

416 Rec'd PCT/PTO 12 JUN 2000

WO 99/29870

PCT/AU98/01023

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## (2) INFORMATION FOR SEQ ID NO:1

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature  
(B) LOCATION 1...1362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1

25 TTCTGTGTC TGGCAAAAGT TATAAAAACA AAAAAAGGCC TTGCACTTAA TCTGAAAGGA 60  
AAACCGCTGC CCGAGATGCT GGCCGAACCG GCCCAAAGTC CTACTTACGC GGTGCTGCC 120  
GACGATTTTG AAGGTGTTAT CCCCAGGTG ACGGCTCGTC CGGGGATAA GGTGCTGCC 180  
GGCTCAGCAC TGATGCACCA CAAGGCATAT CCGGAGATGA AGTTTACAAG TCCGGTTAGC 240  
GGCGAAGTGA TCGCGGTGAA TCGCGGTGCC AAGCGCAAGG TGTTGAGCAT CCAGGTGAAA 300  
CCGACCGGAC TGAACGAATA CGAGTCATTC CCTGTGCGGG ATCGGCTGTC CCTCTCTGCC 360  
30 GAACAGATCA AGGAGCTTTT ACTGTCGAGC GGTATGTGGG GTTTTATTAA GCAACGTCCT 420  
TAGCACATAG TGGCTACACC GGATATAGCT CCACGCGACA TTTATATTAC TGCCAACTTT 480  
ACTGCACCAT TGGCTCCGGA CTTCGATTTT ATCGTTCGAG GAGAAGAAGC CGCCCTGCAG 540  
ACTGCCATCG ATGCCCTGGC CAAACTCAGC ACAGGAAAGG TGATGTGGG CCTGAAGCCG 600  
GGTTCATCTC TGGGCTTGCA CAATGCAGAA ATCGTAGAAG TACACGSAOC TCATCCGGCA 660  
35 GGTAACGTGG GCGTGTGAT CAATCATACG AAGCCAATCA ATCGGGGCGA AACGGTGTGG 720  
ACGCTCAAGG CTACCGACCT GATCGTGATC GGACGTTTCC TGCTTACGGG CAAGCCGAT 780  
TTTACCAGAA TGATTGCCAT GACCGGCTCA GACGCTGAG CTCACGGATA CGTCCGTATT 840  
ATGCGGGGTT GCAATGTCTT TGCTTCTTC CCGGCGGAC TCACATAAA GGAATCTCAC 900  
GAGCGTGTGA TCGATGGCAA TGTGCTGACC GGTAGAAGC TCTGCGAGAA GGASCCTTTC 960  
40 CTGTGAGCCC GGTGTGACCA GATCAGGTC ATCCCGAAG GCGACGATGT GGACGAACTC 1020  
TTGCGGGTGG CTGACCCCG TCTCGATCAG TACAGCATGA GCAGAGCTTA TTTCTCTTGG 1080  
TTGACGGGGA AAAACAAAGA GTACGTACTC GATGCCCGGA TCAAGGGTGG CGAACGTGCT 1140  
ATGATCATGA GCAACGAGTA TGACCGGCTT TTCCCGATGG ACATCTATCC GGAGTATTG 1200  
CTCAAGGCTA TTATAGCATT CGACATCGAC AAGATGGAGG ACTTAGGCAT ATATGAAGTG 1260  
45 GCTCCGGAGG ACTTTGCCAC TTGCGAATTT GTGGATACAT CCAAGATCGA GCTGCAGCGT 1320  
ATCGTTCCCG AGGGCTTGGA TATGCTCTAT AAGGAATGA AT 1362

## (2) INFORMATION FOR SEQ ID NO:2

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature  
(B) LOCATION 1...603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

75 GAACAAAGCA AGTGTTACAT GGATAAAGTG AGCTATGCTC TGGGATTGAG CATCGGTAAT 60  
AATTTCAGAT CTTCGGGCAT CGACAGCGTC GTTATGATG ATTTATGCA AGGTCTGTCT 120  
GATGTACTGG AAGAAAAGC CCCTCAGCTC TCGTATGAG AGGCCAAGCG CGAAATAGAG 180  
GGGTATTTC TGGATTGCA GCAGAAGGCT GTCAACTGA ACAAGAGGC CGGAGAAGAA 240

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5 TTCTCAAGA TAAATGCACA CAAGGAAGGT GTGACGACCT TACCGAGGG CTTGCAATAC 300  
 GAAGTCATTA AGATGGGAGA GGGCCCGAAA CCCACCCTTT CGGACACGGT AACCTGTCAT 360  
 TATCAGGGTA CGCTCATCAA CGGTATCGTT TTGATAGCT CTATGGACAG GGGAGAACCG 420  
 GCCAGTTTCC CTCTAAGAGG AGTTATAGCC GGCTGGACGG AGATTCTTCA ATTAATGCCCT 480  
 GTAGGATCCA AGTGGAAAGT AACTATACCG AGCGATCTGG CGTATGGAGA TCGTGGTGCC 540  
 GCGGAACATA TCAAACCGGG TAGTACGCTC ATTTTATAA TCGAATTAT GAGTATCAAC 600  
 AAA 603

10 (2) INFORMATION FOR SEQ ID NO:3

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 837 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...837

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3

35 CAAAAAACA AACGAAGAT GAAAAAAGCA TTAATTATG GTGCTGCTCT TTGGGAGCA 60  
 GTGCTGCTCT CAAGTGCTCA GTCTTTGAGC ACAATCAAAG TACAGAACA TTCAGTACAG 120  
 CAACCTCGTG AGGAAGCCAC TATTCAGGTT TGTGGAGAAT TGGCAGAGCA AGTTGACTGC 180  
 ATTGGGACAG GTAATTCTGC AATCATAGCC GCTGCAGCGA AATTGAAAG CGATGATCTC 240  
 GAAAGCTATG TTGGCTGGGA GATCATGAGT GTTGATTTCT TCCTGGATA TAAAGCGTGC 300  
 AAGTACACAT CTGCAGTCTG GGCTGATGAT ATGACCATTT TGGCCAATC AGAAGATAGT 360  
 GATCCCGAAA TGCAGACTAT CAACAATCTT GCTCTCAAGA CTAGTGTCAG GATTGAAGCC 420  
 GGCAAGAATT ACATAGTTGG TTATATTGCT AATACCGCAG GTGGACATCC TATCGGATGT 480  
 GATCAGGGCC CTGCGGTGGA TGGTTATGGA GATTGTTTT CTATATCAGA AGATGGTGGT 540  
 GCTACTTTCC CTCGGTTGGA ATCTCTTCAT CAAGCAGTTC CTACCTTAA TTACAACATC 600  
 TATGTCGTTG TTCATTTGAA GAAGGGTGAA GGTGTTGAGG CTGTTCTTAC CAACGACAAG 660  
 GCTAATGCTT ATGTTTCAGAA TGGCGTTATC TATGTAGCCG GAGCTAATGG TCGTCAGGTA 720  
 TCTCTGTTCC ACATGAACGG TAAGGTTGTT TATACCGCGG TTAGCGAAAC GATTGCAGCT 780  
 CCTCAGAAGG GCATGTATAT CCTCCGTGTA GGTGCTAAGA GCATCAAGCT GGCTATC 837

50 (2) INFORMATION FOR SEQ ID NO:4

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 471 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...471

70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4

75 CGTGATTCC TGCCGGAGAA AGCTCTCTAT ATCGGCTGJC GCGTGGAGAC GCAAGAGGGG 60  
 CATGCCGTAG GTTTCGGAAT GGATGACGGC CTGCGGATGA AAGGCAAGGG CGATCTGGTC 120  
 GGGAGCTATC TTCCCGGTGC TGCTCCGATG CCTTTGTCC CGCTTCTGA TATCCGGCT 180  
 CGTTCGATGG ATGCCAATTT TTATATCTAT TCTCGTATT CACTGGGTTT GGGCAGCGAC 240



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5 GATGTTCTCC AGCATAGGAT GAAAGTGTAT CCCAACCCCTG CCACGACGGA GCTGCATGTG 300  
 GAAGCCCTGT CCGCATGGGT GGGCGAGCAG GCTGCGGTAT ATGATATGCG TGGTCGTGCG 360  
 GTATCGGCTC GGACGGTGA TAGCGAGAAG CTGTGCATCG ACATTGCCTC ACTGCCCGTG 420  
 GGGCTCTATA TGCTGCGCAT CGGCAGCTAC TCGGCCAAGT TCGAGAAGAG A 471

## (2) INFORMATION FOR SEQ ID NO:5

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1686 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1686

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

30 ACAAGAAATG TTTCATCAT AAAAATGCCA AGAATTATGA AATTA AAAAT TGCACCTCAGA 60  
 CTGCTGCTGG CGACTTTTGC CATAGTTTGA TTTAGCCCTC TGGCCAAGGC CCAGATGGAT 120  
 ATTGGTGGAG ACGATGTATT GATCGAGACG ATGTCCACCC TATCAGGATA TTCAGAGGAT 180  
 TTTTATTACA AGATGGCTGT GGCAGACAAT GGATGGATCT ATGTGATGT' GGATTTCTCT 240  
 CGTATTATT TTGATGATGT CAGGCTGTAT CGTTCCAAAG ACGGTGGTGC TACTTACCAA 300  
 AAGTTAGGGT CTTTGGGGTC TTTGGTGCTT TATGACTTCG ATGTCTCGCA TTGCGATTTT 360  
 ATTGTAACGG GAAAGGATGA AGATGATATC AATGTTTGA CAGTCATGAC AGCATTTCGAA 420  
 TATGTAGGTG GTACTATTGG CAATGGCGTT TTGCTGATGC ATCGCCATGA TGCAGATATC 480  
 AATAATACAG AGTGTGTGTA CAAGAAGGAT TTCCCTAATA ATAGACTGAT GGGTGTAGCC 540  
 ATCGCCTCCA ACTACCGTGC GCCCTCTCCT TACGGTTTGG GGGGCGATCC TTTTGTCTC 600  
 GCTGTCCGCG TTAGTGGCTC CGGAAGCGAT CACAGCTTCT TGGACTATAT TTTTTCGTTA 660  
 GATGGTGGAG TACACTTTGA GCAAAAGCGT ATTTACACAA GACCCCAAAA ACTGACTATC 720  
 AATAGAGTAG ACCTTTCATT AGGCAGTACA TCTCCTTCTC TTGGATTAA TACTTGGCCA 780  
 CTAAATGGAG TCGTATTGTA AATGAATAAG AACCTTGATG GCTTCGACAT TGGTTTCATT 840  
 TCCAACITTG TGGACTATGA TCCCGCTAT GCGTGGTCTG AACCGATAAT AATAGAAGAA 900  
 45 TTGGATGACA ATTCCGATAA TACCGTGGGT GGAGCACTAA GTATAGAGAT CCAAATGATG 960  
 TACCCGGGCC ATTACGTATA TCCGAAGCAA TCTTTCAATT ATTCTCCCGG ACATACACCG 1020  
 ACAAGAAAG ATCTGGTCTT TAAACACTGT ATAGGTATTC CGGCTTTGGC ATACGATAAG 1080  
 GAAGGCGATC GTTATCTGAC TACTTTTCAA GATCACAATC TAATGAGATA CAGATGGATC 1140  
 50 AAATACGATG ACATTAATCT TTTTATGGT TGGAGTTGCC CATATGTATA TGCAAAAGAA 1200  
 GCTAAAGATA AAAAGAGGCG CCGTCCGCAA GTAGCACTCA ATCCTACCAA TGGAAAGGCT 1260  
 TGTTGGGTAT GGCATACTCG CAAGAGCCCA TATGATGAAA CCAAACCA CA TCCACTCCT 1320  
 GTAATTATTA AACATTTCCT ATGGTCCGAT ACGGAGTGGG TACATGCTCT GGAGGTGGGG 1380  
 GACGATTGCG AGAAGGAGGG TAGCATGAAG CTCTACCCCA ATCCTGCCAA AGAATATGTT 1440  
 55 CTGATCAACC TACCCAAAGA AGGGGGGCAC GAGGCACTCG TATACGACAT GCAGGGCCGA 1500  
 ATCGTGGAGA AAGTTTCATT TTCAGGGAAA GAATATAAGC TGAATGTGCA GTATCTGTCC 1560  
 AAAGGTACGT ACATGCTGAA AGTTGTAGCG GATACGGAGT ATTTCTGTGA AAAAATCATT 1620  
 GTAGAG 1686

## (2) INFORMATION FOR SEQ ID NO:6

- 65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1173 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 70 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- 75 (vi) ORIGINAL SOURCE:

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(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

10 CAAATGAAC GATTACTCCC CTTTCTCCTT TTAGCAGGAC TCGTAGCCGT AGGAAACGTG 60  
 TCTGCTCAGT CACCCCGAAT CCCTCAAGTG GATGTACACA CTCGCATCGC AAGAAATGCC 120  
 CGTTATCGAC TGGACAAGAT CAGTGTCCCG GATTCTCGTC AGATATTGGA TTACTTTCTAT 180  
 AAAGAAGAAA CGATACCCAC TAAAATACAA ACGACCACAG GAGGTGCAAT TACAAGCATC 240  
 GATTCCGTTT TCTATGAAGA CGACAGGTG GTTCAGGTGC GCTATTTTGA CAATAACCTT 300  
 GAATTAAAC AAGCGGAGAA GTATGTATAC GACGGTCTA AGCTGGTCCT TCGAGAAATT 360  
 15 CGCAAGTCGC CGACAGACGA AACGCCAATA AAGAAAGTTA GCTATCACTA TCTCTGTGGC 420  
 AGCGATATGC CTTTTGACAT TACGACAGAG ATGAGCGATG GCTATTTTGA AAGCCATACG 480  
 CTTAACIATC TGAATGGAAA GATTGCCCGA ATAGATATCA TGAATCAACA GAACCCATCG 540  
 GCCGAATTGA TCGAAACGGG TAGAATGGTA TATGAGTTTG ATGCCAATAA TGATGCTGTA 600  
 CTGCTTCGTG ACAGTGTAT TCTTCTCCTT CAAAACAAGT GGGTAGAAAT GTTTACTCAC 660  
 20 CGTTATACAT ACGACAATAA GCATTAATGT ATTCTGTTGG AACAGACGA ATTCCGCACC 720  
 CTCACCTTG CCAACAACCT CGAATACGAC ACCACTATCC CTCTGTCGTC TGTATTGTTT 780  
 CCCACGCAATG AGGAGTTCTT CCGTCTCTT CTTCCTCAAT TTATGAAGCA TATGCGTACG 840  
 AAGCAACGCT ATTTCAATTA CTCGGGAGAA GCGTTGTCTG AGGTATGCGA TTACAACATC 900  
 TTCTATACCG ATATGCAGGG TAATGCACTG ACCGATGTTG CCGTGAACGA ATCGATCAAG 960  
 25 ATTTATCCCT GTCCCTGCCAC GGATTTTCTG CGTATAGAAC GTTCGCAACT GCTTCGCTT 1020  
 TCGCTATTG ACATGAACGG GAACTCATC AGAGCTACCG AATTGACAGG CGATTTGGCC 1080  
 ATTATCGGAG TTGCATCTCT TCCGAGAGGC ACTTACATCG CAGAAATAAC TGCTGCAAC 1140  
 AGCAAAACCA TACGTGCAAA AGTATCGCTC AGA 1173

(2) INFORMATION FOR SEQ ID NO:7

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1284 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7

55 AAGAGGAATC CTTACCTTT GACGGCATCA AATCGAAAGA TTTTATAAAA AATGAGACAG 60  
 CATTATCTC TATTTCTTTT TATCTTGTTC CTGCTTCTTG CTTTCTCTTA TGTCCGTTGC 120  
 AGAACAGTCC GACAAACACC TAAGCAGTCC GAACGGTACG TCGTAGTCCT GTCTTTGGAC 180  
 GGCTTCGGAC CGGACTATAC CGATCGGGCA CGTACACCGG CGTTGGATCG GATGGCACAG 240  
 GAGGGATTGA GCGGGTCGCT CCAACCATGC TTCCCTCTCG TTACATTTC CAATCATTAC 300  
 60 AGCATGGCTA CGGGGCTTTA CCCCGATCAT CACGGTATCG TAGCCAAATGA GTTTGTGGAT 360  
 TCGCTACTGG GCATCTTTG TATATCCGAC CGAAAAGCCG TGGAGACCCC CGGATTTTGG 420  
 GCGGGCGAGC CGGTITGGAA TACGGCCGCA CGCCAAGGCA TCCGTACCGG TGTCTACTTT 480  
 TGGGTAGGAT CCGAAACGGC TGTGAACGGA AATCGGCCGT GCGGTGGGAA AAATTTCTCC 540  
 TCCACCGTTC CGTTTCGTGA CCGTGCCGAC TCCGTATCG CGTGGCTCGG ACTGCCCGAA 600  
 AAGGAGCGAC CGCGTTGCT CATGTGGTAC ATCGAGGAGC CGGATATGAT CGGACACAGC 660  
 65 CAAACGCCCG AAAGCCCGCT GACACTGGCA ATGGTAGAGC GATTGGACAG TGTGCTCGGC 720  
 TATTTCCGCA AGCGGTTGGA CTCTCTGCCC ATAGCCGCAC AGACCGACTT CATCATAGTA 780  
 TCCGATCAGC GTATGGCCAC GTACGAAAAT GAGAAATGTG TCAATCTGTC GCATTATCTG 840  
 CCTGCGGACA GTTTCTCTTA CATGGCCACC GGGGCCCTTA CCCACTTGTA CCGGAAGCCC 900  
 TCCTATACCG AGCGAGCTTA TGAGATCTTG CCGGCCATTC CACATATATC GGTTTACCGC 960  
 70 AAGGAGGAGG TGCCCAAGCG TTTCGCTGT GGCACCAATC CTCGTTTGGG CGAACTGGTC 1020  
 GTGATTCCCG ACATAGGCTC CACCGTCTT TTGCAATAA ATGAAGACGT TCGTCCGGGA 1080  
 GCGGCACATG GCTATGACAA CCAAGCACCG GAAATGCGGG CTTTACTCCG GGTGTGCGGA 1140  
 CCCGATTTC GTCCGGGCG TAGGGTGGAA AACCTGCCGA ATATCACCAT CTATCCGCTC 1200  
 75 ATATGAGGCG GTTGGGTAT AGAGCCTGCA CCCAACGATG CGGACGAAAC GTTGCTGAAC 1260  
 GGCCTGATCC GAGACAAACG ACCA 1284

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## (2) INFORMATION FOR SEQ ID NO:8

- 5 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 846 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 20 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...846

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8

25 CTTTCCCGTG GAGTTTTC CCTGATGAT GGCCGAAGAG GAAGCATTCG TGCCTCTTCA 60  
 GGGCATAGGG ACAAATTTT TAAGAATACA ATTATCAGAT TTATCACRAT GAAAGTAGGT 120  
 TTGTTTCATCC CCTGTTATGT CAATGCAATG TATCCGGAAG TGGGTATCGC CACGTACAAA 180  
 CTGCTGAAGA GTTTGGACAT AGATGTCGAC TACCCGATGG ATCAGACATG TTGGGGCCAG 240  
 30 CCTATGGCCA ATGCCGATG CGAACAGAAA GCTCAAAAGC TGGCTTTGCG ATTCGAAGAG 300  
 CTGTTTCGAGT CGTATGATGT AGTCGTAGGG CCATCGGCCA GTTGGCTTGC TTTCGTGAAA 360  
 GAAACTATG ATCATATCCT CAGACCGACA GGACATGTCT GCAAGTCGGC AGCCAAGGTT 420  
 CGGGATATAT GCGAGTTCTT GCACGATGAC CTGAAGATCA CCAGCCTCCC CTCCCGATTG 480  
 35 GCCCATAGAG TGAGCCTGCA CAACAGTTGC CACGGTGTGC GCGAAGTCCA TCTGTCCACC 540  
 CCCAGTGAAG TGCACCGACC GTACCAACAAC AAGGTGCGCC GGCTATTGGA GATGGTGCAG 600  
 GGCATAGAGG TATTCGAGCC GAAGCGAATA GACGAATGCT GCGGTTTCGG CGGTATGTAC 660  
 TCGTGGGAGG AGCCGGAGGT ATCCACCTGT ATGGGGCATG ACAAGGTGCT GGATCACATA 720  
 TCCACAGGTG CCGAGTACAT CACAGGGCCG GACAGCTCGT GCCTCATGCA TATGCAGGGA 780  
 40 GTGATAGACA GAGAGAAATT GCCGATCAAG ACAATTCATG CAGTAGAAT TTAGCAGCA 840  
 AACTTA 846

## (2) INFORMATION FOR SEQ ID NO:9

- 45 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 753 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 50 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 55 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 60 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...753

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

65 CCTCTGAAA AACGAATGGA TATTGTAAGT ATGGCCGATA AAGCTCTTGT ACTGGAGATG 60  
 AGAGATGTGA CGCTCTGTCA GGAGGAAAAC GTCAITTTTC AAAATTGAA TCTGACCCTT 120  
 TCCGCCGGAG ACTTCGTCTA TCTGATAGGC TCAGTGGGAT CCGGGAAGAG CACTTTGCTG 180  
 70 AAGGCTTTGT ATGCTGAGGT GCCTATCTCT GCCGGTTATG CCCCGTGAT AGATTATGAT 240  
 CTGGCAAGT TGAACGGAA GCAGTTGUCC TATCTGCGCA GGAATTTGGG CATTTGTGTT 300  
 CAGGATTTCC AGTTGCTGAA CGGACGTACT GTTGGGAGA ATTTGGATT CGTTTTCGGA 360  
 GCTACGGACT GGAAAAACCG AGCCGATCGC GAGCAGCGTA TCGAGGAGT TTTGACCCGT 420  
 GTGGGAATGT CTCGGAAGGC TTATTAAGAGA CCGCAGAAC TGTCCGGAGG GGAGCAACAA 480  
 75 CGTGTGGGTA TAGCCAGAGC TTTGCTGGCG AAGCCTGCGT TGATCCTGGC CGACGAACCC 540  
 ACAGGCAACC TCGATTCGGT GACCGGATTG CAGATCGCTT CTCTGCTCTA CGAAATCAGT 600

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AAGCAGGGCA CTGCAGTACT TATGAGCAGC CACAACAGCA GCCTGCTGTC GCATCTGCCG 660  
 GCACGGACAT TGGCCGTTTC TAAGAATGGC GATGCCCTCT CTTTGGTCGA GCTGAGTGCA 720  
 GATGCTGTTT CAAGAAAAA TACGGAAATA GAT 753

5

(2) INFORMATION FOR SEQ ID NO:10

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 714 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

25

(A) NAME/KEY: misc feature

(B) LOCATION 1...714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10

30 ACCAGGCATT GTCGGGCTTG TCGCTCTTCC TTTCACCTCA TAAAAACAAG TAAACAATG 60  
 ATTGAAATCA GCAACCTCAC CAAGGTTTTC AGAACAGAGG AAATAGAGAC GGTAGCCCTC 120  
 GATGGCGTAT CGCTCAAAGT GGACAAAGGC GAATTTATCG CCATAATGGG GCCTTCGGGA 180  
 TGGCGTAAGT CCACTCTGCT CAATATCCTC GGCCTTCTCG ACAATCCCAC TTCCGGTATC 240  
 TACAAGCTCG ATGGGGCAGA AGTGGGCAAC CTCGGGAAA AAGACAGGAC TGCCGTCCGT 300  
 AAGGGCAATA TCGGCTTCGT ATTCCAGAGC TTCAACCTCA TCGAAGAGAT GACGGTAAGC 360  
 35 GAGAACGTGG AGTTGCGGCT CGTCTATCTG GGTGTGAAGG CCTCCGAGCG GAAAGAGCGA 420  
 GTGGAGGAGG CACTGCGCAA GATGAGCATC AGCCACCGGG CCGGCCACTT CCCCAATCAG 480  
 CTCTCCGGAG GACCAACAGCA GCGCGTGGCT ATCGCCCGTG CCGTGGTGGC CAATCCGAAG 540  
 CTCATCCTCG CCGATGAACC CACGGGTAAC CTCGACTCCA AAAACGGAGC CGATGTCATG 600  
 40 GAACTGCTCA GAGGTCTCAA TCGCGAAGGT GCAACCATCG TCATGGTGAC GCCTCCGAG 660  
 CACGATGCAC GTAGTGCCGG CCGCATCATC AATCTGTTTC ACGGTAAGAT TCGC 714

(2) INFORMATION FOR SEQ ID NO:11

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1812 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

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(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...1812

65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

AGCAGAGAAA CAAATAGCAA ATCTGAAATG AAAGAATTTT TCAAAATGTT TTTGGCCTCG 60  
 ATCCTCGGGG TTATAACGGC AGGAATCATC TTGTTCTGTA TCTTTCTATT TATCTTTTTC 120  
 GGCATCGTAG CCGGTATTGC CTCCAAGGCA ACGGGAGGAA CCATTCGAA GATCGAAGCA 180  
 70 AACTCCATCC TACATATANA CAATCTTCTT TCCCTGAGA TCGTATCGGC CAATCCCTGG 240  
 AGCATGCTCA CAGGCAAGA CGAGTCCGTA TCGCTCTCAC AGGCAGTCGA AGCCATCGGC 300  
 CAAGCCAAAA ATAATCCCAA CATAACCGGT ATCTTCCTCG ATCTGGACAA CCTTCCGTC 360  
 GGTATGGCAT CGGCAGAGGA ATTGCGTCGC GCGTTGCAGG ATTCAAGAT GTCGGGCAAG 420  
 TTCGTGATAT CCTATGCCGA CAGATACACC CAAAGGGTT ACTACCTCTC CAGTATTGCA 480  
 75 GACAAACTCT ACCTCAATCC GAAAGGAATG TTGGGGCTTA TCGGGATTGC GACCCAAACA 540  
 ATGTTCTACA AAGATGCCCT CGACAAATTC GCGGTGAAGA TGGAGATCTT CAAGGTAGGC 600

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5 ACCTACAAGG CAGCCGCTAGA GCCATTCATG CTCAACAGGA TGAGCGATGC CAATCGCGAA 660  
 CAAATCACCA CATACATAAA CGGGCTTTGG GACAAGATCA CATCCGATAT TGCAGAGTCG 720  
 CGCAAGACGG CAATGGATTG CGTGAAAATG TTTGCCGACA AAGGCGAAT GTTCGGTCTT 780  
 GCCGAGAAAG CGGTGGAGAT GAAGCTCGTG GATGAGCTGG CTIACCGTAC CGATGTGGAG 840  
 AAAGAACTCA AAAGATGTC CCAACGCGGA GAGAAAGATG AACTTCGGIT CGTATCGCTT 900  
 TCTCAGGTTC TGGCCAATGG CCCGATGAAC AAAACGAAAAG GCAGTCGGAT CGCCGTTCTC 960  
 TTTGCCGAAG GTGAAATAAC GGAAGAAATA ATAAAGAAAG CGTTCGACAC TGACGGTAGC 1020  
 TCCATCACAC AAGAACTCGC CAAAGAAATC AAGGCAGCAG CCGATGACGA TGATATCAAA 1080  
 GCGGTAGTAC TTCGTCTCAA TTCTCCGGGA GGTAGTGCTT TCACTTCGGA ACAGATATGG 1140  
 10 AAGCAGGTAG CCGATCTCAA GSCCAAAAAG CCTATCGTGG TCTCCATGGG CGACGTAGCA 1200  
 GCCTCGGGCG GATACTACAT AGCCTGCGCA GCCAACAGTA TCGTGCGAGA GCATACGACT 1260  
 CTGACCGGCT CCATCGGCAT ATTCGGCATG TCCCCGAAGT TCGCGGGCGT AGCCAAGAAG 1320  
 ATAGGAGTGA ATATGGACGT CGTACAGACA TCCAAATATG CAGACTTGGG CAACACCTTC 1380  
 GCTCCGATGA CGGTGGAAGA TCGTGCCCTC ATCCAACGCT ACATAGAGCA GSGCTACGAC 1440  
 15 CTCTTCTCA CTCGCGTATC GGAAGGCGCG AACCGCACCA AGGCACAGAT CGACAGCATC 1500  
 GCTCAAGGCC GTGTATGGCT CGGCGACAAA GCTCTTGCAC TCGGTTTGGT GGATGAGCTT 1560  
 GGAGGTTTGG ACACAGCTAT CAAACGGGCC GCGAAGCTGG CTCAGCTCGG TGGCAACTAC 1620  
 AGCATAGAGT ATGSCAAGAC CAAGCGCAAC TTCTTCGAAG AGTTGCTCTC CTCATCAGCA 1680  
 GCGGATATGA AGTCTGCCAT CCTGAGTACC ATTCTCTCCG ATCCGGAAT AGAAGTTCTG 1740  
 20 CGCGAACTCC GCTCCATGCC GCCCGCTCCT TCGGCGATAC AGGCACGTCT CCCCTATTAC 1800  
 TCTATGCCGT AC 1812

## (2) INFORMATION FOR SEQ ID NO:12

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 972 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 35 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (v) ORIGINAL SOURCE:  
 40 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...972  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12

CTAACGTTGT TTTGTTGCAA CTATTTCAAA CAGATGAGAG CAAACATTG GCAGATACTT 66  
 TCCGTTTCGG TTCTCTTTT CTTCGGGACA GCGATCGGAC AGGCTCAGAG TCGAAACCGT 120  
 50 ACATACGAGG CITATGTGAA ACAGTACGCC GACGAAGCTA TCCGACAGAT GAGCCGCTAC 180  
 AATATACCGG CAAGCATCAC CATAGCACAG GCTTTGGTGG AGACAGGAGC CGGAGCCAGT 240  
 AACTGGCCA GCGTACACAA CAATCACTTC GGGATCAAT GCCACAAATC GTGACGGGCG 300  
 AAGCGCACCT ATCGTACCGA CGATGCGCGG AACGAATGCT TCCGACGCTA TTCGGCCGCT 360  
 CGCGAATCGT ATGAAGATCA TTCCCGATTT CTGCTCCAAC CACGCTATCG TCCCTGTGTC 420  
 55 AAATCGACA GAGAAGACTA TCGGGGCTGG GCTACGGGGT TGCAACGCTG TGGCTATGCC 480  
 ACCAATCGGG GCTATGCCAA TCTGCTGATC AAGATGGTGG AGCTGTATGA GCTATATGCT 540  
 TTGGATCGCG AGAAGTACCC CTCATGGTTC CACAAGTCTT ACCCGGGGTC CAACAAAAA 600  
 TCCATCAAA CGACCAAGCA GAAGCAGAGC GGAATCAAGC ACGAAGCTTA CTCAGCTAC 660  
 GGACTGCTCT ACATCATAGC CAAGCAAGGC GATACCTTCG ATTCTTTGGC CGAAGAGTTC 720  
 60 GACATGAGAG CCTCCAACT GGCCAAATAC AACGATGCTC CCGTGGATTT CCCGATCGAA 780  
 AAGGGCGATG TGATCTATCT GGAGAAAAAG CACGATGCTC CCATCTCAA ACACACACAG 840  
 CACGTAGTGC GTGTGGGCGA TTCATGCAC AGTATCTCCC AACGCTATGG CATCCGGATG 900  
 AAGAACCTCT ACAAGCTCAA CGACAAGGAT GGCGAATATA TACCCAAGA GGGCGATATA 960  
 CTGCGCTTGC GC 972

## (2) INFORMATION FOR SEQ ID NO:13

- 70 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1599 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 75 (ii) MOLECULE TYPE: DNA (genomic)

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
10 (B) LOCATION 1...1599

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:13

15	AGGATCCCCG	ACGAGCAGAC	CGGACGTATC	ATGGACGGAC	GTCGATATTC	GGATGGCCTC	60
	CATCAGGCTA	TGCAAGCCAA	AGAGCATGTG	AAAGTAGAGG	CTGCGACACA	GACATTGCA	120
	ACTATCACTT	TGCAGAACTA	TTTCCGCATG	TATCATAAGC	TGGCAGGGAT	GACCGGTACT	180
	GCTGAACCTG	AAGCGGGAGA	GCTTTGGGAC	ATCTACAAC	TGGACGTTGT	AGTTATTCCG	240
	ACAAACAAGC	CTATCGCCCG	TAAGGATATG	AATGATCGTA	TCTATAAGAC	GGCAGGTGAA	300
	AAATATGCAG	CAGTTATCGA	AGAGATTGTA	CGTCTTGTG	AAGAGGGCAG	ACCTGTACTT	360
20	GTCCGCTACT	CTTCGGTGGG	AAATCCGAA	TTGTTGAGCC	GTATGTTACG	CTTGGCTGGC	420
	ATCCAACACA	ATGTACTCAA	TGCCAAATTG	CATCAGAAAG	AGGCCGAGAT	TGTAGCTCAG	480
	GCCGCTCAGA	AAGGAACCTG	TACCATCGCA	ACGAACATGG	CCGCTCGTGG	TACCGACATC	540
	AAGCTCTCTG	CCGAGGTTAA	GAAAGCCGGG	GGTTTGGCTA	TCATTGGTAC	GGAAAGGCAC	600
	GAATCCAGAC	GAGTGGACAG	ACAGCTTCGT	GGTCGTTCCG	GCCGTCAGGG	TGATCCCGGT	660
25	TCGTCCATAT	TCTATGTTTC	CCTTGAAGAT	CATCTGATGC	GCCTCTTTGC	CACAGAAAAG	720
	ATTSCATCAT	TGATLGATCG	TTTAGGTTTC	AAGGAAGGAG	AAGTGCTCGA	AAACAACATG	780
	CTGASTAAGT	CCGTGGAGCG	TGCTCAAAAG	AAGGTGGAGG	AGAACAACCT	CGGTATCCGT	840
	AAACATCTGC	TTGAGTACGA	TGATGTAATG	AATTCGCAGC	GTGAAGTCAT	TTATACCCGT	900
	CGCCGTCATG	CTTTGATGGG	AGAGCGTATC	GGTATGGATG	TACTCAATAC	CATATACGAC	960
30	GTATGTAAGG	CTCTGATTGA	CAATTATGCA	GAAGCCAATG	ATTTGGAAGG	CTTCAAGGAA	1020
	GATCTGATGC	GTGCACTCGC	GATAGAATCT	CCTATCACGC	AAGAAATATT	CAGAGGTAAG	1080
	AAAGCAGAAG	AGCTGACCGA	TATGCTTTTC	GATGAAGCTT	ACAAGTCTTT	CCAACGTAAG	1140
	ATGGATCTGA	TGCGAGAAGT	GGCCACCCCT	GTGGTTCATC	AGGTATTCTG	GACCCAAGCC	1200
	GCCGTGTACG	AGCGCATCTT	AATCCCCATT	ACGGATGGTA	AACGTGTCTA	TACATAGGA	1260
35	TGCAATTTCG	GTGAAGCGGA	TGAAACTCAA	GGGAAAAGCA	TCATCAAAGA	ATTTGAGAAA	1320
	GCTATCGTAC	TGCATCATAT	CGATGAGTCT	TGGAAAGAAC	ATCTGCGTGA	GATGGACGAG	1380
	CTTCGTAATT	CGGTCAGAA	TGCCAGCTAC	GAAAACAAAG	ATCCACTACT	TATCTATAAA	1440
	CTCGAATCTT	ACGAACGTGT	CCGCAAGATG	GTAGAAGCCA	TGAACCGTAA	GACCGTAGCG	1500
	ATCCTAATGC	GTGCTCGGAT	ACCGGTACCG	GAGGCTCCTT	CCCAAGAAGA	GCTGGAACAC	1560
40	AGGCGGCAAA	TAGAAATCCG	ACATGCAACC	CAACAACGT			1599

(2) INFORMATION FOR SEQ ID NO:14

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
50 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

55 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
60 (B) LOCATION 1...2160

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:14

65	AAATCTTGCC	GTGTTATTGG	CCAGACGAGG	CGATACGGAT	GCTGCCCTGT	CGGACTACGA	60
	CCGTGCCATC	AAAGCCTATC	CGGAGTTTGC	CGATGCCTAT	TTCAATCGCG	GCCTGCTGTT	120
	GCTTTCCGCG	GGAAAGGCCA	AAGAAGGCAT	CGCCGATCTG	AGTCGGGCAG	GCGAATACGG	180
	GCTCTACAAG	GCGTACAACA	TCATCAAAAG	AATGAGCACG	AAGTCATGAT	CTCCGTCAT	240
70	AACTGCAGTG	TGATTTCCGG	CACCCGTLTG	CTCTTCGATC	AGGTATCATT	CGTCATCAAC	300
	AGCGCGGACC	GTATCGCTCT	TGTAGGGAAG	AACGGTCCCG	GCAAGAGTAC	GCTGCTCAAG	360
	CTGATTGCCG	GCATGGAAGA	ACCGACATCC	GGACACATAG	CACGCCCAAA	GGGGATCCGC	420
	ATAGGCTATC	TGCCCGAGGT	GATGCGTTTG	CAGGACGGAC	ACACGGTTTA	CGAAGAGGTC	480
	GAGCAGGCTT	TCAACGATAT	TCGCCAAATA	GAGGAAGAGA	TACGGCGTCT	GTCCGATGAA	540
75	ATGGCCGGAC	GTACGGACTA	CGAATCGGAT	GACTATATCC	GACTGATAGA	GCATTATACG	600

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5 AATATGAGCG AGACCCCTCTC TCTCATGCAG CAGGGCAACT ATCATGCTGC GATCGAACAG 660  
 ACATTGATCG GTCTGGGCTT CGGCCGAGAG GACTTCCACC GCCCCACAGC CGATTTCAGC 720  
 GGAGGATGCG GTATGCGGAT AGAGCTGGCC AAATTCTGTC TCCAACGCC CGAAGTTTIG 780  
 CTGCTCGAGC AGCCGACCAA TCAGCTCGAC ATCGAATCCA TCGGCTGGCT GGAGCAGTTC 840  
 ATCGCCACCA ATGCAGGAGC CGTTATCCTG GTGTCGCAGC ACAGGGCATT CATCGACAAT 900  
 ACCACGACAC GCACATATCGA AATAGAACTG GGACATATA' ACGACTACAA GACCAACTAC 960  
 AGCCACTATG TGGAGCTGCG CGAAGAGCGG CTGCGACAGC AGATGCGTGC CTACGAGAAT 1020  
 CAGCAGAAGA TGATCCGCGA TACGGAGGAC TTCATCGAAC GATTGAGATA CAAGGCCACG 1080  
 AAGTCCGTAC AGGTACAGAG CCGGATCAAA CAGTTGGAGA AAGTAGAGCG CGTGGAGATA 1140  
 10 GACGAGCGGG ATCGTTGCGC ATTCACTTC CGCTTTATCC CGGCACAGCC TTCCGGCAGT 1200  
 TATCCGCTAA TAGTGGATGA TTTGGCCAAG GCTTATGGCG ATCACCAGGT GTTTCCGGA 1260  
 GCTACATACA CCATCGAAAG AGGCGAAAAG GTGGCTTTCG TAGGCAAAA CGGTGCCGGC 1320  
 AAAAGTACCA TGGTCAAGTG TATCATGGGA GAGCTGACAG ACTACACCGG CNAAGCTCGAA 1380  
 CTGGGGCACA ACGTGCAGCT GGGCTACTTT GCCCAAAACG AAGCCCAAGA GCTAAGAGGG 1440  
 15 GATCTCAGCG TATTCGACAC GATAGACCGT GAGGCCGTGG GCGACATCCG TCTGC3CCTG 1500  
 AACGATTTGC TCGGGGCTTT TCTCTTCGGG GCGAAGCAT CGGAAAAGAA AGTAAGTGTC 1560  
 TCGAGTGGAG GAGAACSAGC ACGATTGUCT ATTATCAGGC TTTTGCTACA GCCGGCTAAC 1620  
 TTCTTATTC TCGATGAGCC GACCAATCAC CTCGATATGC GCTCGAAGGA TGTAAGTAAA 1680  
 GAGGGCATCA AGAACTTCGA TGGGACTGTC ATCGTAGTAT CTCACGACCG TGAGTTCCTC 1740  
 20 GATGGGCTTG TCAGCAAGGT GTATGAATT GCAGATGGAC AGGTGAACGA ACACCTCGGA 1800  
 GGTATATACG ACTATCTCCG GACCGCGGT ATGCAGACCG TGACAGAGCT GGAGCGAACC 1860  
 ACTACGATCG AAACAAAAC CACACGGGAG GCTATACCTG AAACGGGAGC CAAAGCGGAC 1920  
 TACCGTCGGC AAAAGGAGGT AGCCAAACAG CTGCGCACGT TGGAGCGAAC CGTAGCAACC 1980  
 25 TGCGAGSAGC GGATCGGAAA ATTGAGAGTC GAATTACAG CAATAGAGAT GCTACTGCAA 2040  
 GATCCGAAAC ATCGGACTGA CGCGAATCTG TTCGAGCGAT ACGCGGCGAT GAAACAAGAA 2100  
 CTCGAAAAGG CCATGGAGGA CTGGGAACAG GCTTCCGAAG CTTTATCCGA AGCCCAAGGA 2160

30 (2) INFORMATION FOR SEQ ID NO:15  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1158 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 40 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 45 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1158

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15  
 TATTTGAAGC TATTAATACT ACAAAATAGCC TTGATGAATT TCTTAAAAAA AGAACCGTTT 60  
 AAAATATTCT CTATGATTTA TCTGCTGTTA GATACAATAA CAAACCGTGC CGGTACAGAA 120  
 55 CGCGCCGTGA TCAACTTGGC TAACAACCTG CATGCCAATG GTCATCGCGT ATCATTAGTC 180  
 AGCGTTTGTA CAAAAGAAGG AGAGCCTTCC TTCCAAGTAG AAAAAGGAAT AGAAGTACAC 240  
 CATCTCGGAA TTAGGCTTTA TGGCAATGCA TTAGCCCGCA AAACAGTATA TTTCVAGGCT 300  
 TATCGAAGGA TAAAAGCCCT ATACAAGAAG CGTGAACCGG TTTTATTGAT AGGGACTAAT 360  
 ATTTTATCA ATACATTTT GTCTCAGATC AGTAACAGAG GCAGAATATT TACGATCGGA 420  
 60 TGCGAACATA TCTCTTATGA TATTGCCCGC CCTATTACAA AACGCATAAG GGGGTTTCTG 480  
 TATTGAGGUC TTGATGCCGT TGTAGCACTG ACAAAGAGAG ATCAGCAATC GTTCGAGGCA 540  
 ATCTTACGTG GACGCTCTAA AGCATATGTC ATACCCATC AAGTTTCATT TACTACAGTC 600  
 CAAAGAGATG CTACTACTCA CAAACAAATG TTGGCGATTG GCAGGCTTAC CTACCAGAAG 660  
 GGTTTTGAAT TCATGATAGA AGATGCATCA CGAGTGCTGC GAGAAAGGCC TGATTGGAAG 720  
 65 AATATGGAGT CGCAATAGA AATACATCCA TCTACACCGG AAATTTCGCA ATACTACGAA 780  
 TCATCTGCTA TTTATCTAAT GACGTCCCGT TTCGAAGGAC TAACATGGT ACTTCTCGAA 840  
 GCAGAAGCAT ATGCACTACC TATAATCTCA TACGATTGTC CGACCGGCC GAGGGAACCTG 900  
 ATCGAAAACG GTCGCAATGG TTTCTTGTG CCAATGGAAG CACATGAAGA CTTCGCGGAT 960  
 70 AAGTTACGCT TATTGATGGA TGATGAAACT CTTCGTAAGA AAATGGGACA AGAATCAGAG 1020  
 TTGATGGTCA AATCTACTC TCCGGCAAAAT ATCTATGAAT GTTGAAGAA ACTATTCGTC 1080  
 GAAATCGGCT ACATGAAT 1140  
 1158

75 (2) INFORMATION FOR SEQ ID NO:16

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1965 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

ACAACGAAAG	AAAACGAGAC	AACACAAAA	AACGAATAA	GAATTATGGG	AAAAATCATT	60
GGAAATTGACT	TAGGCACAAC	GAACCTTGT	GTCTCTGTAT	TGGAAGGTAA	CGAACCTATC	120
GTTATTACAA	ACAGTGAGGG	CAAGCGCAGA	ACGCCCTCGG	TAGTGGCTTT	TGTGGATGGT	180
GGCGAGCGTA	AGGTGGGCGA	TCCGGCCAAG	CGTCAGGCCA	TCACCAATCC	GACCAAGACG	240
ATATACTCTA	TCAAACGCTT	CATGGGCGAA	ACTTACGATC	AGGTTTCCAG	AGAAGTGGAG	300
AGAGTGCCAT	TCAAGGTAGT	ACGTGGGGAC	AATAATACTC	CGCGCGTAGA	TATAGACGGT	360
CGTCTCTATA	CGCCGCAGGA	AATTTCCGCC	ATGATCCCTC	AGAAGATGAA	GAAGACGGCC	420
GAAGACTACC	TCCGTCAGGA	AGTAACGGAG	GCCGTGATCA	CTGTGCCCGC	ATACTTCAAC	480
GACGCTCAAC	GTACGGCAAC	GAAAGAAGCA	GGAGAGATCG	CCGGCCGTAA	AGTTCGCCGT	540
ATTGTGAACG	AGCCTACGGC	AGCTTCTCTG	GCCTACGGTC	TGGACAAGTC	CAATAAGGAT	600
ATGAAGATCG	CTGTCTTCGA	CTTGGGTGGC	GGTACCTTCG	ATATCTCTAT	CTTGGAAATTG	660
GGCGACGGCG	TTTTCGAAGT	GAAATCGACC	AACGGTGATA	CGCACCTCGG	AGGAGACGAC	720
TTCCGACCACG	TGATCATTGA	CTGGCTGGCA	GAAGAGTTCA	AGTCTCAGGA	AGGTGTGGAT	780
CTTCGCCCAGG	ATCCTATGGC	TATGCAGCGT	CTGAAAGAAG	CTGCCGAAAA	AGCCAAGATA	840
GAGCTCTCCA	GCACTTCATC	TACGGAGATC	AACCTCCCTC	ATATCATGCC	GGTGAACGGC	900
ATCCCCAAGC	ACTTGGTGAT	GACGCTTACA	AGGGCTAAGT	TCGAGCAGTT	GGCCGATCGT	960
CTGATTCAGG	CATGTGTGGC	ACCCTGCGAA	ACGGCCTTGA	AAGATGCCGG	TATGTCACGT	1020
GCCGATATCG	ATGAAGTGAT	TCTCGTAGGT	GGTCCACAC	GTATTCCTGC	TATTACAGGAG	1080
ATTGTGGAGA	AGATCTTCGG	TAAGGCTCCG	TCCAAGGGTG	TGAATCCCGA	CGAAGTGGTA	1140
GCTGTGGGTG	CGGCTATTCA	AGGCGGTGTT	CTGACCGGTG	AGGTAAGGGA	TGTCTTGCTG	1200
TTGGAGGTTA	CCCCCTTGTC	GCTCGGTATC	GAGACTATGG	GAGGCGTGAT	GACTCGCTTG	1260
ATCGATGCCA	ATACCACTAT	CCCGACGAAG	AAGAGCGAAA	TCTTTACCAC	AGCAGTGGAC	1320
AATCAACCTT	CGGTAGAGAT	TCATGTACTT	CAGGGTGAGC	GTTCCTTTGGC	TAAGGACAAT	1380
AAGAGCATCG	GCCGTTTCAA	CTTGGACGGT	ATTGCTCCGG	CGCCCCGTCA	GACACCCGAG	1440
ATCGAAGTAA	CGTTTGACAT	CGATGCCAAC	GGTATCCTGA	ATGTAACGGC	TCAATGACAAA	1500
GCTACCGGCA	AGAAGCAGAA	TATCCGCATC	GAAGCCTCCA	GCGGTTTGTC	CGATGATGAG	1560
ATCAAGCGCA	TGAAGGAAGA	GGCGCAGGCC	AATGCCGAAG	CAGATAAGAA	AGAGAAAGAA	1620
CGTATCGACA	AGATCAATCA	GGCCGACAGC	ATGATCTTCC	AGACGGAAAA	GCAGTTGAAG	1680
GAGTTGGGAG	ACAAATTCCC	GGCCGACAAG	AAGGCTCCGA	TGGATACCGC	TCTCGACAAA	1740
CTGAAAGAG	CACACAAAGC	ACAGGATGTA	GCTGCTATCG	ATACAGCCAT	GGCCGAACCTG	1800
CAACCCGCTC	TTTCCGCAGC	GGGCGAAGAG	CTTTACAAGA	ATGCCGGAGC	AGCCCAAGGT	1860
GGCGCACAA	CCGGTCCGGA	CTTCGGCGGT	GCTCAAGGTC	CCTCTGCCGG	TGATCAGCCC	1920
TCTGACGACA	AGAACGTCAC	AGACGTAGAC	TTCGAGGAAG	TGAAG		1965

(2) INFORMATION FOR SEQ ID NO:17

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1401 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature



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(B) LOCATION 1...1401

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:17

```
5  AAGTGGGCAC GTACAACTAC TTTAAGGATA TCGAACGCAA CAATCTATAA AACTATGCGC 60
   TACGACTTAG CTATCATCGG TGGAGGGCCG GCCGGTTATA CGGCTGCCGA ACGTGCTGCC 120
   AAAGGTGGCC TGAACCCCT CCTAATTGAG AAGAATGCTC TCGGTGGTGT ATGCTCTAAC 180
   GAAGGATGTA TACCGACCAA GACGCTACTC TACTCGGCCA AAGTGCTACA TCAAAATGCT 240
   ACGGCATCTA AATATGCAGT AAGTGGAACG GCGATGGAC TTGACCTCGG CAAGGTGATT 300
10  GCCGAGAAAG GTAAAATCAT TCGCAAGCTG ACTGCAGGCA TCCGTTACCG CTGACAGAG 360
   GCCGGAGTAG AGATGGTGAC GGCAGAACTG ACCGTAACTG GATGCGATGC AGACGGCATC 420
   ATCGGCATTA CTGCGGGCGA AGCAGAGTAC AAAGCTGCGA ACCTGCTACT ATGTACCGGT 480
   TCGGAGACGT TTATTCCACC CATCCCCGGA GTGGAGCAGA CAGAGTATTG GACAAACCGT 540
   GAAGCTCTAC AGAACAAAGA GATTCCGACC TCTCTCGTCA TCATCGGTGG TGGAGTGATC 600
15  GGARTGGAGT TCGCTTCTTT CTTCACCGGT ATCGGTACGC AAGTGACAGT GGTGGAGATG 660
   CTGCCGGAAA TACTCAACGG TATCGATCCC GAACATGCAG CTATGCTACG CGCTCACTAT 720
   GAAAAGAGAG GAATCAAATT CTACCTCGGG CACAAAGTAA CATCGGTTCC CAACGGAGCT 780
   GTTACGGTAG AATACGAAGG AGAAAGCAAA GAGATCGAAG GAGAAGCTAT CCTGATGAGT 840
   GTGGGACGTC GCCCCGTGCT GCAAGGATTC GAGTCGCTCG GATTGGTGCT TGCCGGSCAA 900
20  GGTGTAAAGA CTAATGAGAG GATGCAAACT TCCCTGCCCA ATGTCATATG TGCAGGTGAT 960
   ATTACAGGCT TCTCGCTTTT GGCACATACC GCTGTACGGG AAGCAGAGGT AGCAGTAGAT 1020
   CAGATTTTGG GCAAAACAGA CGAAACGATG AGCTACCGTG CCGTACCAGG TGTGGTGATC 1080
   ACCAATCCCG AGGTCCCGGG TGTGGGAGAG ACGGAAGAAT CGCTTCGCAA AGCAGGACGT 1140
   GCCTACACTG TTCGTGCGCT TCCTATGGCC TTCTCCGGTC GATTTGTAGC AGAAAACGAA 1200
25  CAAAGCAATG GAGAGTGCAA ACTACTACTT GATGAAGAGA ACCGCTTGAT CGGAGCACAC 1260
   CTCATTGGCA ATCCGCGCGG CGAACTCATC GTAACCGCTG CCAATGGCCAT CGAGACCGGC 1320
   ATGACGGATC GACAAATCGA ACGAATCATA TTCCCTCATC CGACTGTAGG CGAAATCCTA 1380
   AAAGAAACTC TCGCCGGAGG T 1401
```

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(2) INFORMATION FOR SEQ ID NO:18

```
35  (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 2835 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: double
     (D) TOPOLOGY: circular

40  (ii) MOLECULE TYPE: DNA (genomic)

     (iii) HYPOTHETICAL: NO

     (iv) ANTI-SENSE: NO

45  (vi) ORIGINAL SOURCE:
     (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

     (ix) FEATURE:
50  (A) NAME/KEY: misc feature
     (B) LOCATION 1...2835
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(x1) SEQUENCE DESCRIPTION: SEQ ID NO:18

```
55  CCTAAGATAC TTATGGAATT GAAAAGATTT TTATCACTTG GTCTTCIGCT TGTGGGATTC 60
   ATTCGGATGA AGCTTTCTGC CCACAGGCT CAGCCACTCC CTACAGATCC GGCTGTTCGT 120
   GTCCGTAAGT TGGACAACGG ATTGACTTAT TTCATCGTTC ACACAGAGAA CCCGAAAGAT 180
   CGTCCGGATT TCTTTATCGC ACAAAAGGTA GGTTCATTC TTGAGAGAGA TAGCCAGTCC 240
   GGTTCGGCTC ACTTCTTGGA ACACATGGCT TTCAACGGTA CGAAGAACTT CCCCAGTAAG 300
   AACTTGATCA ACTATCTCGA AACGATCGGT GTACGTTTCG GTCAGAACTT GAACGCTTCT 360
60  ACOGGATTTC ACAAGACGGA ATATACGATA ATGGATGTGC CGACTACACG TCAGGGAATC 420
   ATCGACTCCT GCTTGCTTAT CCTGCATGAT TGGAGTAACA ATATTACCTT CGACGGGCAT 480
   GAGATCGACG AGGAGCGCGG TGTGATCCAG GAAGAGTGGC GTGCTCGTCG CGATGCCAAC 540
   CTTGATATGT TCGAGGCTAT ACTTGCCAA GCTATGCCGG GTAATAAATA TGCAGAACGC 600
   ATGCCCATCG GTCTGATGGA CGTGTGCTC AACTTCAAGC ATGATGAGCT GCGCAACTAT 660
65  TATAAGAAAT GGTATCGTCC CGACTGCAA GGTCTGGTGA TCGTGGGAGA TATCGATGTG 720
   GACTATGTGG AGAACAGAT CAAGAAGCTC TTCAAGGACG TTCCTGCTCC CGTGAATCCA 780
   GCAGAGCGTA TCTATACGCC GGTAGAGGAC AACGATGAGC CTATCGTAGC CATTGCTACU 840
   GATGCTGAGG CTACTACCA GCACTCTCC ATCAGCTTCA AGAGCGACCC CACTCCTCAA 900
   GAAGTGGAGG GATCGATATT CGGACTTGTG GAAGACTATA TGAACAGGT GATCACTACA 960
70  GCGGTGAATG AGCGTCTGTC CGAGATTACT CACAAGCCTA ACGTCTCTTT CCTCAGTSCA 1020
   GGAGCTTTCT TCTCTAACT CATGTACATC ACCCAGACTA AGGACGCATT CAATTTTGT 1080
   GCCAGGTTTC GTGAGGGTGA AGCGGAGAAA GCGATGAACG CATTGGTGGC AGAGATAGAA 1140
   AGCCTCGCTG AGTTCCGGTAT CACCAAGGCG GAATACGATC GTGCACGCAC GAATGTGCTC 1200
   AAGCGATACG AGAATCAATA CAACGAAGA GACAAGCGTA AGAACATGC TTATGCCAAT 1260
75  GAATACTCCA CCACTCTCAC CGATGGCGGC TATATCCCGG GTATTGAGGT GGAATATCAG 1320
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5 ACGGTGAATG CTTTGTCTCC TCAGGTTCCCT CTGGAAGCAT TCAATCAGGC TATTGCCCAA 1380  
 ATGATCGATC CGGTGAAGAA TGCTGTCTGT ACCCTCACCG GTCCCTTCAA GGCTGAAGCC 1440  
 AAGATTCCGA GCGAAGCAGA CTTCCTCGCT GCTTTCAAAG CTGCTCGTCA GCAGAAAGTA 1500  
 10 GAAGCCCAAGA AAGACGAAGT CTCCGACCAA AAATTGATGG AGAAAGCTCC TAAGGCCGGA 1560  
 AAGATCGTTT CCGAGAAGAA AGATCAGAAG TTCGGTACCA CGGAACCTAC CCTTAGCAAT 1620  
 GGCAATCAAAG TATACCTCAA GAAGACCGAT TTCAAATCAA ACGAAATCCT GATGAGTGCT 1680  
 CTCAGCCCGG GTGGTATCCT CTCCGGAAAG CATGCTCCCA ACCAATCTGT GATGAATTCT 1740  
 TTCATGAACG TGGGTGGCTT GGGCAACTTC GATGCTATCC ACCTGGATAA GGTGCTGACA 1800  
 15 GGTGCTGTCT GTTCCTATC TCCCTCTTTG TCTCTGCTCA GTGAAGGTCT TTCGGGCAAA 1860  
 ACGACTGTAG AAGATATGGA AACTTTCTTC CAGTTGATCT ATCTCCAAAT GACTGTAAAC 1920  
 CCGAAGGATC CCGAAGCGTT CAAGGCCACA CAGGAAAAGT TGTACAATAA CTTGAAAAAT 1980  
 CAGGAAGCCA ACCCGATGGC TGGGCTTATG GACTCTATCC GTCATACCAT GTACGGCGAT 2040  
 AATCCGATGA TGAACCCAT GAAAGCTGCT GACGTGGAGA AAGTAAATTA CGATCAGGTA 2100  
 20 ATGGCTTTCT ACAATGAGCG ATTCTGCTGAT GCCGGCGACT TTATGTTCTT CTTTATCGGT 2160  
 AATCTGGATG AAGCCAAAGT GAAGCCATTG ATCGAAACTT ATCTGTCTTC ATTGCCCAAC 2220  
 CTCAAGCGTG GCGATAAGAT GAATAAGGCT CAGGTACCGG CTGCCCGTTC GGGAAAGATC 2280  
 GATTGCAAGT TCGAGAAGGA AATGGATACT CCTTCGACTA GTATATTCTG TGTCTGTCTC 2340  
 GGAAATGTGG AATATACGCT CAAGAACAGT CTCCTGCTGG AAGTCTTCTC AGCCGTAATG 2400  
 25 GATCAGGTGT ACACGGCTAC CGTTCGCGAG AAGGAAGGCG GTGCATACAG TGTGGCTGCA 2460  
 TTCCGGCGGT TCGAGCAATA TCCTCAGCCC AAGGCTCTGA TGCAGATCTA TTTCCCCACG 2520  
 GATCCTGTCT GTGCCGAGCA AATGAATGCT ATCGTTTTTG CTGAGTTGGA GAAGCTTGCC 2580  
 AAGGAAGGCC CCAATGTGGA ATACTTTAAG AAGACTATCG AAAACCTGAA TAAGCAGCAC 2640  
 AAAGAAAGTC TGGGTGAGAA TCGTTTCTGG CTCGAAGCCA TGAAGGCGTC TTTCTTCGAA 2700  
 30 GGAAATGACT TCATCACAGA CTACGAATCC GTACTGAACG GTCTTACTCC TGCTGAATTG 2760  
 CAAAAGTTTG CCGCAGACCT GTTGAAGCAG CAGAAATCGG TTGTTGTCAT GATGGCTCCT 2820  
 GTTGCAAAAG CTCAA 2835

## (2) INFORMATION FOR SEQ ID NO:19

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2058 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 40 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 45 (A) ORGANISM: PORPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2058  
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19

TACACTATGA GTAAGAAAGG AACAAATCGGG GTAACGAGCG ACAATATATT CCCCGTCATC 60  
 AAAAAAATCC TGTACAGCGA CCATGAGATA TTCTGCGGTG AGATCGTCTC CAATGCGGTG 120  
 GATGCTACCG AGAAGCTGAA AACGCTTACA TCCGTGCGCG AATTCAAAGG CGAGACGGGT 180  
 55 GACCTCCGCG TAACGGTCAG CGTGGATGAA GTGGCAGCA CGATCAGGT CAGCGACCGC 240  
 GCGGTAGGGA TGACCGAAGA GGAGGTGGAG AAGTACATCA ATCAGATTGC TTTCTCCAGT 300  
 GCGGAAGAGT TTCTTGAAAA GTACAAAGAC GACAAGGCGG CCATTATCGG CCACTTCGGA 360  
 CTCGGATTTT ACTCGGCTTT CATGGTGTCC GAGCGAGTGG ACGTGATCAC GCGCTCTTTC 420  
 60 CGAGAAGATG CTACGGCGGT GAAATGGAGC TGGCAGCGAT CGCCGGAATA CACGCTCGAA 480  
 CCTGCGGACA AGGCTGACCG TGGCACCAGC ATCGTGATGC ACATCGATGA GGAGAATAGC 540  
 GAGTTCTCTA AAAAAAGAAA GATAGAGGGG CTCCTCGGCA AATACTGTAA GTTCTTACC 600  
 GTGCCGATCA TTTTCGGCAA GAAGCAGGAA TGGAAAGACG GCAAGATGCA AGATACGGAC 660  
 GAGGACATTC AGATCAACGA CACACATCCT GCTTGGACCA AAAAGCCTGC CGACCTCAAG 720  
 65 GACGAAGACT ATAAGGAATT TTACCGTTTG CTCTATCCCA TGTCCGAAGA GCCTCTCTTC 780  
 TGGATCCACC TCAATGTGGA CTATCCGTTT AATCTGACAG GTATCTCTA TTTCCGGAAG 840  
 ATCAAAACAA ACTTGGATCT GCAGCGCAAC AAGATTGAGC TCTACTGCAA TCAGGTTTAC 900  
 GTCACCGATG AAGTACAGGG TATCGTGCCG GACTTCTCTA CCTCTCTGCA CGGGGTCTATC 960  
 GATTCCGCGG ATATTCCCTT CAACGTATCG CGCTCTCTATC TGCAGAGCGA TGCCAAATGTG 1020  
 70 AAGAAGATCT CGTCTCATAT CACCAAGAAG GTGGCAGACC GTCTGGAAGA AATTTTCAA 1080  
 AACGACCGCC CCACATTCTG GGAGAAATGG GATAGTCTGA AGCTCTTCTG CGAATACGGT 1140  
 ATGCTGACGG ATGAAGATT CTATGAGCGT GCAGCCAAAT TCTTCTTTT CACCGATATG 1200  
 GACGGACACA AGTACAGGTT CGACGATAC CGAACGCTCG TCGAAGGTGT ACAGACGGAT 1260  
 AAGGACGGAC AGGTAGTGTA TCTCTATGCT ACGGACAGG ATGGACAGTA CAGCCACGTG 1320  
 75 AAACGTGCAT CCGACAAAGG CTACAGCGTG ATGCTGTTGG ATGGTCAGTT GGATCCGCAT 1380  
 ATCGTGAGCC TGCTGGAGCA AAAGTTGGAG AAGACACACT TTGTCGCTG CGATAGCGAT 1440

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ACGATCAACA	ATCTGATCCG	CAAGGAGGAA	AGAGCCGAAG	TGAAACTGTC	CGATACGGAG	1500
CGCGCCACTC	TCGTGAAGCT	GTTCTGAAGCA	CGCCTGCCAC	GGGACGAGAA	GAAGCACTTC	1560
AATGTAGCTT	TCGAATCGCT	CGGAGCCGAA	GGTGAAGCCA	TCCTTATCAC	ACAAGCCGAA	1620
TTTCATGCGCC	GTATGCGCGA	TATGGCACAG	CTGCAGCCGG	GAATGAGCTT	CTACGGCGAA	1680
CTCCCGGATT	CGTACAACTC	GGTACTTAAT	ACCGATCATC	CGCTCATCGA	CAGGGTACTC	1740
TCCGGTGAGA	AAGAATCGGT	AGAGCCTTCG	CTCACAGAGC	TTAGAGCGAA	AATCGCCGAG	1800
CTGAAAGCGG	AAGAGGCCAA	GCTGCTCGAT	GAGGAAAAAG	GGAAGAAACC	GGAGGAAATC	1860
CCTGTTGCCA	CGAAGGAAGC	CAAGGAGAAC	AACGCCGTCG	AACAGGCCAA	AACCGAAGGC	1920
AGTATCAACG	ATCAACTGAC	CAATATGCTC	CAGGACAACG	AGCTGATAGG	TCAGCTCATC	1980
GACTTGGCTC	TGCTCGGAAG	CGGATTGCTG	ACGGGAGAGG	CTTTGGCCGA	ATTCATTCGT	2040
CGCAGCCAGC	GTCTTCTC					2058

## (2) INFORMATION FOR SEQ ID NO:20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1446

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20

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GACAATCGAC	AGAAAAGACC	GTGCTTCAAC	GCCAAATTTGT	ACTTTTACCG	TGCAATGGAA	60
AAACTGATCG	ATATTTTGGT	CGTAGACGAT	GATGTGGCAG	TCTGTGCCGC	ACTGCGTCTG	120
GTGCTCAAGC	GAGCGGGCTA	TAATCCCGTT	ATAGCCAACA	GTCCCGACGA	AGCTTTGTCC	180
ATAATGCGGA	ATCCTGATGG	CGGCPTGTAAG	CCGGCTGTGA	TTCTGATGGA	TATGAATTTT	240
TCCCTTTTGA	CCTCCGGCAG	GGAAGGATTG	GAAGTACTGG	AGAAGATGCA	GATATTCACT	300
TCCTGCCCTG	TCATACTGAT	GACGGCTTGG	GCTTCGATTTC	CACCTGGCACT	GGAGGGAAATG	360
AGGCTTGGAG	CTTTGACTTT	CATAGGCCAAG	CCATGGGACA	ACGATCGGCT	CCTTCGTACC	420
ATAGATACGG	CCTTGCACTC	GGCTGCTCCC	TCAGCTGTGG	CGAATCCATC	GGAACAGTCT	480
GACAGAGATA	CAGCCCGTCA	GCCGAAAGCT	ACAGTCCAAG	AGAATGACCC	CTGTGCCCAT	540
ATCATAGGCC	GGAGCGATGC	CATCTGTAAG	ATCAAGGAAC	GGATACGCCG	CATAGCTCCC	600
ACCCATGCCT	CTGTGCTGAT	CACGGGCGAG	AGCGGTACGG	GCAAGAGATT	GATAGCCGAA	660
GCTCTGCACC	GTGGGAGCNA	ACGAGCCTCA	GCCGCATTCT	TCAAGGTCAA	TTTGGGTGGG	720
ATTCCCGAAA	GTTTGTTCGA	AAGTGAGCTG	TTGCGACATA	AGAAAGGAGC	TTTTACCAAT	780
GCTTTTTCGG	ACAGGAAAGG	ACGGTTCGAG	CTGGCTGATG	GCGGCACGAT	CTTTCTGGAC	840
GAAATAGGCG	AACTACCGGT	CGGCAACCAA	GTAAVACTGC	TGCGAGTGCT	ACAGGAACAG	900
ACATTCGAGC	CGTTGGGCGA	GAGCGTCTCC	CACCGATGGG	ACATCCGTGT	GGTATCGGCT	960
ACGAATGCTT	CCTTGGAGCG	AATGGTAGCC	GAAGGACGTT	TCAGAGAGGA	CCTCTACTAT	1020
CGAATCAACC	TGATACATCT	GCATCTGCCT	CCGCTGCGTG	AGCGTCAGGA	GGATATACAG	1080
CTGCTGGTGG	AAGCCTTCAG	TGAAGCCTTT	GCCCAATCGA	ACGGATTGCC	CCATGCGGTT	1140
TGGAGTGCGG	AAGCTATGCG	ACGTATCTGT	GCCATGCCCC	TACCGGGCAA	TGTACGCGAA	1200
CTGAAAAACG	TAGTGGAGCG	TACGCTATTG	CTCTCGGGAT	CGAGAGAAAT	CAGTGGCCGG	1260
GATGTGGCTG	ACTTCGCTTC	GCAGGTGACG	GCAGCAGACC	ACTCCGACGA	ACGGGCTTTG	1320
ACCGACATGG	AGGAAGCTGC	TATCCGAGAG	ACGCTGACTA	AATACACCGG	CAACGTTAGT	1380
CGTGTGCGAC	GAGCCTTGGG	ATTGAGCCGG	GCAGCTCTTT	ACCGGCGAAT	GGAGAAATAC	1440
GACTTG						1446

## (2) INFORMATION FOR SEQ ID NO:21

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21

AGATCTCTGC	AATCATTTC	AAATAAAAA	CACTCAAGTA	TGCTTAAGAT	AAAGAACCTC	60
CACGCCACAG	TACAGGGCAA	AGAGATATT	AAAGGAATCA	ATCTGGAGAT	CAATGCCGGA	120
GAGATTTCATG	CTATCATGGG	GCCGAACGGA	TCGGGGAAVA	GTACGCTCTC	TTCCGTTTGG	180
GTGGGACATC	CCTCCTTTGA	AGTCACGGAA	GGAGAGGTGA	CATTCAATGG	AATCGACCTG	240
CTCGAATCTG	AACCGGAAGA	ACGTGCACAC	CTCGGACTCT	TTCTCAGTTT	CCAATATCCG	300
GTCCGATCC	CGGGCGTCAG	CATGGTGAAT	TTCTATGAGG	CAGCTGTCAA	TGAACATAGG	360
AAAGCGATCG	GAGCAGAACC	CGTATCGGCA	AGCGACTTCC	TCAAGATGAT	GCGAGAGAAG	420
CGTGCCATTG	TGGAGCTGGA	CAACAAATTG	GCCAGCCGTT	CTGTGAACGA	AGGCTTCTCC	480
GGTGGAGAAA	AAAGAGGAA	CGAAATCTTC	CAAATGGCTA	TGCTCGAACC	CAAGCTGGCT	540
ATTTTGGACG	AAACCGATAG	CGGGCTCGAT	ATCGACGCTC	TCCGCATCGT	AGCAGGCGGG	600
GTAACCGGAC	TCCGCTCTCC	GGAGAATGCT	GCTATTGTGA	TCACACACTA	TCAGCGTTTG	660
CTCGAGTACA	TCAAGCCGGA	CTTCGTACAC	GTCTTTACA	AGGGGCGCAT	CGTCAAGTCG	720
GGAGGAGCCG	AGCTGGCTCT	CACGCTCGAA	GAAAAAGGCT	ACGACTGGAT	CAAGGAAGAG	780
ATAGGAGAA						789

(2) INFORMATION FOR SEQ ID NO:22

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1386 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22

AGCATGGCTA	AGGAGAAAAC	GATCTACGTC	TGCCGTTTCT	GCGGAACCAA	ATACGCCAAA	60
TGGCAAGGCA	ACTGCAATGC	CTGTGGAGAG	TGGAAGTSCA	TTGATGAGGA	GAAGGTGCCG	120
GCACCGGCAT	CGGGCAAGCA	TGCACCCAAG	AGTTTTATGC	CTCGGGAGCA	GGACAACCGG	180
CCAAGACTCT	TACAGGATGT	GGAGTCCGGC	GATGAAGAGC	GTATTCCGCT	CGGCGATGAA	240
GAGTTCGACC	CCGTACTGGG	TGGAGGAATT	GTCAAAGGAG	CATTTGTCTT	GCTTGGCGGC	300
GAGCCGGGAA	TCGGTAAGTC	CACGCTTATC	CTCCAGACGG	TGCTGCGTCT	GCCGCAGTTG	360
CGCACGCTCT	ATGTGTCCGG	CGAAGAAAGT	GCCCGACAAC	TGAAGATGCG	CGCCGAACGA	420
CTGGGGCAAG	CCATGAATGG	GTGCTACGTA	TACTGCGAAA	CGAATATAGA	GAGGATACTC	480
TCCCGTGCAG	AAGAACTCAC	ACCGATCTTC	CTCGTGATAG	ACTCTATACA	GACGCTCTAT	540
ACCGAGGAA	TGGAAAGCTC	GGCCGGCAGC	GTGGGGCAGA	TCCGCGAATG	TGCCCGCTTA	600
CTGCTCAAAT	ACTGCAAGAC	TACGGGTATC	CCCGTCATCG	TCATCGGACA	CATCACCAAA	660
GAAGGTAGCA	TAGCCGGACC	GAAGGTGCTG	GAGCATATAG	TGGATACGGT	GCTTCTCTTC	720
GACGGGGATA	AGCATCATCT	CTACCCGATA	CTCCGAGGAC	AGAAGAACCG	CTATGGCAGT	780
ACTTCCGAGC	TGGGGATATA	CGAGATGCGG	CAGGACGGTC	TGCGTGGCGT	GGAGAATCCG	840
AGCGAACATC	TCATCACACG	CAATAGGGAA	GACCTCAGTG	GCATAGCCAT	AGCCGTAGCG	900
ATGGAGGGCA	TTCCGCCGAT	ACTCATCGAA	GCGCAGGCTT	TGGTCAGCTC	GGCCATTAT	960
GCCANTCCGC	AGCGTTCGGC	CACGGGCTTC	GATATTCCGC	GGATGAACAT	GCTCTTAGCC	1020
GTACTGGAGA	AACGTGCCGG	CTTCAAGCTC	ATACAGAAGG	ATGTGTTTCT	GAACATTGCC	1080
GGAGGTATCA	AAATAGCCGA	TCCGGCTACG	GATCTGGCCG	TTATCTCGGC	AGTGTGGCGG	1140
TCGAGTCTGG	ACATCGTTAT	CCGCGCGGCC	GTATGCATGA	CGGGCGAGGT	CGGACTCTCC	1200
GGAGAGATAC	GTCCCGTGAG	CCGCATCGAG	CAGCGCATAA	CGGAAGCGCG	TCGCATAGGG	1260
TTCAVAGAGA	TATTGGTACC	GGCCGATAAT	TTCCGGCAGG	AGGATGCCGG	CCGCTTCGGT	1320
ATTCCGCTCG	TGCCGCTCAG	AAAGGTGGAG	GAAGCCTTCC	GCCATCTGTT	CTCGAAAGGA	1380
AGAGAA						1386

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## (2) INFORMATION FOR SEQ ID NO:23

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1119 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1119
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23

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25  GGGTCTTGTG GAAGTAGCCC AGCAATTGGC CGATCAGGST GTTCGCGTTG TGATCSCCGG      60
    ATTGACATG GACTTTCGAC GTCACCCCTT CGGACCTATG CCGGGCTTGT GTCCCATAGC      120
    CGACTCCGTG ACCAAAGTTC ATGCCGTGTG TGTGGAAATG GCGCGATTGG CCAGCTATTC      180
    TTCCCGTCGT GTCCAAGGCG ATCAGCAAGT GATGCTGCGC GAACTGAACG AATACAGTCC      240
    CCTCTGCAGA ACCTGCTACA GGAAATGCAG TTCTCCCCCA CAAACAGAAG AAATCCATTC      300
    GACAATATGA ATAGCAGACA TCTGACAATC ACAATCATTC CCGGCCTCTC CCTCTTTGTA      360
    CTGACATGGG GCGGCTGCTC CGTAGCCCAA CAAGATACGC AGTGGACTCT CGGCGGAAAG      420
    CTCTTTACTT CGGCGTGGAT ACAACGTTTC GCCGAATATC AAGCGCTTTG CATTGAGGCA      480
    TACAACATCG CTACGGAAG AGTGGAGCCT CTACCGGCAG AACGTAAACA AGGAGATAGG      540
    CCTTATGCCA TGGTAACGGA CATAGACGAA ACCATTTTGG ACAATAGGCC TAACTCCGTG      600
    TATCAGGCTC TCAGGGGCAA GGATTATGAT GAAGAGACTT GGGGGAAATG GTGTGCACAG      660
    CGCGATCGCG ACACACTGGC AGGAGCTTTG TCTTTCTTCC TCCATGCAGC GAACAAGGGG      720
    ATCGAGGTCT TTTACGTCAC CAACCGCAGA GACAATCTGC GCGAAGCAAC TCTTCAGAAC      780
    CTTGAGGTTT ACGGATTCCT CTTGCGGAT GAAGAACATT TGCTTACGAC CCATGGGCCA      840
    TCCGACAAAG AACCCCGTCG GCTCAAAATA CAGAACAGT ATGAAATAGT ATTGCTCATA      900
    40  GGAGACAACCT TGGGCGACTT CCACCACTTC TTCAATACGA AAGAAGAGTC CGGACGCAAA      960
    CAGGCTCTGG GCCTGACAGC CGGGGAGTTT GGCCGGCACT TCATCATGCT GCCCAATCCC      1020
    AACTACGAT CTGGGAACC GGCATGGTAC GGCGGGAAGT ATCCGCCACT GCCCGAAAGA      1080
    GACAAAGCAC TTAACAACCT GCACTCAGC AACAGCAGA      1119

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## (2) INFORMATION FOR SEQ ID NO:24

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1278 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1278
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24

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70  CGTTGGGTT TTTCTAATT TGTGGCCATG AGCACCAATA TAGATGTACA ACAGATCAAA      60
    CAGCGTTTCG GCATCATCGG TAGCAGTCCG CTGATGGAAC ATGCCATACG AGTGGCAGCA      120
    CAGGTGGCTC CTACCGACAT GTCGTCCTC GTGACGGGCG AGAGCGGTTC CGGGAAAGAG      180
    TTCTTCCAC AGATAATCCA CTAATAACGC GCCCGGAAC ATCATAGCTA CATTGCAGTC      240
    AATTGCGGAG CCATCCCGGA AGGAACATC GATTCCGAGC TGTTCCGACA CCGCAAAGGT      300
    TCCTTTACCG GAGCCGTATC GATCGCAG GGTACTTTCG AAGAAGCATC CGGCGGCACG      360
    75  ATCTTTCTGG ACGAAGTGGG CGAACTGCCT TTGCCACGCG AGGCGAGGCT GCTGAGGGTG      420

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5 CTGGAGACGG GCGAGTTCAT CCCCCTAGGA GCCAGCCAGT CGCAGAAGAC GGATGTCCGT 480  
 ATCGTAGCGG CGACGAATGT GAACCTCAAG GAGGCGGTAG CGAACGGGAA GTTCCGGGAA 540  
 GACCTCTTCT TCCGGCTCAA TACGGTACCG ATCGAGGTGC CTGCGCTGCG TATCGGACCG 600  
 GACGACGTGC CCTTGTCTTT TCGCCGATTC GCGCCGACA GCGCCGAGAA GTATCGGATG 660  
 CCTCCGCTGC GCCTATCGGA CGAAGCCCGT ACCATATTAA TCGGTACCG CTGGCCCGGC 720  
 AATGTGCGAG AGCTGCGCAA TATAACCGAC AGGCTGAGCA TCCTGGAGGA GGAGCGGACG 780  
 GTATCGGCAG AGACCATCAC TCGCTACCTG GACGCTGAGG GGATGCAAGA CCTCCACCCC 840  
 GTCGTGATCC GACGGAACGA AACGACCGAA GCGGACAAAC AAATCCCCCA TTACGAGCGC 900  
 GAAATCATCT ACCAGGTGCT ATACGATATG AAGAAAGAGA TAGCCGATTT GAAGGGGATG 960  
 10 ATGAACCGCC TGGCGCACCA CGAACAGCCC TCATGGCCTG TAGGGTCGGA CGTCTGGGGC 1020  
 AACGACGACA AGCGACCCGC AGATCCGAAG TGGGGCGTCA GCACGCACAA GGCCCCCATC 1080  
 GCGAACCGCG CAGAACCCGT GGAGCCGATA CAGGAAGCCA GCGAATACAC CGAGGATCCG 1140  
 GTTTCGCTGG AGGAGGTAGA GAGAAAATG ATTTCCCTTG CATTGGAACG CCACCGCGGA 1200  
 AGGCGCAAGC AGACAGCCGA GGAATGAAG ATTTCCGAGC GGACACTATA CCGTAAATTC 1260  
 15 AAGGAGTATG GACTGGAA 1278

(2) INFORMATION FOR SEQ ID NO:25

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1959 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 25 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 30 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: FORYPHYROMONAS GINGIVALIS  
 35 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25

40 AAAAATCTTC CGAGGTACGC TCCGGCATTT GGCAGAAATC GTAAAGGGA ACAACCTGAC 60  
 CCTGACAACG ATGATAGTCG TGGGAGAAGC CATAGACAAT CGGGAAGGGC TGTCAAGGTT 120  
 GTATGCCGAC GAATTCAAAC ACCTCTTCCG CACATGATCC TACTCTTCGG CGGTACTAAG 180  
 GAAGGCCGTG CCGCAGCTCG CGTGCTGGAT GAAGCGGGAA GTCCGTTTTT CTACTCCACC 240  
 45 AARGGCAATC TGCAAGAGAT CCAGAGTAGC CACGGCCATC GTCTGACAGG AGCCATGACG 300  
 GTTGCCGACA TGGTTTCGTT TTGTCGGAAA GAAGAGATCC GACTGATCGT GGACCCCGCT 360  
 CATCCCTTTC CGAAGAATT GCACGCTTCA GTGGCAGAAG CTTCTGAACA AACAGGTATC 420  
 CCGTAGTAA GATACGAGAG ACAATACCTT CCACGCGAAG AAGGTATCGT CTGGTGTGCA 480  
 50 AACTACGATA CGGCTGCCGA GCGGATGCTT GGCGATGGCG TGCAGCGTCT GCTGATGCTC 540  
 ACAGGAGTGA ATACGATCCC CAAGCTGGCT GCTTCTGGA AAGAGCGCAC CACCTTTTGC 600  
 CGCATATTGA AGCGAGACGA ATCGGTTGCT TTGGCAGAGA AGAACGGCTT TCCTGCGGAG 660  
 CGCATCGTTT TCTTCGAACC GCATGCGGAC GAGGAGCTGA TGCAAGCCGT TCGCCCGGAT 720  
 GCCATTATCA CAAAAGAAAG CGGAGAGAGC GGTACTTCC GAGAAAAGAT AGAAGCTGCC 780  
 CGACGGATGG GCATCCGTAT ATATGCCGTC GTACGTCCCC CTTTGCCTCC TTCATTCAIT 840  
 55 CCGTATAGGG GGCCTGTGCG TTGAGACGG GCGGTAGAAC GCCTCGTGCC GGGATTCCTT 900  
 TCACTCCGAA GCGGATTAC TACCGGCACC ACAGCTACCG CTGCAGTAGT AGCAGCCATG 960  
 TACCGATTGA TGGGGCTTGG CTCTCTGCCG GAAGCTCCCG TAGAATTGCC TTCGGGCGAA 1020  
 ATAGTCAGTC TGCCCATAGC GAAATTCGA GAGGAAGAAG ATGCTGTGCT ATCCGCGATC 1080  
 60 CTGAAGAGAT CAGGTGATGA TCCGGATGTG ACCAATGGCA TGGCGGTATG CGCTACGATC 1140  
 AGGCTCAATC CCGAACATGA GGAAGTCCGC TTCCTGCAGG GTGAAGGGGT GGGGGTATG 1200  
 ACGCTCCCGC GCCTCGGTCT GGAGGTGGA GGTCCGGCTA TCAACCTCGT ACCTCGACGA 1260  
 ATGATGACAG CAGAGGTACG CCGACTCTAT GCGCAGGGAG GTGTGGATAT TACGATTAGC 1320  
 GTACCCGAAG GCGGAGAGGC TGCTACCCAG ACATTCAATC CCGGACTCGG CATAAGGGAC 1380  
 GGCATCTCTA TTATCGGAAC ATCGGGAGTC GTGAACCTT TTTCGGCGGA AGCGTTCGTT 1440  
 65 GGTGCCATCC GTAAGCAAGT GGGTATTGCC ACCGCCCTGG GAGCCAATCA TATCGTCCTC 1500  
 AATTCCGGAG CCAAGAGTGA GCGTTATGTA AAAGGAGCCT ATCCGGCACT CATTCCACAG 1560  
 GCCTTTGTGC AGTATGGCAA TTTCGTCCGC GAATCACTCA GTTGTGTAGC TTCTTCCCT 1620  
 TCTGTCCSTT CGGTAACGGT AGGAATCATG CTCGGCAAAG CAGTGAAACT CGCCGAAGGC 1680  
 70 TATCTGGATA CGCAGAGTAA AAAGGTAGTG ATGAATCGGG ATTTCTGCA CGAACTGGCT 1740  
 CGTCAGGCAG GTTCTTCGGA AGACATCCAT GCCAATATAG ACAGCTGAA TTTGGCTCGT 1800  
 GAGCTATGGA CTATGCCGAG TCGGAGGAGC AGCGATCGAC TGCTACGAAA GATTGCCGAA 1860  
 CGATCTTGGG AAATTCGCCG CCCATCGGTA CCATCGGCCG AATTAGAATC CCTGCTGATC 1920  
 75 GATGAGTCCG GAGCGATTGC TTTTCGTATC GGTGGAGAA 1959

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## (2) INFORMATION FOR SEQ ID NO:26

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1353 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1353
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26

```

25 CAACAAAGAC CACATAGAAT TATTATGTTG AGGACTTTCC GAATCGGTGG TATTCACCCC      60
   CCGGAAAACA AGTTGTGGGC AGGCAAGCCC GTAGAGGTGT TGCCTATCCC CTCACAGGTA      120
   GTCA'FCCCTC TTGGTCAGCA CATCGGTGCA CCGGCAACTG CCACGGTCAA GAAAGGGCAT      180
   GAAGTTAAGG TCGGGACTAT CATTGCTCAG GCCGGAGGAT TCGTATCAGC TAATATCCAC      240
   TCATCTGTST CCGGTAAGGT GCTGAAGATC GATAACGTAT ACGACTCAAG CCGCTATCCC      300
   AAGCCCGCAG TCCTCATTTAG CGTAGAAGGT GACGAATGGG AAGAGGGCAT CGATCGCTCA      360
30 CCAGCCATCG TCRAAGAATG CAATCTGGAT GCAAAAGAAA TCGTAGCCAA AATTTCGCA      420
   CCGGTATTGG TGGGTCTTGG CGGTGCTACC TTCCCTACCC ATGTGAAGCT GTCCCTCCT      480
   CCGGCAACA AGCTGAGAT CCTGATCATC AACCCGCTAG AGTGCGAGCC TTATCTGACG      540
   AGCGACCATG TCCTTATGCT GGAGCACGGC GAAGAGATCA TGATCGGCGT GAGTATCCTG      600
   ATGAAAGCCA TTCAGGTAAA CAAGGCCGTC ATCGGAGTTG AGAATAATAA GAAAGATGCT      660
35 ATTGCTCACC TCACCAAACT GGCCACTGCA TATCCGGGCA TAGAGGTAAT GCCGTGAAG      720
   GTGCAATATC CTCAAGGCGG TGAGAAGCAG CTGATCGATG CAGTGATCCG CAAGCAGGTA      780
   AAAAGCGGTG CCTTGCTAT CAGCACAGGT CCGGTAGTAC AAAACGTGGG TACGGTATTC      840
   GCCGTGTACG AAGCAGTACA GAAGAACAAG CCTCTGGTGC AGCGCATCGT GACGGTTACA      900
   GGAAAAAAAC TGCTCGTCC GTCTAACCTC CTCGTTCGTA TAGGTACTCC TATTGCGGCT      960
40 TTGATCGAAG CAGCAGGTGG CTTGCCGGAG AATACGGGCA AGATCATCGG CGGAGGTCCG      1020
   ATGATGGGAC CGCTCTGTCT GTCAACGGAT GTGCCGTGTA CCAAGGCCAG CTCGGGAGTA      1080
   TTGATTCTCG ATAGAGAAGA GGCAGTTCCG AAGCCTATGC GCGACTGTAT CCGATGCGCC      1140
   AAGTGGCTCG GAGTGTGTCC GATGGGACTC AATCCGGCTT TCCTTATCGC CGACACCTTA      1200
   TATAAGAGCT GGGAAACAGC GGAATAAGGC AACGTGGTTG ACTGTATCGA ATGCGGTTCT      1260
45 TGCAGCTTCA CTTGCCGGC CAACCGTCCT CTGCTGGATT ATATCGGCA AGCCAAGAAG      1320
   ACTGTGTGAG GTATCCAAAG AGCAGTAAG CAA                                     1353

```

## (2) INFORMATION FOR SEQ ID NO:27

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1467 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1467
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27

```

75 ATGAACTCTC AAAAGAAAGA GGCTTTTAAT ATGAAAAGAA TACAACCTAC TCTTATCGCT      60
   CTCTTCGCCG CTGTTCGCCG TTTGGTCGCT CAAAATGCTT ACGAGGGAGT AATTCATAT      120
   AAAATTTGCT TGGACAAAAC CGGAAACAAG GTTGTACTGA ATGGTCCGGC AGATATGAGT      180
   AATTTAAGC TCAGAGCAC TCAGATGATC ATTGTTACGC CTATTCTTCG TTCAGAAGAT      240

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5 GGTACCAGCC GGGTGGAAIT TCCTTCGGTA GTCATTACAG GCCGCAATAG AACAAAACCT 300  
 CTCAGCGGTG AAATCGCATT TAGTTCGGCT TTGCCCAAG CAAAACATGC AGCTCAATAC 360  
 ATTCGCCGTC ATAATGGGAA GAGCGAGCAG TTTGCTTTTA CAGGAGAACA TGCTTATGCA 420  
 TCATGGATGA TGGATGCCAA GTTTGTGGTT CGTGAGGAGG TACGAGGTTG TGCTAAATGC 480  
 CCTGTAGGTC TCTCGAGTAA TATTGTCTCT TTTGATCCAC TCTTCAATCC GGCAGAGGCT 540  
 CCTTATTGT TGGCACACAT TACTCGGCA GAAGAAGTGG AAAACAGCG AGAGTCCAGC 600  
 TTCGATGCTT ATATCAACTT CAAAGTCAAT AAGGCAGATG TCCTTCCTGA GTATCGCAAC 660  
 AATAAGGCGG AGTTAGAGAA AATCAAAGAA TTTGTAAGCA CCGTTAAGGC TAATCCAAAC 720  
 10 TATTGGGTGA ATAAATGAT CATCGAAGGG TTTGCTTCTC CCGAGGCTTC AATAGCCAC 780  
 AATAAGGCTT TGTCGAGCG CCGTGTCTAA AGACTCGCGG AAGATTGGT GCGTAAGTAT 840  
 GGCAAAACAT TGCCGAATAT AACCCTGAA TTCGCGGTG AAGATTGGAA GGGGCTGAAA 900  
 CTGGCTATCG AAAAGAGTGA TATAGCCGAT CGTGACCGCG TATTGGAGAT AATCAACTCC 960  
 GATAAATATG CCGATGATGA TGCACGTGAA CAGGCTCTGA AGCAACTTTC GTCTTATCGT 1020  
 15 TATATCTTGG ATCAGATCTA TCCGAATTG CGTGCATAA CGATAACCAT GGGGTATATC 1080  
 GTTCGTGATT ATACCCTCGA AGAAGCTCGT GAAATCATA AGACTGCTCC GAAAGAACTT 1140  
 AGTGAGGCGG AAATGTACCG TGTGGCAATG TCTTATCTG AGGGGCACCA AGAGCSTTTG 1200  
 TTTGCTCTGA ATACGACCCT TAAGTATTTT CCTGAAAGTG TAACGGGCGG AATCAATTTG 1260  
 GCTGTAGCCG CTTTTAATGG TGGAGAGCTT CAACAGGCAA TTGCTCTGTT GAGTCCGATT 1320  
 20 CAGACAGAAA AGGGTGTAG CAATATCCTT GGAGCTGCTT ATGCTCGTAC GGGAGATTTT 1380  
 GCTCGTGCCG AACCTTCTT CCGTAAGGCC GTTGCAGAAG GAGATGCAAA TGCGCAGCGC 1440  
 AACCTCGATA TGCTGCTTGG CAAAAAG 1467

## (2) INFORMATION FOR SEQ ID NO:28

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1152 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28

50 GACATGGCAG AAAAAAGAGA CTATTACGAA GTCCTCGGTG TATCGAAGAA TGCCACCGAC 60  
 GATGAACCTGA AAAAAAGCATA TCGCAAGAAG GCTATCCAAT ACCATCCTGA TAAGAACCCC 120  
 GGTGACAAGG AGGCCGAAGA GCACTTCAAA GAGGTAGCTG AAGCTACGA CGTATTGAGC 180  
 GATCCGCAGA AGCCGAGTCA ATATGACCAG TTCGCCATG CCGGATTGGG CCGAGCTGCC 240  
 GGTGAGGTTT TCAGCGGAGG CGGTATGTCC ATGGAGGATA TTTTCAGTCC CTTCGGTGAT 300  
 CTATTCCGTG GGTTCGGCGG TTTCCGCGGA TTCTCCGATA TGGGCGGTGG CAGTCCGAGA 360  
 CGTGTTCGCA GAGGCTCTGA CCTGCGAGTA CGAGTGAAGC TTTCTTTGGC CGATATAAGT 420  
 55 AAAGGTGTGG AGAAGAAAGT GAAGGTAAAA AAGCAGGTAG TGTGCAGCAA ATGTCGTGGC 480  
 GATGGCACGG AAGAAGCCAA TGGCAAGACT ACCTGCCAGA CCTGCCATGG AACCGCGGTG 540  
 GTTACACGTG TGAGCAACAC TTTCTTGGG GCCATGCAGA CCCAGAGCAC TTGTCCCACT 600  
 TGCCACGGAG AGGGTGAGAT CATCACGAAG CCATGCTCCA AGTGTAAGGG CGAAGGTGTG 660  
 GAGATCGGCG AAGAGGTGAT CTCATTCCAC ATCCCTGCCG GTGTAGCCGA AGGAATGCRA 720  
 60 ATGTCCGTGA ACGGCAAGGG AAATGCCGCG CCCCAGGAGG GCGTGAATGG CCACTTGATA 780  
 GTCGTGATCG CCGAGGAACC GGATCCGAAT CTGATCCGCA ATGGCAACGA TCTGATATAC 840  
 AATCTGCTTA TATCCGTTCC GTTGGCTATA AAAGGAGSTA GTGTGGAAGT GCCGACGATA 900  
 GACGGACGAG CCAAGATCCG CATCGAGGCG GGGACACAAC CCGGCAAGAT GCTGCGTTTG 960  
 CGCAATAAGG GATTGCCAGC CGTAACCGGC TATGCCATGG GAGACCAACT GGTGAATGTC 1020  
 65 AATGTCTATA TCCCGAATC GATCGATGCC AAAGATGAGC AGGCTATCGC AGCGATGGAA 1080  
 AACTCGGACA GCTTCAAACC TACCGATGCT GCTCGTAAGG ATATAGACAA GAAATACAGA 1140  
 GAGATGCTGG AT 1152

## (2) INFORMATION FOR SEQ ID NO:29

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 927 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular



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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29

```

CGATTGCGATT CAACAACATAA TGTCTCACAA ATTAATTAA GAACAGAGAT GAAAAAACTG      60
ATTTTAGCGA CTITGGGACT TATGGCCATT GCCATGCTCT CATGTTCAAG CAACAACAAG      120
GATTTCGAGA ACAAAGGGGA GGCTACTCTT TTGGTAACGT TTGGTAGCTC CTATAAAGCT      180
CCACCGCGAAA CCTATGCGAA GATTGAGAAG ACTTTTGCCG CAGCTTATCC CGATCAAAGG      240
ATAAGCTGGA CATACACGTC TCTATTATC OGAAGAAGAC TGGCTCAGCA GGGTATTTAT      300
ATCGATGCTC CGGATGAGGC TTGGAGAAA TTGGCTCGTC TGGGTATATA GAAGATCAAT      360
GTACAGAGTC TTCTGTGAT TCCCGGCCGA GAATATGATG AGATGATCGA CTTTGTCAAT      420
AAGTTTAAGG CAGCACATAG TGATATTACT GTGAAGTAG GGGCTCCGCT TTTGATACC      480
GATGAAGATA TGGCGGAGGT GGCAGAGATC TTGCACAAGC GTTTTCAGCA AACGATAGAG      540
AAAGGTGAAG CTATTGTATT CATGGGACAC GGCACCGAGC ATGCTGCAA TGACAGGTAT      600
GCCCCATCA ATAAGATCAT GAAGAATAT AGCAAGTTCA TGATCGTCGG AACCGTCGAG      660
TCCGATCCCT CTATCAATGA TGTATTGCC GAACTGAAAG AAACCGGTGC CACGGCCGTA      720
ACAATGATGC CGCTGATGAG TGTGGCAGGC GAACATGCTA CGAATGATAT GGCCTGAGAT      780
GAGGACGATA GCTGGAGAGC GTTGCTGACC AATGCCGGCT ACACAGTTTC TATAGACAAG      840
CTGGACAATG GCATTTCTC AGCTCTTGGG GATATAGAAG AGATCCGGAA TATCTGGCTC      900
AAGCATATGA AAGCCACCTC TGCTCGC                                     927

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(2). INFORMATION FOR SEQ ID NO:30

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1473 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30

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CGGAGAGATG CGCGGAGGCA ACTGGTACGC CGTAGGAGGA AAGAGCTATC TGGCACAGCA      60
AATACGCGAT GCGGAGGAG AGTATTTCTT GAAAGACGAT CAGCGATCCG GTGGTGTTC      120
CCTCGACTTC GAGACGGTCT ACAGCCGATC CGATTGGGCT CGCTACTGGC GAATCCTCAA      180
CAGCTATCCC GGGGAGTTCG GTTACGAAGC TTTGAAAGCC GAAGACAGCC GATATGCCGA      240
TTTCAGGGCA TTCAAGGAAA AAGGCGTGAT ATACTGCAAC CTGAGGGAAA CAGCCTTCTA      300
CGAACTCATG CCGATGCATC CCGATTGGGT GCTGGCCGAT CTTATCGCTA TCTTGACCCC      360
CGGACTACTT CCGGACCACC AACCCGATTT CTATTATTG CTCCAATGAC ATCUGTCAGC      420
CACTTACGTA CAATTTCTGT CGCAGGTATC CTGGCTGCGC TGGGAGGGGC TGTACTCATT      480
CTCTTCGGGG TTAATCTCTT CCTCGGCTCG GTGGCTATTC CGATGAGCGA GATCTTCCGA      540
CATCTTTTTT CAGATCGTCC CGAAGGAGGA GAAGCACTCG TGCACTACAA TATCCTATGG      600
AAATCCCGCC TGGCCGAAGC CCTCACGGCT GCTTTGCGG GCGCAGGTTT ATCCGTTAGT      660
GGCTTCGAGA TGCAGACCGT CTTTCGCAAT CCTTTGGCCG GTCCGTCGCT TCTCGGCATC      720
TAGTCCGGTG CCAGTTTGGG TGTTCGTTTG GTCGTTCTGC TGAGCGGCTC GCTGGGAGGA      780
GTGGCATTGA GTAGCCTGGG TTATATGGGC GAGGTGCCCC TGAATATAGC CGCTGCCGTA      840
GGCTCGCTGG CAGTAATGGG GCTGATCGTT TTTGTACGCA CCAAGGTGCG CAGCCACGTT      900
ACGCTGCTCA TTATCGGCGT TATGATCGGA TATGTAGCCA CTGCCGTCAT CCGGGTATTC      960
AAGTTTTTCA GTATCGAAGA AGATATTCGG GCATACGTTA TTTGGGGGTT GGGCAGCTTT      1020
TCCCGTGCCA CGGATTGCGA ACTGAGTTTC TTTGCCATTG TGATGTTGAT CTTTATTCGG      1080

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5 GCCGGTATGC TCCTTGTCAA GCAGTTG/AT CTCTTATTGC TGGGAGAAAG CTACGCACGT 1140  
 AATCTGGGAC TGAATACTCG TCGGGCACGG CTGCTCGTGA TCTCTTCCGC CGGTTTGCTC 1200  
 ATCGCTACCG TCAGGSCCTA TTGCGTCCCG ATCGGCTTTT TGGGGATGGC TGTGCCACAC 1260  
 TTGGCACGSG TTATCTTTCA CACATCGGAT CATCGGATCC TGATGCCTGC TACCTGTTTG 1320  
 ATTGGAAAGTG CTCCTGGCTCT TTTCTGCAAT ATCATTGCTC GTATGCCGGG GTTTGAGGGG 1380  
 GCTTTGCCCC TGAATTCGCT AACGGCTTTG GTGGGAGCAC CTATTATCGT CACCGTTTTG 1440  
 TTCCGGCGCA GACGCTTCAA GGAAGAAACC GAC 1473

## (2) INFORMATION FOR SEQ ID NO:31

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2289 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2289

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31

35 CATTTTTTAG TAACGATTAT GCGGACAAAA ACTATCTTTT TTGCGATTAT CTCTTTTATT 60  
 GCTCTATTGT CGTCTTCTCT GTCCGGCTCAG AGCAAAGCCG TTTTAACCGG TAGTGTGTCTG 120  
 GATGCCGAAA CCGGAGAGCC TCTTGCCGGT GCTCGAATCG AAGTCAAAACA CACCAACATA 180  
 GTAGCCGGTG CGATGCGCGG CGGACATTTT GAGATCAAGA ACCTGCCCGC AGGGCAGCAT 240  
 ACTATTATAT GTTCGTTGGG GGGCTATGGA CAGAAAGAGG AGGTGGTTGC CATCGAAGCC 300  
 GGACAGACCA AAACGATCTC TTTTGCAATT CGATGCGGAA CGAACAACTT GGAGGAAGTC 360  
 GTCGTTACCG GTACCGGTAC ACGTTACCGC TTGGTCCGAT CTCCTGTGGC AACGGAAGTC 420  
 40 CTTACCGCTA AGGACATAGC CTCCTTCTCG GCTCCTACTT CCGAGGCTTT ATTGCAGGGG 480  
 CTGAGTCGCT CTTTGTGACT CGGCCCAAT CTGATGGGCT CTTTCATGCA GCTGAACGGC 540  
 CTTAGCAGTA AGTATATCCT CATCCTTATC GATGGTAAGC GTGTGTACGG CGATGTAGGC 600  
 GGTGAGGCGG ATTTGAGTCG TATTTCTCCT GATCAGATCG AACGGATCGA ACTGGTGAAA 660  
 GGTGCTTCGA GTTCGCTCTA CGGATCCGAT GCCATCGCCG GGGTAATCAA TGTGATCACA 720  
 45 AAAAAGACCA CGAATCGACT GAGTGCATAT ACGTCACATC GCATATCGAA GTACAACGAT 780  
 CGGCAAAACCA ATACTTCGCT CGATATRAAC ATCGGTAAGT TCAGTAGCAA TACCACTAT 840  
 TTCTTCTACC ATACGGAATG CTGGCAGAA ATGCGGTTCT AAATAAAAAA GAAAAAAGGA 900  
 TCCGGCGAAC CGGTCTTGGA GGAAGCGTAT AAGAAAACTT TTGCTGCACA GGAATAATCAG 960  
 GGTGTAAGCC AATCGCTTTC CTATTATGCA ACTAACCAATC TTAGCTTCAG CGGAAATGTG 1020  
 50 CAGTACAATA AACGTGAGT CTTCACTCCG ACTTTTTCCG AAAAAGAGGC CTATGACATG 1080  
 GATTATCGTG CTTTGACGSC TTCACTCGGT ACGAACATAT TTTTCCCAAA TGGTCTGCAT 1140  
 ACGCTTTCTT TCGATGCCGT CTACGATCGC TTCCGTTTCG GATATTTGTA TCATGACAAG 1200  
 GACAGCAGTG AGAGCCTGAT CAACAACCAA GGTGAGACCG AGCAACCCAC ATTCTTTCCG 1260  
 GGTGAGCTAC GCAATAAAAA CGATCAGATC CGATACACCG CAGAGGCTCG CGGTGTATT 1320  
 55 ACCTGCGCTT ATGCGCAGAA ACTGACCGGC GGTITGGAGT AITTCGCTGA GGAATTGATC 1380  
 TCTCCCTATA ATTTGATTAC CGACAAGGCA GATGCTTCCA CGCTCTCTGC TTATGTACAA 1440  
 GATGAATGGA AACCGCTCGA TTGGTTCAAT ATGACAGCCG GTTTCGCTCT GGTACACCAT 1500  
 CAGGAGTTCT GTACACGAAT GACGCTAAG GTATCCATAC TCGCCAAGTA TGGGCGCGTG 1560  
 AACTTCCGCG CTACGTATGC TAACGGCTAT AAGACTCCCA CGCTGAAAGA GCTTTTTGCA 1620  
 60 CGGAACGAAC TCACCACTAT GGGTTGCGAC AATCTCTATC TCGGCAATGC GGATCTTAAG 1680  
 CCACAGATGT CGGATTATTA TGCTTTGGGC TTGGAGTACA ATCAAGGCCCT TATCTCGTTC 1740  
 AGTGCAACGG TTTATGACAA TGAACCTCGC AATCTGATCT CCTTTATGGA TATACCGACC 1800  
 TCACCCGAGC AGGAAGCTCA GGAATCAAG AAAACCAAGC AGTATGCCAA CATAGGAJVA 1860  
 GCTCGCAGCC GCGGCTTGA TGTCTTATGT GATGCTCTA TCGGTTGGGG TATCAAGTTA 1920  
 65 GGAGCCGGAT ACAGCCTCGT GGAAGCTAAG AATCTCCAGA CGGATGAGTG GCTGGAAGGA 1980  
 GCTCCACGTC ATCGTGCCAA TGTGACGCGC GATTGGGTTT ACTACTGGGG TCAGTATAGA 2040  
 CTTGGCGTGA GCCITTTCCG CCGTATTGAG AGCGAGCGTT ACTACAAAGA CGGCAATGCT 2100  
 CCGGACTATA CCTGTGGCGC ACTCGCCACA TCGCATCGTT TCGCTCATTT CCGCCACATC 2160  
 70 ATCCTGGATG GAACGCTCGG TATAGACAA CTGTTTGACT ACGTGGATGA TCGTCTCATG 2220  
 GGTGTCAATT ATGCTACCGT AACGCCGGGA CGTACTTTCT TTGCTCAAAAT AGCGATTTCGA 2280  
 TTCAACAAC 2289

## (2) INFORMATION FOR SEQ ID NO:32

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1095 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRAINEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32

25	TTTCCTTATT	TCGTTATTCA	TCTGATCAAA	CATATTATCA	TTATGACGGA	CAACAAACAA	120
	CGTAATATCG	TATTCOCGCG	GTTCCTCCTC	TTGCTGGGAG	TCATCGCAGT	GGTGACGATC	180
	GTTCGGTTTT	TCATGCTCAG	ACCGGCCGAG	GAGATTATCC	AAGGACAGAT	AGAAGTGACC	240
	GAATACCGAG	TGTCCAGCAA	AGTGCCCGGG	CGCATCAAGG	AACCTAGGGT	ATCCGAGGGA	300
	CAGCAGGTGC	AGGCCGCGCA	TACCCCTCGT	GTGATCGAAG	CCCCCGACGT	AGCGGCTAAG	360
	ATGGAGCAGG	CAAAGGCTGC	CGAAGCAGCT	GCACAGGCTC	AGAACGCCAA	GGCTCTCAAA	420
30	GGAGCAGCCA	GCGAACAGAT	ACAGGCAGCC	TATGAGATGT	GGCAGAAAGC	TCAGGCCGGC	480
	GTAGCCATAG	CGACCAAGAC	ACACCAAGCG	GTGCAGAAC	TCTATGACCA	GGGAGTGGTA	540
	CCGGCTCAGA	AGTTGGAAGA	AGCCACTGCC	CAGCGGATG	CGGCCATCGC	TACGCAAAAA	600
	GCGGCCGAAG	CCCAAGTACAA	TATGGCTCGC	ACCGGTCCCG	AACGCGAAGA	CAAGCTGGCA	660
	GCTTCTGCCC	TCGTGATAG	AGCGAGAGGA	GCCGTGCGCG	AGGTGGAGTC	GTACATCAAC	720
35	GAAACCTACC	TCATCGCCCC	ACGGGCGAGC	GAAGTGTCCG	AGATATTCCC	CAAGCCGGGC	780
	GAACTCGTAG	GTACCGGCGC	ACCTATCATG	AATATCGCCG	AGATGGGCGA	TATGTGGGCC	840
	AGCTTTGCCG	TTCTGTAGGA	TTTCCTCAGC	AGCATGACCA	TGGGAGCCGT	TCTGGAGACT	900
	GTGGTGCCCG	CTCTGAATGA	AGAAAAAGTA	CCCTTCAAGA	TCACATTTCAT	CAAGAACATG	960
	GGTACCTATG	CTCCCTGGAA	AGCGACCAAG	ACAACAGGGC	AGTACGACCT	GAAGACCTTC	1020
40	GAGGTAAAGG	CCACCCTTGC	GGATAAAGAC	AAGGCACAAA	AGCTACGCCC	GGGTATGTCC	1080
	GTGATCATAC	GCAAG					1095

(2) INFORMATION FOR SEQ ID NO:33

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 960 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRAINEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33

65	CCGCAATCCT	CTCCTGATCG	AAGAAGCTTC	CAAAACGTCA	TGAATAAATA	TCATTCTCAA	60
	AGCGTTTTAG	AGGTGCGCAA	AATTGGGATT	GTGATTATCT	TTGGGCCCAT	AGTACGGAAT	120
	GTACATCAAC	AACCCCTTTT	TTTAAGCCAT	AAATCAATTA	TGCGTATTGT	CAGTAAITTT	180
	TTGTTCTGCT	CTTTTTCGGT	TTTGCTTTTT	GCATCATGCC	GTTCACGCG	AGAAAAAGGTC	240
70	CTTTACCTGC	AAGATATCCA	AACCTTTTAA	CGGGAGATT	TCGCTAAACC	ATATGACGTA	300
	AAATTTGAGA	AGGACGATGT	GCTGAACATC	CTTGTCAGCA	GTAGAGACCC	GGAGCTTTCA	360
	ACGCCCTACA	ACCAAGTGT	GACCACTCGT	GCACTGGCCC	GCAACGGCTA	TGGAACGAAC	420
	TCGAACGAAG	GCTTCCTGGT	CGATTGCAAA	GGGTACATCA	ATTATCTTAT	TTTAGGCCAG	480
	ATCTATGTAG	AGGGCCCTAC	TCGTACCGAA	CTGGAGAAGG	AGATACAGAA	GAGGATTATT	540
75	TCCAGTGGAT	TTATCAAGGA	TCCTACGGTA	ACGGTGACGC	TTCAAAATTT	CAAGGTGTCT	600

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5 GTTTTGGGAG AGGTGAATCA TCCGGGTTCC ATGTCGGTAA AAGGAGAGCG AATAACTCTT 660  
 TTGGAAGCGA TCGGAATGGC CGGAGACCTG ACAATCTATG GTCGCCCGCA TCGGGTTTTT 720  
 GTGATTAGAG AAACCGATGG GCATCGCGAG GTTTTCCAGA CGGATCTCAG AAAGGCCGAC 780  
 TTGCTCGCAA GCCCGGTGTA CTATCTGCAT CAGAACGACG TCATCTATGT GGAGCCGAAC 840  
 GACAAAGAAA CACAGATGAG CGAGATCAAC CAGAATAATA ACGTAAACGT ATGGCTGAGT 900  
 GTTACCTCCA CTTTGGTATC CATTTCACG CTGACGATTA CGATAATAGA TAAGACCAAA 960

## (2) INFORMATION FOR SEQ ID NO:34

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1746 base pairs  
 (B) TYPE: nucleic acid  
 15 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 20 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 25 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1746  
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34

TCAAAAATAG TACTACGAAA GTTTTGTACC TTAGCGCGCA TGA AAAAGAC CAATCTGTTT 60  
 TTATCTCTGC TGGTGATCTT TATCACCAGT AGTTTATGA CTGCCTGTGC ACAGAAGTCC 120  
 35 AAGACGAACA AACTCACCAG AGAAGATCGG AGCCGCAATG AGTATGTACA GTCGATGGAT  
 GTGCTTAGCA ATATTATCGG TAACGTCAGG CTGTATTTCG TCGATACCAT AAGTATCAAA 180  
 CATATGACTC GGCCTGGTAT AGATGCGATG TTGGGCGGGC TTGACCCCTA TACCGAATAC 240  
 ATTCCTTAGC AGGAAATGGA TGAAGTAAA TTGATGACTA CGGAGAGATA TGCCGGAGTC 300  
 GGAGCTATCA TATCGCAGCG CCCGGATAGT GCTGTGATTA TCCAGAGACC TATGGAAGGT 360  
 40 ATGCCCGCAG ACGAAGCAGG ATTGATAGCA GGCGACCGCA TCCTGACTAT CGATGGGAAA  
 GACTTCCGCA AATCCACCAC ACCGAAAGTA AGCGAACGAC TGAAGGGAT AGCCGGTACT 420  
 GTTGCAAAAG TGACAGTAAT GCGCTATGGC GAAACCAAAC CTCGACTTTT TTCCGTGAAA 480  
 CGTCAAAAGG TGATATGAA TTCCGTCACT TACAGCGGAA AGTGCAGAAG AGGTGCGCAC GGCCCTGTTG 540  
 TATATCCGCT TGAACAACCT TACGGACAAA AGTGCAGAAG AGGTGCGCAC GGCCCTGTTG 600  
 45 GATCTCTGTC ACAAACAAAG AGCGAAAGGT CTCATTTTGG ATTTAAGAGG CAATGGTGGC  
 GGACTGATGC AGGCTGCTAT CGAGATAGTC AATCTGTTCG TCCTAAGGG CAAAGAGGTG 660  
 GTAACGACCA AAGGTGCGAT TGCAAGAGTC GCGTCCGTAT TTCGCACATT GACTGAACCG 720  
 ATCGACACGA AACTCCCGAT AGTAGTCCTG ATCGATGGAC AATCGGCATC TTCTCGGAG 780  
 ATTGTAGCCG GAGCACTGCA GGATATGGAC AGGGCTGTAC TGATGGGACA AAAGAGCTAT 840  
 50 GGCAAGGGG TTGTACAAAC GACTCGTCAG CTACCATACA ACGGCGTGAT CAAATTGACT  
 ACGGCCAAGT ACTACATCCC AAGCGGACGT TGTATTCAAC GTTTGGACTA CAGCCGACCC 900  
 AATCGGACAG GTATGGCAAC GGCCATTCCCT GACAGTCTGC ACAAAATCTT TTACTGCT 960  
 GCCGGAAGAC GTGTAGAAGA TGCAAGAGGA ATCCTGCCTG ACATCGAGGT CAAACAAGAT 1020  
 ACAGCTGCGA CATTACTTTA TTATATGGCC ATCAATATG ACGTTTCGA TTTCGTCACA 1080  
 55 GGTATGTGTC TCAAGCATAA AACGATTGCC AAGCCGAGG ATTTTCCAT AACGAACGAG  
 GACTATGCGC CTTTCTGCAA GATGATGGAA GAAAAGAAAT TTGACTATGA TCGCCAGAGT 1140  
 GGCAAGATGC TTGACAACTG GGAGGAAGTG GCTAAGATAG AAGGCTACCT GCCGGAAGCC 1200  
 AACTCGGAGC TTAAGCACT ACAGCAAAAG CTAACACCCA ACCTGTCCG TGATCTGCTA 1260  
 CGATTCAAAA AGGAGATAAC AACTATCTC AACAATGAGA TTGTCACTCG CTATTATTAT 1320  
 60 GAGCGAGGCA GTATCCGCCA GAGTTTGGCG GAAGATAAGG TAGTCAAGA AGCTATTAAG  
 CTGCTGAAG ACCATCCGGA ACAAATTCGA CAGATCCTTG CAGCTCCGAA AGCAGAGAA 1380  
 AAAGGG 1440  
 1746

## (2) INFORMATION FOR SEQ ID NO:35

- 65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2955 base pairs  
 (B) TYPE: nucleic acid  
 70 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 75

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...2955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35

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GTAACAGACA AAATGCCAAA CAAAGGATTT GTGATTGTTA TCACATCGGC TCTGGCCATC 60  
 ATCTGTGCGT TTTACCTGTC ATTCTCTTTC GTTACGAACC GTTACGAAAA GAAGGCTAAG 120  
 GCGATGGGCG ATGTTGCCGG AATGGCCTAT CTTGATTCCA TGTCGAATGA GAAGGTCTGG 180  
 TTCGGCTACA CGCTGAAAGA AGCTCAAGCC CAGCAAATTG GTCTTGGCCT TGACTTAAAG 240  
 GGGGGTATGA ACGTTATCTT GAAACTTAAC GCAAGCGATC TGCTTCGTAA CCTCTCTAAC 300  
 AAAAGTTTGG ATCCCAACTT CAACAAGCT CTGAGAATG CTGCCAAGAG CACGGAGCAA 360  
 TCCGACTTCA TCGATATTTT CGTGAAGGAA TATCGCAAGC TCGATCCCAA CGGTGCGTTG 420  
 GCGGTATCTT TCGGTTCCGG TGACCTTCGC GACCAGATTA CCGCAAAGTC TACGGATGCA 480  
 GACSTAGTGC GTCTGCTCAA AGAAAAATAT AATAGTGCTG TAGAAGCTTC GTTCAATGTG 540  
 CTCGGTGCTC GTATCGATGC TTTCGGTGTG GTTGACCTTA ATTTGCAGCG ATTGGAAGGG 600  
 CRAAGGCGTA TCGTTGTGCA ACTCCCGGA GTGAAAGACC CTGAGCGTGT TCGTACCTTT 660  
 TTGCAACGCA GTGCCAACCT ACAGTTCTGG CGTACATACA AATTGGAAGA GGTGAGCGGA 720  
 GACTTGATCG CTGCCAATGA TCGTCTGAGC GAATTGGCTA TGAACAACAC GGATGCTACC 780  
 CCGGAAACAG AGCCTGCAAC TACTGACTCT GTAGCTGCAA CAGCCGATTC TGCTGCTGTA 840  
 CAAGCTGTAG CTGATTCTGC TAC1GTAGCA CAAAAGAGGG CCAAGGATGC TACTCGTAAA 900  
 GACGCTACTT TCTCTCTGCT TACTCCCGTG AATCGTGCGG GTGCAGTAGT GGGTGTGGCT 960  
 CGTCTGTCTA ATATGGCTCA GATATCTGAA ATGCTCCAGC AAGCTCACGA TCTGAAGGTT 1020  
 ACACGTGAAG ATGTGCTTTT CCTCTGGGCT GCTAAAGCAA TCGAAGACCC CGAAACCAAA 1080  
 AAGGAGACCG ACCTCTACGA ACTCTATGCT ATTCGTACCA ATCGTACGGG AGATCCTGAT 1140  
 TTGGGAGGTG ATGTAGTGAC TTCCGCCAAG AGTGATATCC AAAATGACTT CGGTGCTTCC 1200  
 GAACCGATCG TTTCGATGAC GATGAATGAA GAAGGTGCTC GTAAATGGGC GCGTATCACA 1260  
 AAGGATAACG TGGGACGGGC AATCGCTATC GTTTTGGATG GTGTGGTTTA TTCTGCTCCG 1320  
 AACGTGAATG ATGAGATCAC GGGCGGTGCG TCTCAGATCT CCGGGCACTT CACCGTGGAG 1380  
 GAGGCGGTG ACCTTGCCAA CGTACTCAAC TCCGGTAAAA TGGATGCTAC GGTAAAGCATC 1440  
 GAACAGGAAA ACGTGATTGG TCCTACGCTG GGTGCCGAGT CCATTAAAGC CGGATTCCTG 1500  
 TCGTTCCCTG TCGCTTTGGT TATCCTGATG TGTACATGT GTCTGGCTTA CGGTTCTTG 1560  
 CGGGGTCTTA TCGCAACCGG CGCATTGATT GTAAACAGCT TCTTACATT GGGCGTATTG 1620  
 GCTTCTTTCC ATGCCGTGCT GACCTCTCG GGTATCGCAG GTTTGGTGTG GACGCTGGGT 1680  
 ATGGCTGTGG ATGCCAAGCT ACTTATCTTC GAGCGTATCA AAGAAGAGCT TCGTGCCGGT 1740  
 AAGACTCCGA TTCTGTGCCGT TACGGATGCT TATGGCAACG CTTTCTCTGC CATCTTCGAC 1800  
 TCGAACGTTA CGACTATTAT TACCGGTATC ATCCTATTCC TCTACGGGAC GGGGCCGATT 1860  
 CGCGGTTTTC CCACTACGTT GATTATCGGT CTTATCGCTT CTTTCATTAC GGC1GTCTTC 1920  
 TTGACTCGTA TCGTCTTGA GAACTGGCG AAAAAAGGTC GTTTGGATTA GATTACATTC 1980  
 ACTACGAGCA TTACTCGCAA TCTCCTTGTC AATCCCTCAT ACAACATCTT GGGTAAGCGC 2040  
 AAGACCGGCT TTATCATTCC GGTGATTATC ATCGTTTGG CACTTATAGC TTCATTTACA 2100  
 ATCGGTCTCA ATAGGGGTAT TGAATTCTCC GGAGGACGTA ACTACGTAAGT TAAATTCGAC 2160  
 CAGCCTGTAT CTTCCGAAGC CGTTCGTTCC GCCTTGCTTT CTCCCTGCA GGAAGAGGTA 2220  
 TTGTTTACCT CCATCGGTAC TGAAGGGACA GAGGTGCGTA TATCTACGAA CTATAAGATC 2280  
 CAGGAGGAAA GCGAAGAAAC TGAAGCAGAG ATTAAGTACA AATTGTATCA GAGCCTGAAA 2340  
 GGTTTCTACA CCCAGCAGCC TACTGCTGAT CAGTTCTTGG ACAATATCAT TAGCTCTCAG 2400  
 AAAGTAAGTC CCAATATGTC GAGTGACATC ACGAGAGGTG CTATTTGGGC TGTGCTGTTA 2460  
 TCGATGATCT TCAATGGCCAT TTATATCTG ATTCTGCTTC GTGACATTTT TTTCTCTGCC 2520  
 GGGGTATTCT TATCTGTGGC CGCTACTACA TTCTGCATTA TTGCTCTGTA TCGGTTGCTG 2580  
 TGGAAGATTCT TGCCCTTCAC CATGGAGATC GATCAGAACT TCATCGCTGC TATCTGGGCT 2640  
 ATCATCGGTT ACTCGCTCAA TGACACCGTG GTTGATTTG ACCGTATCOG AGAGACGATG 2700  
 AAATTGTACC CCAACAGAGA TCGCTATCAG GTGATCAACG ATGCCCTTAA TTCAACATTG 2760  
 GGTCCGAACAT TAAATACGTC TTGACTACG TTTATCGTTA TGTGGTAAAT CTTCACTTTT 2820  
 GGAGGTGCTA CGATGCGTAG TTTCAGTTTC TCGATCCTGC TCGGTATCGT TATCGGTACA 2880  
 TACTCTACGC TCTTTGTTGC TACACCCCTT GCCTACGAGA TCCAAAGCG CAAGCTCAAC 2940  
 AAAGCAGCTA AGAAA 2955

(2) INFORMATION FOR SEQ ID NO:36

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3138 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

SUBSTITUTE SHEET (Rule 26) (RO/AU)

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORPHYROMONAS GINGIVALIS

5 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...3138

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36

GACTTCCCTT	GGGTAGGGT	AAAACCGGAG	AAGAAAGAA	AACAACATAA	CAGTAATAAT	60
TTTAAGTTTA	ACGCAAAAGA	AAAGTCTATG	AAAAGAATGA	CGCTATTCTT	CCTTTGCTTG	120
CTGACGAGCA	TTGGGTGGGC	TATGGCCAG	AATAGAACCG	TGAGGGGTAC	AGTTATCTCC	180
TCCGAGGATA	ATGAGCCCT	GATCGGCGCG	AATGTCTGG	TTGTCCGAAA	CACCACTATC	240
GGTGCTGCAA	CGACTTGGG	TGGCACTTC	ACGCTTAGCG	TGCCTGCCAA	TGCCAAAATG	300
TTGAGAGTGT	CCTATTCCGG	TATGACTACC	AAAGAGGTGG	CCATCGCTAA	TGTGATGAAG	360
ATCGTACTGG	ATCCGGAATC	TAAGGTTCTG	GAGCAGGTAG	TTGTATTGGG	TTACGGTACG	420
GGACAGAAAC	TCAGCACTGT	TTCCGGTTCT	GTGGCCAAAG	TGTCCAGCGA	AAAGCTCGCG	480
GAAGAGCCCG	TTGCCAATAT	CATGGATGCC	CTCCAAGGTC	AGGTAGCCGG	TATGCAGGTT	540
ATGACTACTAT	CCGGTGACCC	TACTGCCGTC	GCTTCTGTGG	AGATCCATGG	TACAGGGTGG	600
TTGGGGGCAA	GCTCTGCACC	ATTGTATATC	GTGGATGGTA	TGCAAACTTC	TTTGGATGTT	660
GTGGCTACGA	TGAATCCGAA	TGATTTTGAA	TCTATGTCCG	TTTGAAGA	TGCTTCTGCA	720
ACATCTATTT	ATGGAGCTCG	TGCTGCAAA	GGAGTCGTTT	TCATTCAAA	GAAGAAAGGT	780
AAAATGAGCG	AGAGAGGTGG	TATTACCTTT	AATGCCAGTT	ACGGGATTTC	TCAATCCTG	840
AAATAAAGC	CCCTTGATAA	TATGATGACT	GGAGATGAAT	TGCTGGATT	TCAGGTGAAG	900
GCTAGGTTTT	GGGGGAACAA	TCAAACCGTT	CAGAAGGTTA	AAGATATGAT	CCTTGCCGGA	960
GCTGAAGATT	TGATGGCAA	TTATGATTCT	TTGAAGATG	AGTATGGTAA	GACATTGTTC	1020
CCAGTGGATT	TTAATCATGA	TGCAGACTGG	CTCAAGGCTT	TGTTAAAC	AGCACCCACC	1080
AGTCAAGGTC	ATATTCTTTT	CTCCGGAGGG	TCTCAGGGAA	CTTCATATTA	TGCCCTCTATA	1140
GGCTACTTCG	ATCAGGAAGG	TATGGCTCGT	GAACCGGCAA	ATTTAAGCG	GTATAGTGGC	1200
CGGCTCAATC	TGAAAGTCG	TATCAATGAA	TGGCTGAAAG	TTGGTGCAAA	TTTGTCTGGT	1260
TTCGATAGCGA	ATAGACGATC	TGCCGACTAT	TTTGAAAGT	ATTATATGGG	GTCAGGTACT	1320
GGCGGTGTTT	TAAAGATGCC	TGTTTATTAT	AACCTTTTGG	ATGTGAATGG	GGATTAGCA	1380
ATGTGTCTATT	ACATGTATGG	AGCTACCGA	CCTTCTATGA	CAGAACCGTA	CTTCGCAAAA	1440
ATGAGACCGT	TCAGTTCCGA	ATCACATCAG	GCCAAATGTA	ATGGTTTCGC	CCAGATTACT	1500
CCGATCAAGG	GCCTTACTTT	AAAGGCACAG	GCTGGTGTTC	ATATTACTAA	TACTCGCACT	1560
TCTTCTAAGA	GAATGCCCAA	TAATCCGTAT	GATTCTACTC	CTCTGGGGA	AAGAAGAGAA	1620
AGAGCTTATC	GAGATGTTAG	CAAGTCTTTT	ACAAATACGG	CTGAATATAA	GTTTCAATTT	1680
GATGAAAAAC	ATGATCTTAC	AGCATTGATG	GGGCATGAA	ATATTGAATA	TGAAGGGGAT	1740
GTTATTGGGG	CATCTTCTAA	AGGATTGAA	AGTGATAAGT	TGATGTTACT	GAGCCAGGGA	1800
AAACCGGAA	ATAGTTTGTC	TTTGCCCTGAA	CACAGAGTCG	CTGAATATGC	CTATTTGTCT	1860
TTCTTTAGTC	GTTTAAATTA	CGGTTTGGAC	AAATGGATGT	ATATAGATT	CTCTGTTCTG	1920
AATGACCAAT	CCTCTCGATT	CGGATCCAAT	AATAGAAAGC	CGTGGTTCTA	TTCTGTCGGT	1980
GGATGTTTG	ACATATATAA	TAAATTCATT	CAAGAAAGTA	ATTGGCTCAG	TGATCTTCGA	2040
CTGAAATAGA	GTTATGGTAC	AACGGGTAA	TGGGAGATTG	GTAATTACAA	CCACCAAGCA	2100
CTCGTTACTG	TGAACAATTA	TACTGAAGAT	GCTATGGGCG	TTAGCATTTT	TACAGCAGGC	2160
AAACCGGACC	TCTCGTGGGA	AAAGCACTCT	CAGTTCAACT	TGGGTTTGGC	TGCAGGGGCT	2220
TTCAATATTC	GCTTATCTGC	AGAGGTAGAT	TTCTATGTCC	GCACATACGA	TGATATGTTG	2280
ATTGATGTCC	CGATGCCTTA	TATCAGTGGT	TTCTTCTCAC	AGTATCAGAA	TGTAGGCTCT	2340
ATGAAATAA	CGGGTGTAGA	CCTTCTCTTT	AAGGGGACGA	TCTACCAAAA	TAAGSACTGG	2400
AATGTATATG	CTTCTGCGAA	TTTCAACTAC	AATAGACAGG	AAATAACAAA	GCTTTTCTTC	2460
GGTCTCAATA	AGTACATGTT	GCCTAATACC	GGTACTATAT	GGGAAATTGG	GTACCCCAAT	2520
TCGTCTTATA	TGGCTGAATA	TGCTGGAAATC	GACAAAAAAA	CCGGTAAGCA	GTTGTGGTAT	2580
GTTCTCTGGT	AAGTCGATGC	GGATGCTAAT	AAAGTTACAA	CAAGCCAGTA	CTCAGCTGAC	2640
TTGGAGACAC	GAATGTATAA	GTCTGTACT	CCTCCTAATA	CAGGTGGTTT	CTCCTTAGGT	2700
GCTTCTTGGG	AAGGACTTTC	TTTAGATGCT	GATTTTGCTT	ACATCGTTGG	TAAATGGATG	2760
ATCAATAATG	ACGTTACTT	TACAGAGAAT	GCAGGTGGAT	TGATGCAATT	AAATAAGAT	2820
AAATGCTAT	TGAATGCCCTG	GACAGAGGAT	AATAAAGAAA	CAGATGTTCC	AAATTTGGGA	2880
CAGTCTCTCT	AGTTTGATAC	GCATTTGTTG	GAGAATGCTT	CTTTCCTGCG	TTTGAAGAAT	2940
CTCAAACTCA	CCTATGTACT	CCCCAATAGT	CTTTTGTCTG	GGCAGAAATG	GATTGGTGGA	3000
GCTCGTGTCT	ATTTGATGGC	GCGCAATCTG	TTAACTGTTA	CAGAGTATAA	AGGCTTTGAC	3060
CTTGAAGCAG	GGGGGAATGT	GGGAAAAAAT	CAATATCCTA	ATTCTAAGCA	GTACGTTGGC	3120
GGTATTCACT	TGCTTTTC					3138

(2) INFORMATION FOR SEQ ID NO:37

(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2607 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (Rule 26) (RO/AU)



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(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38

CTTTCGTACA	GTGGAGAGAG	CGATGCAAAA	GAGTCTGATC	AGAATTGCCG	GAAATGTACC	60
TTCATCGGCT	TTGAAAAACG	AGTAAATACG	ATGCGACTGA	TCAAGGCTTT	TCTCGTGCAA	120
CTCTTACTGC	TCCCCATTTT	CTTCTACAAG	CGGTTTATAT	CGCCGCTTAC	ACCGCTTCA	180
TGCGGGTTTA	CCCCCTCATG	TTCGTCTAT	GCCATCGAAG	CCTTACGTAA	ATATGGCCCG	240
GGCAAGGAC	TATTGCTGAG	CATCAAGCGT	ATTCTCCGCT	GTGACCCGTC	GGGTGGAAGT	300
GGCTATGACC	CCGTTCCG					318

(2) INFORMATION FOR SEQ ID NO:39

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2583 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39

TTAGAGATGG	CATACGACTT	TACACAAACA	TTCCGCAACA	GCCTGGAGTA	CAGCTATCAG	60
GAAGCAACCC	GTCTCGGCGT	CGTAGCCGTG	ACGCAAGATA	TGCTCGTACT	CGGTATCATT	120
CGCGACGGAG	ACAATGGCGC	GATCGACATC	ATGCGGCACT	ATGGGATCAA	CTTGTACGAA	180
CTCAACCGGT	TGATCGAGTT	GGAAGCCATC	GCCGAGAGTT	TGCTGCTTTC	GCCTGAGGGA	240
TGCGCCATCT	TCACCCCTTC	GGCTCGGGAG	GCTATCGATG	ATGCCACAGA	CATCTGTGCC	300
GACATGGAGG	ACGAGGCCGT	CAGCCCGGTC	CATCTGTTGC	TGAGTATCCT	CAACTCGACA	360
CAGGAGAGCT	TAGTACAAAA	GATAITTTAT	AAACAAGGTA	TAAAAATAGA	CACCATCCTG	420
TCGGATTACT	TCGGACAGCG	CAACCCCTCC	GAAGGGAAGT	CTCCCTCCGA	AATGGAGATC	480
CTCGACGGGT	ACCAAGACAA	CGACTTCGAC	GACGAAGAGG	ACGAATCCTC	TCCGCCTTCC	540
GGGAATAGCG	CGACAGGCGG	AGGCTCCGGC	GACGCCCCCG	AACAGAATAC	CGGCGGAGGC	600
GATACTACCA	CCACGACACG	GAGTGGAGGC	GACACGCCCTG	CACTGGACAC	CTTCGGCACC	660
GACATCACTG	CCATGGCGGC	AGCAGGCAAG	CTCGACCCCG	TAGTGGGTGG	GGAGCAGGAG	720
ATCGAAAGGG	TGATACAGAT	ACTCAGCCGG	CGCAAAAAGA	ACAATCCGGT	GCTCATCGGC	780
GAACCCGGTG	TAGGCAAGAG	TGCCATCGTG	GAAGGACTGG	CCGAACCGAT	CGTGAACAGG	840
AAGSTGAGCC	GTATTCTTTT	CGACAAGCGG	ATCATCAGCC	TCGATTGGGC	TCAGATGGTA	900
GCCCGCACCA	AATATCGCGG	ACAGTTGCAA	GAGCGGTTGA	TAAGCGTGCT	CAATGAGCTG	960
AAGAAGAATC	CGCAGATCAT	CCTCTTCATC	GACGAGATAC	ATACCATCGT	GGGAGCAGGC	1020
TCTGCAGCCG	GATCGATGGA	TACGGCCAAT	ATGCTCAAAC	CCGCTCTTGC	CCGTGGACAG	1080
GTACAGTGCA	TCGGAGCCAC	TACGCTGGAT	GAGTATCGTA	AGAACATAGA	AAAGGACGGA	1140
GCACTCGAAC	GCGGCTTCCA	GAAGGTGCGG	ATAGCCCCCT	CGACTGCAGA	AGAAACGCTG	1200
ACCATCCTCG	AAACATCAA	AGAGAAATAC	GAGGACTATC	ACGGTGACG	CTATACGGAC	1260
GAAGCGATCA	AAGCGGCAGT	GGAAGTGAAC	GATCGCTATG	TATCCGATCG	TTTCTTCCCA	1320
GATAAGGCGA	TAGATGCCAT	GGACGAGGCT	GGCGCGAGCG	TCCATATCAC	CAATGTGGTG	1380
GCTCCGAAG	AAATCGAGAT	ACTGGAGGCC	GAATTGGCAT	CGGTGCGAGA	GAACAAGCTC	1440
TGCGCCGTAA	AGGCTCAGAA	CTACGAACTG	GCTGCCTCCT	TCCGCGATCA	GGAGCGGCGC	1500
ACTCAGCAGC	AGATAGCGGA	AGAGAAGAAA	AAATGGGAAG	AGCAGATGTC	CAAGCACCGC	1560
GAGACCGTGG	ACGAGAATGT	AGTGGCGCAT	GTAGTGGCGT	TGATGACAGG	CGTTCGGGCT	1620
GAGCGGCTGA	GCACGGGCGA	AGCGCAACGT	CTGCGCACGA	TGGCAGATGA	TCTCAAGACC	1680
AAAGTAGTAG	GTCAAGGACAC	AGCCATCGAA	AAGATGGTGC	ATGCCATCCA	CGCAATCGT	1740
CTGGGACTTC	GCAATGAAAA	GAAACCGATC	GGTTCTTTCC	TTTTCTCTCG	CCCCACGGGG	1800
GTAGGCAAGA	CCTATTGTCG	CAAGAAGCTC	CGCGAATACC	TGTTGAGGGA	TGAGAATGCC	1860
ATGATCAGGG	TGCATATGAG	CGAGTATATG	GAGAAGTTCT	CGGTTTCGGG	TCTCGTGGGT	1920
GCCCCCTCGG	GATATGTGGG	CTATGAAGAA	GGCGGCCAAC	TGAAGGAGCG	CGTAAGACGC	1980
AAACCTTATT	CCGTGGTTCT	CTTGGATGAG	ATCGAAAAGG	CGCATGCCGA	TGTCTTCAAT	2040
CTGCTCTTAC	AGGTGATGGA	CGAAGGTGAG	CTGACCGACA	GTCTGGGACG	GGCGGTGAAT	2100
TTCAAGAACA	CCGTGATCAT	CATCACCTCC	AACGTGGGTA	CAGCCAGGCT	CAAAGACTTC	2160





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## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...897

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41

```

TTAAAAAGG AGATAACTAT GAAACAGAAC TACTTCAAAA GAGTCTGCTC ACTGCTTTGG      60
CTGGTTTAC CCATGCTTAT TATGCCATTG GAAGTAGCAG CTCAGAGAT TATCCGAAC      120
GAAGAGCTGT TGAATCATT GACTTTCGTT GCACCGGTTG AGGAGACAGA CGCAATAGAG      180
GCAGAGGTAG AAGCTCTGCA GGAGATAGTC GCTACTGAGG AGATTGCGGA GCAGGCTGTT      240
CGTTCTTTATA CTTACACGGT CTATCGTGAT GGCCTGAAGA TTGCTTCAGG ATTGACTGAG      300
CCCACTTTTC TCGATGAAGA TGTTCTGCGC GCGGAACATA CCTACTGCGT AGAAGTACAG      360
TATCAGGGAG GCGTATCCGA CAAAGTATGC GTGGACGTAG AGGTGAAGGA CTTCAAACCG      420
GTTACCAATC TCACCGGAAC TGCTTCCAAT GACGAAGTTT CTTTGGACTG GGACGGTGTG      480
15 GAAGAGAAAG CTGAAGAGCC GGCAAGTGAT AAAGCAGTCA GCTACAACGT CTACAAGAA      540
GGAACCTTGA TCGGTAATAC AGCTGAAACT CATATGTGG AGACCGGTGT AGCCAATGGT      600
ACATACATCT ACGAAGTGA AGTAAAGTAT CCTGACGGTG TATCTCCGAA GGTGGCTGTA      660
ACCGTGACCG TGACCAACAG CTCATTGAGC AATGTAGATG GACAGGCTCC TTACACATTG      720
CGAGTAGAAG GCAAGAAGAT TATTGCGGAA GCCCATGGTA TGATCACGCT CTACGACATC      780
20 AACGGACGTA CCGTGGCGGT AGCCCCGAAT CGATTGGAAT ACATGGCGCA AACCGGTTTC      840
TATGCAGTGC GCTTCGATGT GGGGAATAAA CACCATGTAT CGAAAAATACA AGTAAGA      897

```

## 25 (2) INFORMATION FOR SEQ ID NO:42

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1131 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

## 30 (ii) MOLECULE TYPE: DNA (genomic)

## 35 (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## 40 (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...1131

## 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42

```

TTGTTTAATC ATAAAAAATC ATGGTATGAA ACATTTCAAT TTTATCTCGT TGTTTTCCGC      60
TCTGGCTTTA TTCTTTTGTG TGAAAAATACC CTTGCACAAC AAAAAACAGA GGAGTTTGCA      120
CCTGTGTCCG ATTACGTGC AGAAGCGTAC GGCTCTACCG TTTCTCCTCA CTGGACTCCG      180
CCGTATGACA ATCCGATGAT TCCTCTAAGC GAGAGTTTGG AATCAGGTAT TCCAGCTATA      240
TGGAAGACCA TTGACGCAGA TGGCGATGGC TATAATTGGA TGCATTGAC CAATTCACG      300
GGACAGAGTG GTCTCTGTGT CTCTTCGGCT TCATACATAG GCGCGGTCCG AGCTTTGACT      360
COGGACAATT ATCTGATAAC ACCCGAATTA AAACATACCA CAGACGCGTT GGTGGAAATA      420
ATCTAATGGG TATGTACTCA AGATCTCACT GCTCCATCCG AGCACTATGC CGTTTATTCC      480
TCTTCTACAG GCAATAATGC TGCTGACTTT GTTAATCTCT TATATGAAGA GACTTTGACT      540
GCCAAACGGA TACAATCCCC CGAGTTGATC CCGGGAATC GGACACAAGG TGTTTGGTAT      600
CAAAGAAAGG TGGTACTCCC TAACGATACT AAATATGTTG CTTTCCGCCA TTTTAATTCC      660
ACGGATAAAT TCTGGCTCAA TTTGGATGAA GTATCTATCC TGTATACCCC TCTTCCCCGA      720
AGAGCTCCGT GTCCGCATCC GGGTGGTTAC ACTTATCTCT TATTCCGTGA TGGACAAAAG      780
ATAGCGAGTG GATTGTCCGC ATTGGCATAT ATCGATACGG ATGTACCGTA TGGGACTCAA      840
GACTATTGTG TCCAAGTCAA TTATCTGCAA GGAGACTCGT ATAAAGTCTG CAAAAATATA      900
GTGGTGGCAA ATTCTGCAA CATCTATGGG GCGGATAAGC CTTTTCGCTT GACCGTGGTT      960
GGCAAGACCA TTGTAGCGAG TGCTTTCAA GGAGAGATCA CTCITTATGA CATTCGTGGC      1020
CGGCTGATAG CTTCCGGCTG CGATACGCTT AGGTACAAAG CGGAAATGG TTTTACCTC      1080
65 ATTAAATAC AGGTAACCG AACTGTCTAT ACTGAGAAAA TCCAAATCCA A      1131

```

## (2) INFORMATION FOR SEQ ID NO:43

## 70 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2547 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

75

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(ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 5 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS  
 10 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2547  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43

15	TTCCGSAATAT	CACCTTCAAT	GAAAAAAGT	TTTCTTTTAG	CCATAGTAAT	GCTCTTTGGC	60
	ATTGCCATGC	AGGGACATTC	TGCTCCGGTT	ACGAAAGAGC	GAGCTTTGAG	TCTGGCTCGG	120
	CTGGCTTTGG	GACAGGTATC	CTTGGGAATG	GGACAAACAG	CAGTATCTGA	CAAGATTTC	180
	ATCGATTACG	TTTATCGGCA	AGGAGATGCT	GAGAGGGGTA	TCACATCACA	AGAGGAAGGC	240
20	TCTCCTGCAT	ATTTTATGT	ACCTAATCGT	GGAAATAATG	AGGGCTATGC	TCTTGTAGCA	300
	GCAGATGACA	GAATACCGAC	AATTTTAGCC	TATTCACCCA	TTGGCCGTTT	CGACATGGAC	360
	AGTATGCCGG	ACAATCTTCG	CATGTGGCTA	CAAAATTACG	ATCAGGAAAT	AGGCCGTGTA	420
	CTTTCCGGAA	AAGCTCAGCT	CAATGAAGAG	ATATTACGTA	CCGAGGGCGT	ACCGGCTGAA	480
	GTACATGCTC	TGATGGATAA	CGGTCAITTT	GCCAACGATC	CCATGCGATG	GAATCAAGGT	540
25	TACCCATGSA	ACAATAAGGA	ACCACTGCTT	CCTAATGGCA	ATCATGCCTA	TACCGGCTGT	600
	GTGCTACTG	CTGCAGCACA	AATCATGCGC	TACCATAGCT	GGCCGCTTCA	AGGTGAAGGC	660
	TCTTTGATT	ATCATGCAGG	TTCAATAGTT	GGCAACTGGT	CCGGCACATT	TGTTGAAATG	720
	TACGACTGSA	TCAATATGCC	CGGAAATCCC	GACCTTGATA	ATCTGACTCA	ATCTCAAGTG	780
	GATGCCTACG	CCACACTGAT	GCGTGATGTG	AGTGCACTCG	TTTCGATGAG	TTTTTATGAA	840
30	AATGGAAGTG	GTACGTACAG	CGTTTATGTA	GTAGGAGCCT	TGCGAAACAA	CTTTCGCTAC	900
	AAGCGTTCAC	TGCAGCTACA	TGTACGGGCC	TTATATACCT	CACAGGAGTG	GCACGATATG	960
	ATCCGCGGGG	AACTTGCCCTC	CGGAAGGCCG	GTCTATTATG	CAGGGAATAA	CCAGAGCATA	1020
	GGACATGCTT	TGCTTTGCGA	TGGTTATGCT	TGGGATGGTA	CTTTCCATT	CAACTGGGGT	1080
	TGGGAGGGTG	TTTCCAACGG	CTTCTACAAA	CTAACACTCC	TCTCGCGGAC	TTCTTTGGGT	1140
35	ATCGGAGGTA	AGGGAATAGG	TTTTACCATT	TATCAAGAGA	TCATCACCGG	TATCGAACCG	1200
	GCTAAGACTC	CCGCTGAAGC	CGGTACAGAT	GCCTTGCCGA	TCTTGCCACT	GAAAGACATA	1260
	GAAGCCGAGT	ATAAAAGTGA	ATCCGGATTG	AACGTAGGGT	ATTGATATA	TAATACAGGT	1320
	GAGAGGCAAT	CAATCTCTGA	CCTCGGATAC	AGATTGAACA	AGGCTGACGG	AGAAGTCATA	1380
	GAGGTGAAAA	CTTCATCTAT	CAATATCTCT	TGGTACGGAT	ACGGAGAGCA	TCCGAGAGT	1440
40	TTCTCATTTG	CACCTAATCA	GTTGTCACAA	GGAAATCAACA	CCATCACCOCT	ACTTTATCGT	1500
	CGCACAGGCA	CGGAACAGTG	GGAGCCGGTA	CGGCATGCAC	AGGGAGGATA	TGTCAATAGC	1560
	ATTAAGATAA	ATACGACAGA	CCCGAACAAAT	GTCTAGTCA	CGGTAGATAA	TAACGAAGGC	1620
	AAGCTCAGTA	TGCTCCCAAA	CAGCTTTGTC	GCAGATCTGA	ATTCTTATGA	ACATAGTACG	1680
	ATTACAGTAC	AGTTCAATAG	CGACAGCCCT	GATGAGATCC	GTACACCCGT	AGCCTTTGCT	1740
45	CTATCTACAG	GAGCTACTGC	GGACGATGTA	ATATCTTTGG	GCTGGGTAA	GGCTGAAGTT	1800
	CCGGGCGGTA	GCAGCAACTA	TCCGGTGGTT	TGGTCTAAAG	ACGTTCTCAC	TCTCTCGGAA	1860
	GSCGACTATA	CATTGTGGTA	TAGATTTTCC	ATCAACAACC	AAAAGGATGA	ATGCAAAAAG	1920
	ATCGGAAGCG	TGTCAGTAAA	AACACCGACA	GAGTATACGC	AUCCCTTATT	CGAAGTGGGC	1980
	CATAATGACA	CTTCTACCTA	TACGCTGGAT	ATGGCACACA	ACAGAGTATT	GCCCCACTTT	2040
50	CACTCAAAA	ATCTCGGATT	GCCTTTCAAT	GGTGAGTTGG	TTGTTGTTT	CCGCCAACA	2100
	CAATCCTCAT	CGGGTCTTT	ATGGGAGCT	CAAGAAACAG	TACATATCAA	GCAAGGAGAA	2160
	ACTTTCGTAT	ATAAACCTGT	TGTCGAAGGC	CCTATACCTG	ATGGATCCTA	TCGTGCGACC	2220
	CTCCATGCAT	TCGTAAACGG	ACAACAACAG	TTGTACCTCA	AGGGGAAAAG	GAACCTACAG	2280
	GTGAAGATCG	TCAATGGTAC	AGCCGTAGAA	GCAATAGAA	CGTCAGAAGA	GATCAGAGTA	2340
55	TTCCCTAATC	CGGCACGCGA	TTATGTGGAA	ATATCGGCAC	CTTGCAATCC	CCAAGAAACA	2400
	TCTATCATTC	TTTTCGATCT	GTCAAGCAAG	ATTGTCATGA	AGAATAGTTT	ATCAGCGGGG	2460
	CATGGCAGAA	TGGATGTGAG	CCGACTTCCT	AATGGGGCCT	ACATCCTTAA	GGTGGATGGA	2520
	TATACGACGA	AAATAAATAT	AGTGACAC				2547

(2) INFORMATION FOR SEQ ID NO:44

(1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 885 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 65 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 70 (vi) ORIGINAL SOURCE:  
 75

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(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

5 (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...885

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44

10 ACGAAGAAAA CACTGATGAA AAAGCTATT CTCTCGCTCA CGAGTCTTGT AATGGTCTTC 60  
GCTGTTGCAA GTTGGGATAT AATCGACAAG GATCAAACCC TCTTGCCGGC TCCGACCAAT 120  
GTGACACCCG ATAATCCGGA TGACAATCCT TCGGAGATCG ACATTACGCA GACGCACACA 180  
GAAAAATATG TTTTGGCTGA AGAATTTACC GGCCAAAAT GTCTCACTG TCCGAAAGGT 240  
CATGCCAAAC TGGCGGCTCT CAAGGAGCAA TACGGTAAGA GATTGACTGT TGTCGGTATA 300  
CATGCCGGCC CTGGATCTCT CGTGCCACCT CTTTCCGTA CAGAAGCCGG AGACGCATAT 360  
15 TATAGCAAGT TCGCCAATAA TACCCCTCTC CTGCGCTGA TGGTTTCGGC CAAAAAGTTC 420  
GGCTCTTCT ACCTTTATGA TAAGAGCTAC AAAACGTGGG ACGTGCCAT TCCGAGCAG 480  
ATGGAGCAAA AGGCGAAGAT CAATATCTTT GCCGTGGCCG AATACACCGA TACCCAAAAG 540  
ATCAAGTGA CTGTAAAGG TAAATACTG GAGGGGAATA CACTCCGAA GTCCATGGTT 600  
CAGGTGTATC TGTGGAGGA TAAGCTGATC GCTCCGAGG TGGATGGCAA TACGACGTC 660  
20 GAGAAATACG AGCACAATCA CGTGTTCGGT GGAGCCGTTA ATGGTATTG GGGCGAAGAA 720  
TTTGTGAATC TCAAAGATTA TTTGTATACT TACGCCGTTG AACCGCTCTC GGGTATGTCC 780  
TTCGTAGCCG AGAATTATTC GATTGTGGCT TTTGTATACG ATGTGCAGAC GTTCGAAAGT 840  
TATGACGTTG TGCATGTAA GATCAATCCG CAATCCGATG GCAAA 885

25

## (2) INFORMATION FOR SEQ ID NO:45

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 690 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

35 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

40

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

45 (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...690

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45

50 ACGAATAAAA AAGAAGAGAC ANTGAAGAAA TCAGTGTAG TAGCCTCAGT TTTGGCCGTG 60  
GCTCTCGTGT TCGCCGGTTG CGGACTGAAC AATATGGCAA AAGGCGGCCT TATCGGCGCC 120  
GGAGTAGGAG GTGCCATTGG TGCCGGAGTA GGTAACGTAG CCGGAATAC GGCTGTCGGT 180  
GCCATCGTGG GTACTGCAGT CGGTGGAGCA GCCGGTGCTC TCATCGGAAA GAAGATGGAC 240  
AAGCAGAAAA AAGAACTGGA GGCCGAGTA CCGATGCTA CGATTAGAC AGTAAATGAC 300  
GGAGAGGCTA TTCTGGTTAC TTTCGATAGC GGTATCTCT TTGCGACGAA CTCCAGCACT 360  
55 CTGAGTCCCA ACTCACGCAC TGGCGTGACG AAGTTTGCTG CAAACATGAA CAAAAACCC 420  
GACACGGATA TTCGTATCGT AGGCCATACG GACAATACCG GCTCCGACAA GATCAACGAT 480  
CCTCTGCTG AGAGACGTGC AGCCAGCGTA TATTCTTCC TGAATCTCA GGGTGTGAGT 540  
ATGTGGGCA TGGCAGCCGA AGGGCGTGG AGCCATGAAC CGGTTGAGA CAATAGCACA 600  
60 GTTGCCGGAC GTTCGGCCAA CCGCGTGTG GAGGTTTATA TCTTGCCGAA TGCCAAGATG 660  
ATCGAACAAG CACAGCAAGG TACGCTGAAG 690

## (2) INFORMATION FOR SEQ ID NO:46

65

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1026 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

70

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

75

(iv) ANTI-SENSE: NO

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- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 5 (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...1026
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46
- |               |            |            |            |             |            |      |
|---------------|------------|------------|------------|-------------|------------|------|
| MCAGGAACA     | GAAATATGTC | GAATAATCG  | ATCCTTCTGC | TTTGCTGTTT  | GCTGTGCTTC | 60   |
| ATTTCTGCTA    | CGAAGGCTGT | GACCCCGCTC | AGAAATGTGC | GCAATAGCCA  | AGTGAACAGC | 120  |
| AAAGCAAAGA    | CCGAACGTAC | AAAGCCCTCG | GACTCTGTAC | GGTACATTAG  | CAACATGATT | 180  |
| GCAGATCGGC    | TGGAGTTCCG | CAACAGATT  | TCTTCCGAAA | AAGAGGTAAG  | AAAAGCCGAA | 240  |
| 15 TATGAAATC  | GGCTGGCGAT | GGAAGCACTC | AATTACCCTG | CCATAGATT   | ATATGGTGAA | 300  |
| GATTCCTTGA    | GCGAGTATGT | AAACCCCTTC | GTGGGTGCAG | GAACCGATGT  | CGAAATTCCG | 360  |
| AACTCCTATG    | ACATTGATTG | CTCTTCGTTT | GTGATGCCCG | TGGAAGATAA  | GCAGGTCACC | 420  |
| TCTCAATTTG    | GCTACCGTCG | GCGTTTCGGA | CGGATGCACT | ATGGTATTGA  | TCTTTCAGTG | 480  |
| 20 AATCGTGGCG | ATACGATACG | AGCAGCCTTT | GACGGGAAAG | TTCGTGTACG  | CAGCTATGAA | 540  |
| GCGCGTGGCT    | ATGGCTACTA | CATAGTCTTG | CGCCATCCGA | ACGGACTGGA  | GACTGTGTAC | 600  |
| GGACACATGA    | GTGACCAATT | GGTAGACGAG | AATCAGATCG | TTCGAGCAGG  | ACAACCGATC | 660  |
| GGATTAGGAG    | GCAGCAGCGG | TGGAAGCACU | GGTCCTCATC | TTCACCTCGA  | GACCCGCTTC | 720  |
| ATGGGTATTG    | CCATCAATCC | GAGTACCATT | ATAGACTTCG | ATAACGGAGT  | GCCGCTCCGA | 780  |
| 25 GACATTACA  | CATTCAAACG | AGGGAGCAAT | TCTCGCTATG | CAAAAGCCCTC | TAAGACTTCT | 840  |
| TCTCGCTATG    | CAAAAAAGG  | GAAGAAAGGC | AGACAAGCTT | CTTCTCCTAT  | GACCTATAGA | 900  |
| ATCAAAAAAG    | GCGATACTTT | GGAAACAATA | GCCAAAAGGC | ACGGCACTTC  | TGTTCAAGAA | 960  |
| CTCTGTGCTA    | CCATGGGCAT | TGGCAAGAGT | AAATTTTGA  | CTCCGGGCAA  | AGCCTTGAGG | 1020 |
| ATCAAA        |            |            |            |             |            | 1026 |
- 30 (2) INFORMATION FOR SEQ ID NO:47
- (i) SEQUENCE CHARACTERISTICS:  
35 (A) LENGTH: 477 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- 40 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 45 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
50 (A) NAME/KEY: misc feature  
(B) LOCATION 1...477
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47
- |               |            |            |            |            |            |     |
|---------------|------------|------------|------------|------------|------------|-----|
| CCGAGCAAAA    | CGATAATTAA | GACAATGGCA | AAAATCAATT | TCTATGCTGA | AGGCGTCAGC | 60  |
| CTTCCTCGGA    | TCAGAAGACG | GATCGTCGGT | AAGTGGATAG | CCGAAGTATG | CAGCCGATAT | 120 |
| GGGAAAGCGG    | TGGGAGAAAT | CTCCTATCTT | TTCTGTGATG | ACGAATATAT | CCTGAAAGCC | 180 |
| AATCAGGAAT    | TTCTCGATCA | TGACTACTAC | ACCGACATCA | TCACCTTCGA | TTCTGCGGAA | 240 |
| GCGGATACGG    | TGAATGGCGA | CCTGCTTATC | AGTCTCGATA | CCGTACGCTC | GAATGCCCGT | 300 |
| 60 GCTCTTGATC | TTGATACGGA | AGACGAACTG | CATCGTGTCA | TTATCCACGG | CATACTGCAT | 360 |
| CTTTCGGGAT    | TGAAAGACAA | GAGCAAAAAG | GATGAAGCCC | AAATGCGTGC | AGCCGAAGAG | 420 |
| AAAGCCCTTG    | TCATGCTGCG | AGAAACCATC | GGATCGGAGC | TTTCCTTATT | GCATACA    | 477 |
- 65 (2) INFORMATION FOR SEQ ID NO:48
- (i) SEQUENCE CHARACTERISTICS:  
70 (A) LENGTH: 1185 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- 75 (iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48

AAAAATAAAA	CTATGAAGGT	AAAGTACTTA	ATGCTCACAT	TGGTTGGAGC	AATTGCACTG	60
AACGCAAGTG	CACAGGAGAA	TACTGTACCG	GCAACGGGGT	AGTTACCCGC	TAAGAATGTT	120
GCTTTTGCTC	GCAATAAAGC	AGGCAGCAAT	TGGTTTGTA	CACTGCAAGG	CGGTGTTGCA	180
GCGCAGTTCC	TCAATGACAA	CAACAACAAA	GACCTCATGG	ACCGCTTAGG	AGCCATAGGT	240
TCTCTTTCTG	TCGGAAAGTA	TCACAGCCCT	TTCTTTGCAA	CTCGTTTGCA	AAITTAACGGA	300
GGTCAAGCCC	ACACTTTTCT	CGGAAAAAAT	GGCGAACAA	AAATCAACAC	CAATTTTGGT	360
GCAGCTCACT	TCGACTTTAT	GTTTGATGTG	GTTAACTACT	TTGCACCATA	TCGCGAAAAAT	420
CGTTTCTTCC	ATTTAATTCC	ATGGGTAGGT	GTTGGCTACC	AACACAAATT	CATCGGTAGC	480
GAATGGAGCA	AAGACAATGT	GGAATCACTG	ACGGCGAATG	TAGGAGTTAT	GATGGGTTTC	540
AGATTAGGAA	AGCGAGTAGA	CTTTGTGATC	GAAGCACAAG	CAGCTCACTC	CAATCTCAAT	600
CTAAGTCGCG	CATACAATGC	CAAGAAAACT	CCCGTATTGG	AAGATCCCGC	AGGACGTTAT	660
TACAATGGAT	TCCAGGGGAT	GGCTACAGCA	GGTCTTAATT	TCCGCTGGG	AGCCGTAGGC	720
TTCAATGCCA	TTGAHCCAAT	GGACTACGCA	CTTATCAATG	ATCTGAATGG	TCAGATTAAAC	780
CGTTTGCGCA	GCGAGGTCGA	AGAACTCTCA	AAACGTCCTG	TATCATGCCC	CGAATGTCCCT	840
GAAGTAAGTC	CTGTTACTAA	GACAGAAAAAT	ATACTGACGG	AAAAAGCTGT	ACTGTTCCGT	900
TTGACAGCC	ACGTTGTGGA	CAAAGATCAA	TTGATCAACC	TGTATGACGT	AGCTCAGTTT	960
GTAAAAGAAA	CTAACGAGCC	GATTACCGTT	GTGGTTATG	CTGATCTTAC	GGGTAACTACT	1020
CAATACACG	AGAAAATGTC	TGAGCGTCGG	GCTAAAGCCG	TTGTTGATGT	TCGACAGGT	1080
AAATATGTTG	TGCCTTCCGA	ATTAACTCT	GTAGAATGGA	AGGGCGACTC	TACGCAACCG	1140
TTACAGCAAG	AAGCTTGGAA	TCGTGTTGTA	ATCGTTGCGT	CCAAG		1185

(2) INFORMATION FOR SEQ ID NO:49

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1161 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49

TATAAAATGA	CATACAGAA	TATGAAAGCT	AAATCTTTAT	TATTAGCACT	TGCGGGTCTC	60
GCATSCACAT	TCAGTGCAAC	AGCCCAAGAA	GCTACTACAC	AGAACAAGC	AGGATGCAC	120
ACCGCATTC	AACGTGATA	GGCCTCCGAT	CATTGGTTCA	TTGACATTGC	AGGTGGAGCA	180
GGTATGGCTC	TCTCGGATG	GAATAATGAT	GTAGACTTTG	TAGATCGTCT	AAGTATCGTT	240
CCTACTTTCC	GTATCGGTA	ATGGCATGAG	CCTTATTTCC	GTACTCGTCT	CCAATTCACA	300
GGATTTCGACA	TCTATGGATT	CCCGCAAGGG	AGCAAGGAGC	GTAAACCACAA	TTACTTTGGA	360
AACGCCACCC	TTGACTTCAT	GTTGATCTG	ACGAACTATT	TCGGTGTATA	CGTCCCAAT	420
CGTGTCTTCC	ATATCATCCC	ATGGGCAGGT	ATAGGATTTG	GTTATAAATT	CCATAGCGAA	480
AACGCCAATG	GTGAAAAAGT	AGGAAGTAAA	GATGATATGA	CCGGAACAGT	TAATGTCCGT	540
TTGATGCTGA	AAATCCGCCCT	ATCAAGACTC	GTAGACTTCA	ATATTGAAGG	ACAAGCTTTT	600
CGCGGAAAGA	TGAATTTAT	CGGGACAAAG	AGAGGAAAAG	CAGACTTCCC	TGTAATGGCT	660
ACAGCAGGTC	TAACTTCAA	CCTTGGCAAG	ACAGAGTGGA	CAGAAATTGT	TCCTATGGAC	720
TATGCTTTGG	TCAATGACCT	GAACAACCAA	ATCAACTCAC	TTCCGCTCA	AGTGAAGAG	780
TTGAGCGCTC	GTCTGTTTC	ATGCCCTGAA	TGCCCTGAGC	CTACACAGCC	TACAGTTACT	840
CGTGTAGTGT	TTGACAAATG	GGTTTACTTC	CGTATCAATA	GTGCAAGAT	TGATCGTAAT	900
CAAGAAATCA	ATGTTTACAA	TACAGCTGAA	TATGCGAAGA	CCAAACAACG	ACCGATCAAG	960
GTACTAGGTT	ACGCTGACGA	AAAAACCGGT	ACTGCGGCT	ATAACATGAA	GCTTTCAGAG	1020
CGTGTGCAAA	AAGCGGTAGC	CAAGATGCTT	GAAAAGTATG	GTGTTTCTGC	GGATCGCATT	1080
ACAATTGAAT	GGAAGGGCTC	ATCAGAGCAA	ATCTATGAAG	AGAAGCCTTG	GAATCGTATT	1140

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GTAGTAATGA CTGCAGCGGA A

1161

## 5 (2) INFORMATION FOR SEQ ID NO:50

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 585 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...585
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50

30 GTAAATGGCA TCATTATGGA ATTTTTCATG TTATTCATAG CGGCGGTTTT CGTTAATAAC 60  
 GTCGTGTCTGT CGCAGTTCCT CGGTATATGC CCATTCTTAG GCGTATCGAA GAAGGTAGAC 120  
 ACCTCAATCG GTATGGGTGC AGCCGTGACA TTCGTATTGG CACTGGCTAC CTGGTTACC 180  
 TTCCTGATTC AGAAGTTCGT TTGGATCGT TTCGGATTGG GCITTATGCA GACCATTTGCA 240  
 TTTATTTTGG TCATTGCCGC CTGGTGCAG ATGGTGGAGA TCATACTCAA GAAAGTATCT 300  
 CCTCCCTCT ATCAGGCACT GGGTGTATTC TTGCCCTTGA TTACGACGAA CTGCTGTGTG 360  
 CTCGGTGTGG CTATTTTGGT TATCCAGAAG GATTATACCC TGCTCCAGAG CTTCGTCTAT 420  
 GCAATATCCA CGGCTATCGG TTTCACCTTG GCAATGGTTA CTTCGCAGG TATTCGAGAG 480  
 35 CAACTCGATA TGACCAATCT CCCCAAAGCT ATGAAGGGAA TACCTTCGGC ACTCTTGGCT 540  
 GCCGTATAT TGGCTATGGC TTCATGGGC TTCAGCGGTA TCGCC 585

## 40 (2) INFORMATION FOR SEQ ID NO:51

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2628 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2628
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51

60 TACCGATCTT ATCGTGGGAT AGGGAGTGGG ACACACTCTC CTAACCTCAA AAACCGACTA 60  
 AAAAGGATCG GAATAAGGAT ACCGAACAGA CACTATATCC ATATCAAGCC AATCAAACCA 120  
 65 AAAAATAAAA TGAACAACCT AAACATTATC AGCTTCATCA TTGCTTTCCT ATTCTTAGGA 180  
 ACGAGCGCAT CGGCTCAGCA ATCGGGCGGA TCCGTTACAG GTACCGTAGT GGACAAVAGC 240  
 TCAAAAGAAC CTATCGCATA CGTACAGTA TTGTCAAAG GAACCACTCT CGGAACCTCC 300  
 ACGGATGCAA ACGGAAACTA CTCGATCAAG GGAATCCCTT CGGGTAATCA AACTATCGTA 360  
 GCCCGACTCA TGGGTTACTC CACTTGGCAA GAAAAAGTAC ATATAGAAAA GGGTGGTTCC 420  
 CGCCACGTAG ACCTCTATCT GACCGAAGAG ATTCTCTCTC TCGATGGGGT AGTGGTATCT 480  
 70 GCCAATAGAA ACGAGACTTT CCGCGCTCAA GCACCTCGT TGGTAACGGT ACTGTCGCGG 540  
 GAACTTTTCC TCAAAACCAA CTCTACCAAC CTGAGTCAGG GACTTAAGTT CCAGCCCGGT 600  
 CTGCGCGTGG AGGACAACTG TCAGAACTGC GGTTCACACC AAGTTCGTAT CAATGGACTC 660  
 GAAGGAGCCT ATTCCGAAAT TCTTATCGAC AGCCATCCCA TCTTCAGTTC GCTTGCCTGG 720  
 75 GTCTATGGCT TGGAGCAGAT GCCTGCCAAT ATGATCGAAC GTGTAGAAGT AATTGCGGGT 780  
 GGAGGTTCCG CTCTGTTCCG CTCTAATGCT GTGGGAGGCG TTATCAACGT AATTACGAAA 840

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GAACCGCTTC GCAATTCGGC CGAGATCAGC CATTCTACGA TGACCTTCGA CCACGCGAAA 900  
 GGGTGGGGGA GCTTCCAAAA TACGACCCAG TTCAACGGTT CTATGCTGAC GGAAGACCGC 960  
 AAAGCCGGTG TCATGGTATT CGGCCAACAC AACTACCGTC CCGGACAGGA TATAGACGGC 1020  
 GACAACTTTA CCGAACTACC CAATCTGCGC AACCGCTCGC TCGGTTTCGG CTCACTACTAT 1080  
 5 AAGACCGGTC TCTACAGCAA AGCAACCGTC GAATATCACA GCATGCAGGA GTACCGTCGT 1140  
 GGTGGCGACA GACTGGACAA TCCTCCTTTC GAAGCCGAGA TAGCGGAATA TCTCCAGCAC 1200  
 TATATCAATG GCGGAAGTTT CAAATTCGAT CAGGGCTTCA GCGGTGGCAA GGATTTCTTC 1260  
 AGTCTGTATG CTTACAGACA AGACGTTTCA CGTCGTAGCT ACTACGGGGG TGGCGACTAT 1320  
 ACCGAAAAATC TGCTGAACGG AGCAGTTTCA AGTGGGAACA CCGAATCGGA CGAATACAAC 1380  
 10 GATGCTTTCA CGGCTCTTAC TTCTACGGG ACTACCAAGG GATTCGATTT GCAAGGAGGA 1440  
 GGTATGTACC GTCATACCTT CGGAGAAAAC TGGGACTTTA CCGGCGGACT CGAATATATC 1500  
 TACCGCCAAC TCGATGACAG AAGCGGCTAC AGACCGAGCA AATAGATCA GAATACCTCT 1560  
 ACTTTTATGC AGTACGACCA GCTCGAATAT AAGACGGAGA AGTTAAGTGC CCTTATCGGA 1620  
 GCACGTATCG ACTATGTTCT CCTCAATCAG GATGGCAAAC GCTATATCGA TCCGCTCTTC 1680  
 15 ATTTTCAGTC CTAGAGCCAA CGTACGATAC AATCCCAATA AGAATCTCAG CTTCCGACTC 1740  
 TCATACAGCG AAGGATTCCG CGCTCCTCAG TATTTGATG AAGATCTGCA CGTAGAGTTG 1800  
 GCCTGGTGGTA CTCTTTCAG CCGTGTCTTT TCCCCCAATC TGAAAGAAGA ACGTTACGA 1860  
 AGCATCAGTG CTCTTTCGA TTTATACCA AGAGCCGACG AATGGCAATT CAATATCATG 1920  
 GGAGAAGCCT TCTCCACCTT TATCAGCAAT CAGTTCAAAC CATOCGATAA GGTGGAACC 1980  
 20 ACGAGCATG GCAAGAATG GATCATTCTG ACCATCTACA ACGACAAGGA TGGAGTATCG 2040  
 AAGGTATATG GTGTGAATCT GGAGGGAGA ATGCGCTACA ACAATCTGTT CGACCTCCAG 2100  
 CTGCGCGGTA CATGGCAGAG AAGCGGCTAC GGAAGCATCT ATACCGCTGT GGAAGCGGAC 2160  
 AAAACAACGG GACAAGCCGA GATCTCTGTG AAGAGCTATG TACGCACTCC GAATCTGTAC 2220  
 GGCTATTTCG TTGCTACGGT ACGTCTTACC GAGCACTTCC CCATCAATCT CTCGGTACA 2280  
 25 TTCACGGGCA AATGGATGT AGTACAGGAA GCCTATGAAG GCGATATTCC CGCAGAACAC 2340  
 ATAGCTCCGG ACGGATCGTT CGACTTTGAA ATGAATGGTC AGCAATTCAG AGGTTTGGCC 2400  
 GAAGGTCATG CCAAGCTCGT CAAGACTCCG GCCTTCGCGG ATATAGACCT CAAGCTGAGC 2460  
 CACGACTTCC ACCTTGCTTC CACTATGACC TTGGAATTGA ATGCCGGAAT ACAGAACATA 2520  
 30 TTCAACAGCT ATCAGAAAGA CACGGACAAG GGACCGGTA GAGCTTCTAC TTACGTATAC 2580  
 GGTCTATGCG AGCCAGAAAG GATTTTCTGTC GGTACAAAGA TCAATTTT 2628

## (2) INFORMATION FOR SEQ ID NO:52

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2697 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 40 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 45 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 50 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2697  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52

ATATTGAATC ATTTGAGAAA GACTATGTAC AAAAAGATTA TTGCCGTAGC AGCTCTCTTC 60  
 TGCCGCCAGCA TAGGGATCCT GAAAGGACAG TCCTCGGATC TGACCCCTCA GGATACTATA 120  
 TATAGCCCTG AAATATCCTA TGCCAAGCCT ATTCTAAGA CCATAGCATC TATTGAGATC 180  
 GAGGGAATGA GGTCTTTTCA TGACTTTGTC TTGCGCAATC TTTGAGGCTT GGCTGTAGCT 240  
 60 GATGAAGTCC TGATTCTCTG AGATGCCATG TCTGCTGCCG TGAATAGAAT TATGCGTCAG 300  
 GGCTACTTCT CAAATGTGCG AATCATCGCG GATAAATATG TCGGCAATAA AGTCTATCTG 360  
 AAAATCAITG TCACTGAACG TCCTCGCATC AGTAAGGTTA CTTTTCAGCG GGTAAAGAAG 420  
 TCTGAGAGAG AAGATCTTGA AATGAAAATC GGTCTTCGCG AGGGGATTCA GATGACCAGA 480  
 AATAATGAAG ACAAGGTCAG GCAAATCGTA CAGAAGTATT TTAGTGAGAA AGGTTATCGC 540  
 65 GATGCCAGCA TACGGATAAC GCAGGAACCG GATCTTTCCA AAGATGGCTT TGTCAATGTG 600  
 CTTATCTCGA TTGAGAAGAA AAGCAAAACC AAGGTGAATG AATTTTATTT TTCGGGCAAC 660  
 AAGGCCCTTA GCAATCATAA GCTAAGAATG GCGATGAAGA ACACCAATGC CAAATTCAGT 720  
 CTTAGAAACJ ATATTGCTC ATCTTTCTTG AAATTTTITA GTACTCATAA GTTTGTGGAA 780  
 GAGAGCTACC GTGAAGATTT GGTCCGATTG ATAGAGAAGT ATCAGGAATA TGGATATCGT 840  
 70 GATGCTGAAA TACTGACCGA CAGTGTCGTG AAGGCTCCTG ACGGCAAAAG AGTGGATATT 900  
 TATCTCAACA TCGAAGAGGG GCAGAAGTAT TATATTAAGG ATGTCAACTT TGTGGGCAAT 960  
 TCACATATC CATCGGAGTA TTTGGAACGA GTGCTCGGAA TAAATCCGG AGATGTGTAC 1020  
 AATCAGAGAC GATTGGCTAA GCGTCTCAAT GAAGATGAAG ATGCTGTGGG GAACCTGTAC 1080  
 75 TATAACATG GCTATATTTT TGCTGGGTC GATCCCGTGG AAACAATGT AGTGGGGGAT 1140  
 TCTGTTTCGC TTGATATTCG TATAGCGGAG GGAAGACAG CCAATATCAA TAAGGTGATC 1200



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ATCAAAGGAA ATACTGTCGT GTACGAAGAC GTAGTACGCC GAGAGCTTTA CACAAAGCCC 1260
GGCCAGCTCT TTAGTCCGGA GGATATCATT AACTCTATTG GTCTCATCAA TCAGCTTGGG 1320
CATTTTCGATG CCGAAAATC TATTCCTCGT CCGATTCCCA ATCCCGAAAC AGGAACAGTG 1380
GATATAGAGT ATGATTTGGT GCGGCGTAGC AGTGACCAAT TGGAGCTTTC TGTCGGTTGG 1440
5 AGTCAGTCCG GACTTCTGTT CCGAGGAGCC ATTAAGTTCA CGAACTTCTC TGTCGGCAAC 1500
TTGCTCCATC CCTCGATGTA TAAGAAAGGG ATCATTCCGC AAGGGGATGG GCAAACACTA 1560
TCACTGAGTG CTCAGACCAA TGGAAAGTAC TATCAGCAGT ATAGTGTAC ATTTATGGAT 1620
CCATGGTTTG GGGGCAAGCG GCCGGATATG TTCAGCTTCA GTGCATTCTA TTCCAAGACT 1680
ACGGCGATTG ACTCCAAGTT CTACAATAGC AATGCCGGA ACTACTATAA TGCCCTACTAT 1740
10 AATAGTACT ACAACAATA TAATAGTTAT TACAACGGTA TGTCGAATA TACCGGCGAC 1800
CTCTATACTC AGGCCAGCGA TCCGGATCGT TCGCTTCAGA TGTAGGTAC TTCGATCGGT 1860
TAGCGTAAGC GTTTGACTTG GCCGGACAAT TGGTTCCAGA TTTTACTTTC TCTGAACCTAC 1920
ACCTAGTATA GACTGCGAAA TTGGAGTAC AATACCTTCC AAAATTTCCA TCATGGCTCG 1980
GCTAATGATC TCAACTTGA GCTGCGTCTC TCTCGTACT CCATCGATAA TCCTATTTAT 2040
15 ACCAGAAGCG GATCGGATTT CATGGTTTCT GTTGTGCTGA CTCCTTCTTA TTCTTTGTGG 2100
GACCAATCATG ACTATGCCAG CCAGAACCCTC AGCGTAAGCG ATCGTTACAG ATTTATCGAG 2160
TATCACAAGT GGAAGTTAG AGGACGAGTT TTTACTCCAT TGCTCAATCC TGCTAGCAT 2220
AAATATACAC CGGTGCTCAT GAGTCGAGTG GAAGGAGCAG TTCCTGGTTC GTATATATCC 2280
AATAAGAAAT CTCCTTTCCG TACTTTCTAT ATGGGAGGTG ATGGTATGTC CAGCTATTAT 2340
20 GGTGGCTACA TGAATGAGAC TATAGTTTG CTTGGTTATA AGAACGGATC TATTGCCGCT 2400
AATAACTACG ACTATGCATA TGCTTATATG CCGCTTACGA TGGAACTACG TTTCCTCGATT 2460
CTGTTTGAAG ACTCATTCAA TGCGTGGCTC TTAGCTTTTG CCGAAGCAGG CAATGCGTGG 2520
CGCAGTATCG ACAATTATAA TCCCTTTAAC CTGAAGCGAT CCGCCGGTGT AGGATTGCGT 2580
GTACCGTTAC CGATGGTCGG AATGCTCGGT ATCGATTGGG GATATGGCTT TGACCGTCCG 2640
25 GACAATTCTC TACAGCGAGG AGGAAGCAAT GTCCACTTTG TGCTCGGACA GGAGTTT 2697

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## (2) INFORMATION FOR SEQ ID NO:53

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30 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 531 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: circular
35 (ii) MOLECULE TYPE: DNA (genomic)
    (iii) HYPOTHETICAL: NO
40 (iv) ANTI-SENSE: NO
    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
45 (ix) FEATURE:
    (A) NAME/KEY: misc feature
    (B) LOCATION 1...531

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53

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50 CAAATAAACA TGAATGGCGA TATGAAACGG TTTTGATTI TGATCGGCTT TGCACTGGCG 60
GTAGCTTTCT CCGGTTTTTC CCAAAAGTTC GCTTTGGTAG ATATGGAATA TATCCTCAGG 120
AATATTCCTG ACTATGAGAT GATGAACGAA CAGCTGGAAC AGGTGTCCAA GAAATGGCAA 180
AATGAAATCG AAGCTCTCGA AAATGAAGCC CMACTATGT ATAAGAAGTA TCAGAGCGAT 240
55 CTGCTATTCT TGTCTGCTGC ACAGAAGAAA ACCCAAGAAG AGGCTATCGT AAAGAAGAG 300
CAGCAAGCAT CCGAGCTCAA GCGGAAGTAT TTCGGCCCGG AGGGGGAGCT GTATAAGAAA 360
CGTCCGATC TGATGAAGCC TATTCAGGAT GAGATTGGGA ATGCTATCAA AGAGATTGCC 420
AAGCGTAACA ACTATCAGAT GGTGCTTGAT AGAGGTACGT CCGGAATTAT CTTTGCCAGT 480
60 CCGTCTATTG ACATTAGCGA CCTGTACTG AGCAAGATGG GCTTTAGCAA G 531

```

## (2) INFORMATION FOR SEQ ID NO:54

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65 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 510 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: circular
70 (ii) MOLECULE TYPE: DNA (genomic)
    (iii) HYPOTHETICAL: NO
    (iv) ANTI-SENSE: NO
75

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(v1) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...510

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:54

10	CGAATAAATA AACAAACACGA AATGAAGAAA TTTTCTCTCA TGCTTCTGAT GGCTCTTCCT	60
	TTGAGCCTCT TGGCACAAAA GGTGGCAGTG GTAAACACTG AGGAGATCAT TTCCAAAATG	120
	CCGGAACAAAG TAGCTGCTAC CAAACAGCTC AACGAATTGG CCGAAAAGTA TCGCCTTGAT	180
	CTCAAGAGTA TGGACGATGA GTTTGCCAAA AAGACAGAAG AATTTGTAAA GGAAGAAAGAC	240
15	TCTCTACTGG AGAACATCCG CAATCGTCGT CAGCAGGAAC TTCAGGATAT TCAAACTCGT	300
	TATCAGCAGT CATAACAAAC GATGCAGGAG GATTTGCAA AGCGCCAAAC ACAGCTTTT	360
	GCTCTATCC AACAAAAGGT GGCTGATGCC ATCAAGAAAG TGGGTGACGA AGAAAACGTG	420
	GCCTACATCA TGGAGGCCGG TATGATGCTT TACACCGGAG CTACTGCTAT TGACTTGACC	480
	GCAAAGGTAA AAGCGAAACT CGGAATCAAG	510

(2) INFORMATION FOR SEQ ID NO:55

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2484 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v1) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2484

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:55

45	ATCATGAAGG AAGCTATTCC CCGAAGAAGC AAGTATATAA AGCTCAACGG TATATACAGA	60
	TTGTGATTCA TTCTGCTATG CTGCCCTGCTA TGCTCTCAGG CAGCTATGGC ACAAGGCGTC	120
	AGGGTATCGG GCTATGTGCT CGACCGTGGG GAAAGAGCCGA TCCCGTTCCG CCGAGTCAAA	180
	GTGCGTGGTA CGGGGACAGG CGCAACGACG AATCTGAAAG GATACTACGA GTTTCGGATG	240
	AAGGCCACGA CCGGACAGCAT CACGATCGAG TTCAGCTCCA TGGGGTACCA AGGGGTAAGT	300
50	CGCAGCTTTC CGTCTCTGAC CAAGGACACT CGGCTGAATG TTCGTTTGGC AGAGGCGAG	360
	ATGGAGCTTT CGAGCGTGAC GGTACAGGCC ACAAACGCA GACTCAACAC GATGGAGCCG	420
	GTCAATACCC GAGACCTTCG TGTCAATGCA GGGCCTACGG GAGGGGTGGA ATCGCTCATC	480
	GGAAGCTACG CAGGAGTAAC GCAGAACAAAT GAACTAAGCT CGCAATACTC GGTTCGCGGA	540
	AGTACCTACG ATGAGAATAT GGTCTATGTA AACGAGTGG AGGTTTATCG CCGCTGCTG	600
55	GTTGCTCTG CACAGCAGGA AGGTCTGAGC TTCGTCAATC CGGATCTGAC ACAATCCGTA	660
	CAGTTCTCCG CCGGAGGGTT CACGGCCGAC TATGGCGACA AGATGTCTCT CGTACTGGAT	720
	ATTGCTACA AGCAACCGCA GGAGAAGGAA GGAGCGGTAC TCCTCGGGAT GCTACAATCG	780
	AGTGCCAAAT CGCTCTTGGG CACTACGGAC ACGAAAGCCG AATACGATCC GATCTATGCG	840
60	GACGGACAGA CATTCATGAC GTACCGTTTC AGCCCCAAGC TGTGCGTTAG TTTCTCGGC	900
	AATATTTGCG AATCTCGCTA CAAGTTTGTC CCTCAGACCC GTGAGACGAG CTTCGGTACA	960
	CTGAGCGATG CCAAAAAGTT GAAGATCTTT TTCGACGGTC AGGAACAAGA TCGTTTCCTG	1020
	ACCTACTTCG GTGCTTCAG CATGAATTC GTGCCGAGC ACAAACAGCG GCATACGGTT	1080
	ACGCTTTCCG CCTTCAACAG TAACGAACCG GAGACCTACG ATATTGAGG AGAATACTTT	1140
65	CTGAACGATG TGCAGCTGGG GCGGACGGA ACTGCTTCCA TGGCTTCGGG CTCAGAGAAC	1200
	TCCAACGGCT TGGGCATCGG GCGCAATCAC GAGCATGCCG GCAACAGGCT GAGCTACCGC	1260
	TTGCTGAACA TGGGTTACAG AGGGGAGATG AAGCTGAACG AGAAGCATCG CCTGCAAGCC	1320
	GGCGTATCGG CACAGATGGA GAAATAGCC GACCATATCA CCGAATGGGA ACGGAGGGAT	1380
	TCGGTAGCAT ACAACCTACU TCACTCGGAG ACCGTATTGC TGATGTACAA TAACCTATAT	1440
70	CGCGATACCG AGATGAGGGG AACCGCGCTG TCGGCATTTC TACAGGATCG ATTCAACTTC	1500
	AGCATGGGAG GAGGTACATT TTCTCTCAT CCGGGTATCA GAGCTTCGTG GTGGAGCTTC	1560
	AACNAGGAGT TGCTCGTCAG CCCACGATC AGCGTGGGTT ATTCTCCCGA AAGCAACCCG	1620
	GCTTTGGTAC TGCGTGACGC CGCCGGAATT TATTATCAGG CACCGTTTTC CAAAGAGCTA	1680
	AGGCAGACGC ATAAGGATGC CGAAGGCAAT AACGTGGTTG TCCTCAACGA GAGATCCGC	1740
75	TCTCAGGAG CTTTTCACAT TCTCGCAGGA GCAGACTATA CCTTCGAAAT GGGGGGCGA	1800
	AAATACAAGT TTACGGCAGA GGCTTACTAC AAGAGCCTGT TCAACATCAA CCCGTATATA	1860
		1920

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5 ATAGAGAACG TGAAGATCCG CTATCTGGGC GAAACATCG GTTCGGGTTA TGCTGCGGGT 1980  
 ATCGATCTCA AGCTCTTCGG CGAACTGGTA CCGGAGTGG ATTCGTGGCT GACGGGCTCC 2040  
 ATTATAAAG CCGTCAGAA ACTGGATGGC TACGGTTCTT TACCACTGAT GAACGCACCC 2100  
 ACTTACAATT TCTCCTTCTT CCTTCAGGAG TACGTGCCGG GCAATAAACG CATCACAGCC 2160  
 ACCCTGCGGG CTGCACTAAG CGGAGGATTG CCCCAGCTCA ATCCGAGCAA AGGGCTTAGC 2220  
 TCGCCGGCCT TTACCGCACC GGCCTATAAG CGTGTGATC TGGGGGTAAT GTACAAATGG 2280  
 CTCGACCCGG ATGACTCCTT TGCCGGCCGA AGCAAATGGC TAATGGGAGT AAAAGGGGCC 2340  
 TACATAGGGG CTGACCTCTT CAATCTGTTC GACATGACCA ACGTCAATTC TTACTACTGG 2400  
 10 GTGTCGGATG CCTACCAACA GCAATACGCC GTACCGAACT ACCTGACACG CCGCCAATTC 2460  
 AACCTGCGTC TCCTCGTCGA ATTC 2484

## (2) INFORMATION FOR SEQ ID NO:56

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2037 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 20 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 25 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 30 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2037  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56

CCTATCCCTT TTCTTCTTAA TATGTACAGC GGACATCATA AAATCCATTA TCCTTTTCTT 60  
 ATCCTGTTGG TATGCCCTGC TTTTGCTGCC TGCAAGAGCG TGAAGTTGAA AGATGCGGAG 120  
 AAGGCACATG ATGCCCAAGA GTATACCAAG GCTGCCGATA TGTACAATAC ATTATACAGG 180  
 CGTACCCGAC GAAAGCAGGT GGAGATGAAA GCTTATACGG CTTCGGATC CGGTGAAAAC 240  
 40 TATCGTGCGG CCGGCAGACA AGCCAAAGCT TTGCGTGGCT ATCTGAATGC CAGACGCTAC 300  
 GGGTATCCGG ATTCTGTGGT ACTGCTCCGT TTGGCACAGA CTTATCAGCA AGGAGGTAAC 360  
 TATAAGGAAG CCGAGGTACT CTTCCGTGGA TATCTGGAAG CTTATCCGAA AAGTTATTTT 420  
 GCAGCTATCG GTTTGGAGGG GTGCTCTTTT GCCCGCCAGC AAAAGGAATA TCCTACACGT 480  
 TACCGGATAC GCGAGCTGCT CGAGTGGAAAT TCGGCACGGG GCGACTTCGG CCGGCGCTAT 540  
 45 GCACCCGATG CTTCCGCTCT CTATTTCACA TCGAGCAGAA GCAAAGACGA CGGTTTGGAT 600  
 AATAGCAGCA TACCGGACT GAAACCCAAC GACATTATA TCATCAACG AGATGCACAA 660  
 GACGATGGG GACGTCCCGA TAGCGTGTCC GGAGGAATCA ACACCTCATG GGATGAAGGC 720  
 GTGCCAACA TCAAGCCCGA TGGTAGTACC ATATATTATA CGTTGGCGCA GCAAGGAGCC 780  
 GATTACGACC GTACGGTACA GATCTATTCC GCGCTCGGA GCGGAGAAGG CGGTTGGAGC 840  
 50 AACGGTTCG TCGTGGACAT TATGCGGAT TCGCTCCGTA TGGCTGCTCA TCCCTCTATG 900  
 TCGGCATCCG GCGATTACCT GTATTTCGTC AGCAATATAG CCGGTAGCTA TGGCGGCAAG 960  
 GATATTTATC GTGTCAAGGT GTCGGATCGT TCTTATGGTT CACCGGAGAA TTTGGGGCCT 1020  
 GATATCANTA CCGCGGGGGA CGAAATGTTT CCCTTCATAG ATGGGGATAG TACCCTTTTC 1080  
 TTGCGTTCGG ACGGACACGC CGGTCTGGGA GGACTGGATA TTTTCAAAGC CACGCTGGAC 1140  
 55 TCTACCGGCC AATGGCATGT AGTCAATATG GGACAACCGG TCAATTCCTC TGCCGATGAT 1200  
 TTCGGCTTGG CTGTGGAGCC TAAAGGCAAA AACAAAGAAG AAGCTTTGCC GGACAACGGA 1260  
 GTCAAAGGTG TATTTTGTTC CAACCGAGGC GATGCACGCG GATGGCCGCA CCTCTCCAT 1320  
 TTCGAACTGC CCGCTATCTA CACCGAGATT CAAGGTTATG TGTAGGACAG AGAAGAAAAT 1380  
 CCCATAGCCG GAGCCACTGT CAGGATCGTA GCGGAACGCG GCCCGTAGG ACAGGGATTG 1440  
 60 GTGACTACTC GTGACGATGG CTCCTATAAG ATGAGCGTGC AGGGCGATAC TCGCTATGTA 1500  
 ATGCTTGCCG GAGCATCGGG TTATTGTAAT CAGTACGTAG AACTCAAGAC CGATACCGCC 1560  
 AAGCAGAGTG AGACCTACTA TGTGGACTTT TTCTTTCAT CCGGTGAGAA AGCCGAGGGC 1620  
 TTGCAAAATA TTTTCTATGA TTTCGATAAA GCTACTCTTC GCCCGGAAAG CATGAAGAGC 1680  
 TTGGACGAAC TGATTCTGAT CCTCACGGAC AATCCGATA TFCGATCGA ATTGGGTTG 1740  
 65 CATGCGGACA GGAAAGGCCG CGATGCTTAC AACCTCGGAC TATCTGACCG CAGAGCCAAA 1800  
 TCGTGGTGG ATTACCTCAC GAGTCGTGGC ATAGCGSCCG ACAGGCTTAC GTGGAAAGGC 1860  
 TACGGTAAGT CTGTCCCCAA GACGGTGACA GCCAAAATTG CCGAACGGCA CGATTTCCTG 1920  
 AAGGAAGGCG ATGTGCTCAC CGAGGAATTC GTAGCACCTT TGACCGAGGA GCAGCAGTCA 1980  
 70 GTCTGCGACC AACTGAACCG TCGTACCGAG TTCCGTGTGA TCGAAGAAGA GTTGCCT 2037

## (2) INFORMATION FOR SEQ ID NO:57

- 75 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2316 base pairs

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

5 (ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO  
10 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
(ix) FEATURE:  
15 (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...2316  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57

20	CCTGCACAGC	CGAAAACATA	TTGCATACGA	TACTTTCGGA	GAGAGGTATC	TCCGAGGAGG	60
	CAAAACAGAA	GGACATTGTA	TGCGGACAAG	ATGCGCCGGC	ATATCGTCAA	GTGCTGTCCC	120
	TCCTGCTCCA	TACTCTTGCA	AGAATACTCC	ACAACAGAA	TATTCATTCA	TCACTTTAAC	180
	ATATCAATTA	TTATGAAAAA	GT'TTTCTTC	CGCTACTAT	CGATTGGTAT	TTCAGCGCAG	240
	GCTTTTGCCA	AGACGGACAA	CGTCCCGACA	GATTCTGCTAC	GAGTACACAA	TCTTCAGACC	300
25	GTACAGGTCT	ATTCTACACG	CACGGCCGTA	CCTCTGAAAA	AGATACGGGC	CAAGATGGAA	360
	CTCATCTCAT	CGCGCAACAT	CAAGCAGTCC	GGCTTTAACA	ACATGACCGA	CATCCTCAAG	420
	ACGCAAAATT	CGCTCGATGT	CATACAATAC	CCGGGCTTTA	GTTGCAACAT	CGGTATCCGC	480
	GGTTTCAAGC	CCTCCGGCAA	GTATGTAAAC	GTATTGGTAA	ACGGCATCCC	TGCGGGAAAG	540
	GACAAATATCT	CTACGCTCAA	CACGAGCAAC	ATCGAACAAA	TGAGATCCCT	CAAGGGCCCG	600
30	TTCTCTTCCA	TCTACGGCAC	CAATGCCATG	GGCGGTGTGG	TGAACATCAT	CACCCACAAA	660
	TCCAAGGACA	AGATCCATGG	CAACGTTTCT	CTCTTCGGCG	GTAGCTACCA	GACCATGGCC	720
	GGATCATTCA	ACTTGGGTGG	CCGCTTCGAG	GATATTTTCT	CATTCTGATCT	TAGTCTGGGC	780
	TTGGACAAGC	AGAACAAGGA	CTATAAGACC	GGATCAAAACA	ATTTCCTATC	CCTGAGCAAA	840
	CTGGAAGAAG	CTATAGTAGA	TGTAAATGCT	ACCAAAAACA	AGAAAATGAA	GGGGAGCGAC	900
35	TATACTGTAG	CAACGGGACG	TCTGCGTTTC	GGTATCGACT	TCACGCCCGA	ATGGTCGCTG	960
	AATCTGTATC	AAAACGTAAT	CCTCGGAGAT	CGCATCCCGG	TAGGAGGATC	TATATGGGGC	1020
	GTTTACGGAG	AATCCAAAAA	AAATCTGAAT	CGTTCTTCCA	CCTCTTTCGA	GCTGCTCGGC	1080
	AAACATGGCT	GCCACACGCT	TCAATCTCCC	CCCTACTTCA	ACATAGAGAA	ATCGGAGAAC	1140
	TATAACAATG	CCGATCCAC	CGGTTTCAATC	AACTACAAAA	GCGACTACTA	CACCTATGGT	1200
40	CGCCTACTCC	AGGACAAGAT	TTCTTTTGGA	GGACAAAAA	TGCTACTCGG	TGTCGACAGC	1260
	CGAAACATGA	CGATGGAGTC	AGAAAGATTC	GAGCAGGCAG	GAGTGAATAC	AAAGCCATAC	1320
	AACCCCGGAT	ATGCCACGAA	CAATATCGGT	TTGTTGGGAC	AGGCCAATTT	CTACCTGCTG	1380
	AACGATGCTC	TATCGATATC	TGCCGGTGCA	CGTGCCGACT	TCAATGTTCTT	TGACCTGAAA	1440
45	GCGAACGAGT	ATCTCAACAA	TGAAGCCAAA	CAGGAAACTC	ATAACGTAAT	CAATCCGAAT	1500
	GTCCGAATCA	AATATGAGTT	TGTGAAAGGC	CTTACAGCTC	ATGGTACATT	CGGTAGTGCA	1560
	TTCAATGCTC	CCGATGCTTT	CCAAAAGCA	GGCCAAATAC	TAGGCCCGTT	CGGCACGACC	1620
	ATAGGCAATC	CTGACCTGAA	ACCCGAAAAG	TCCATGACCT	GGGACTTCGG	TATCGGATAC	1680
	AGCAATGGAC	GCTGCGGGAT	CUAAGCCGAC	GTAACCTTAA	CCTATTTCGA	CACCGACCAC	1740
	AAAGATCTGA	TCTTGTCCAG	CCCTGACTAT	GCTAATAATA	TCACCACATA	CATCAATGCC	1800
50	GACAAGGCTC	GTATGAGCGG	TATCGAGGCC	CTTTTGTCTT	ATGACTTCGG	CAGCCTCTTT	1860
	GCCAACAAGT	TCTCTCTCCG	CGCATTTGCG	AATGCCACGA	TCATGCTCAA	TCCGAGATG	1920
	AAGAAAAGCC	AGACCGATGC	CCCTTGGAGC	GAAATGACT	ACGTTCCGAA	GCAGAACATC	1980
	ACCTTCGGTA	TGCAATATCG	TGGCAAAGAA	GGACTTGAA	TGATGCTCAA	CGGTGCTTC	2040
	ATGGGACGCA	GGATCGAGCA	AAACTGGTAT	GCTTACTACC	CCGAAGTTCG	CCCCGAACTC	2100
55	CAGCAACTGC	TTGCAGCAGA	AGAGCCTGAA	TTGGCTGCTC	AGGGACTGCT	CCGTCACTCG	2160
	CAAGCAATGG	TGTTCAATGC	CTCTGCTTAC	TACCACATGA	ACAAGTATCT	CACCTTCGGT	2220
	GTGAACCTGA	ACAACATCTT	GGATGAGCTT	TATACGGAGA	AAGACGGCTA	CCACATGCC	2280
	GGACGTAA	TCATGGGTAA	GGTTATGGTC	AACCTC			2316

60 (2) INFORMATION FOR SEQ ID NO:58  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1452 base pairs  
65 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular  
(ii) MOLECULE TYPE: DNA (genomic)  
70 (iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO  
75 (vi) ORIGINAL SOURCE:

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(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...1452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58

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10  GGCCGGGCCT CTTCCCTTA CAGGCAAATG GATGGCATAC TAAACGATGA ATATAGACAA      60
    GCATCTATGA ACAGGTTTTC AAATCATTGG CCTGCATCC TCGTGGGGTT TGTACTCTGG      120
    TTTGTATCGG CGAGTCGGAC TGTGGCACAA AACGCCTCCG AAACGACGGT ATCGTACGAT      180
    ACGGATACCG CCGTACTCTC CGAAGCCGAT GTGCTTCGSA TCGCTCTTAG TGAGAATGCC      240
    ACAGTGAAG TGGCCGATAI GGATGTGCGC AAACAGGAAT ATGCACGTAG GGCAGCACGT      300
    GCCGATCTCT TCCCGAAAGT AGACCTCAAT GGCCTTTACA GCCATACGCT AAAGAAGCAG      360
15  GTCTTATATA TAGATATGCC CGTTCAGC AGTAGCGAAG GTATCGAAAT GGGGCGTACA      420
    CACAATACGC AAGGAGGGGT GAACGTCTCC ATGCCATTGG TGTCGGCACA GCTTTGGAAA      480
    AGCATTGCCA TGACUGGAGA ACAGCTCGAT CTGGCTCTGG AGAAGCTCG CAGTCCCGA      540
    ATCGATTGG TGGCAGAGGT GAAGAAGGCT TACCTCAGTG TATTGTTGGC CGAGGACTCT      600
    TATGGCGTAT TCAAGCGCAG CTATGACAAT GCTCTGGCCA ATTATAAGAA CATATCCGAC      660
20  AAGTTCGATC GTGGACTTGT GGCCGAGTAT GATAAGATTC GAGCCAATGT ACAGGTACGC      720
    AACATCGAGC CTAACCTCTT GCAAGCGCAG AACTCCGTAG CCCTTGCTCT CTGGCAGCTC      780
    AAGGTCCTGA TGAGCATGGA AGTGGAAACT CCGATCAGAC TCTCCGGTTC ATTGTCCGAC      840
    TATAAGAAGC AAGTCTATAC CGGCTATTTT GCGGCCGATA CGCTTATTTC CAACAACCTCC      900
    TCCCTGCGTC AGCTCGATAT ACAGCGTCGT CTGGCTGTCA GTGCAGACAA GCTGAACAAG      960
25  TACAGCTTCC TGCCTACACT CAATCTGGGA GGGCAGTACA CCTATTGCT CAACAGCAAC      1020
    GACATCAVAT TCTGGGGCGA GGGACAACGC TGGAGCCCTT TCTCCACCAT ATCGCTCAGC      1080
    CTGTACATTC CTATATTCAA TGGAGGCAAA CGTCTGTACA ACGTGAAGCA AAGTGCTTTA      1140
    TCGATCCGTC AGATCGATCT GCAACGACGC CACATAGAGC AATCCATCCG AATGGGAATC      1200
30  AAGAACCAAA ATGACCGTCT GCGTACCTGT ATGCAGAGAT TTGTGGCCTC GGAAGAGGCT      1260
    GTCCGAAGTG CAGAAAAGGG CTATCAGATA GCAGAGAAAC GCTATCAGAC AGGCGAAGGC      1320
    ACTCTCGTCG ACCTCAACGA TGGCGATGTG GCTCTTTTGC AGGCTCGACT CAATTATAAT      1380
    CAGGCCATAT TCGACTTTAT GACCGCAAG GCGGAATTGG ACAAGATGAA CGGCATGGGG      1440
    ATTCGCAAC AA                                     1452

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(2) INFORMATION FOR SEQ ID NO:59

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1620 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...1620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59

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60  TTTCATAACT TTGACTTCCT AAACGGTATA AAATTGTTT CGATGGCAAA TAATACTCTT      60
    TTGGCGAAGA CTGACGTTA TGTCTGCCTT GTCGGTTTCT GTTGGCTCAT GGCATGATG      120
    CACCTCTCTG GGCAGGAAGT CACTATGTGG GGGGACAGCC ATGGAGTGGC GCCGAACCAA      180
    GTGCGCCGAA CGCTGGTGAA GGTAGCCTTA AGTGAATCCC TTCCTCCGGG TGCAAAACAG      240
    ATTCTGATCG GATTCTCTCT TCCGAAAGAA ACGSAGGAAA AAGTCACCGC CCTATATCTC      300
    CTGTGTAGTG ATTCTTTAGC GGTGCGCGAC TTGCCGGACT ACAAGGGCG AGTCTCTTAC      360
65  GATAGCTTCC CGATCTCAA GGAAGATCGT ACCACAGCCC TTTCTGCGGA TTCGGTAGCC      420
    CGACGCGCGT TCTTTTATT GGCTGCGGAT ATAGGGCCTG TTGCTTCTTT TTCCCGATCC      480
    GATACGCTGA CTGCCCGTGT GGAAGAGGTG GCTGTGATG GCGGCCCTTT GCGGTTGAAA      540
    GAGCTGTGCG CTGCCCTCCG TCGTCTGTAT AGGGGGTATG AGGCCCTCTT TGTACCCGGT      600
    ATAGGCGATG CCGGGAACCTA TCGTATCCCG GCCATTTTGA AAACGGCTAA TGGAACTC      660
70  GTCATGCGGC GCAGTACGGA CGGAGGGAAA TCGTGGAGCG ATCCCAGGAT TATCGTACAG      720
    GGAGAGGGGC GCAATCATGG CTTTGGCGAT GTAGCCCTGG TGCAAAACCA AGCAGGAAAG      780
    CTCCTGATGA TCTTTGTGCG TGGAGTAGGC CTGTGGCAGT CTACCCCGA TCGTCTCAG      840
    CGCACTTATA TATCGAAAG TCGGGACGAA GGAAGTACTT GGTGCGCTCC TCGGGATATA      900
    ACCCATTTCA TCTTCGGCAA GGATTGTGCC GATCGGGAC GCACTGCTG GTTGGCCTCC      960
    1020

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SUBSTITUTE SHEET (Rule 26) (RO/AU)

WO 99/29870

PCT/AU98/01023

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TTTTGTGCTT CGGGACAAGG GCTTGTGCTG CCATCCGGTC GTATCACGTT TGTGGCTGCC 1080  
 ATCCGCGAAT CAGGGCAGGA GTACGTCCTG AACAACTATG TCCTCTATAG CGACGATGAG 1140  
 GCGGATACAT GGCAGCTTTC CGACTGTGCA TACCGCCGTG GCGATGAGGC AAAGCTTTCA 1200  
 TTGATGCCCG ATGCCAGGGT ACTGATGAGC ATACGCAATC AGGAGCGGCA GGAGAGCCGA 1260  
 5 CAGGCTTICT TCGCTCTCTC CTCGACGAT GGCCTTACTT GGGAGAGAGC CAAGCAGTTC 1320  
 GAGGCGATCC ATGACCCCGG CTGTAATGGA GCTATGCTTC AAGTGAAAAG GAACGGAAGG 1380  
 GATCAAGTGC TGCACCTCCCT GCCTCTCGGC CCGGATGGGC GTCCGATGG AGCTGTCTAT 1440  
 CTCTTCGATC ATGTCTCCGG CCGCTGGTCC GCTCCCGTTG TTGTCAATTC AGGATCGAGT 1500  
 GCCTACTCGG ATATGACTCT GCTGGCGGAT GGAACGATCG GTTATTTTGT CGAAGAGGGC 1560  
 10 GATGAGATCT CATTGGTTTT CATTCCGGTC GTCCTTGAGC ATCTCTTCCA TGTCCGGCAA 1620

## (2) INFORMATION FOR SEQ ID NO:60

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 879 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 20 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 25 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 30 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...879  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60

35 AAGTCTCGGA GCGATTCGGC TTGCGGTCG GTATGGAGCG CGAATACAAT ATCTGGACTC 60  
 GTCGGTGGGA AACGCATTAC TTGCTTATC CTGTATTCTA TGGCGATAAG AAGTAGTAAT 120  
 ATAGAATCAA TACAGTGCTT TGTGATGAAA AAAGAAAAAC TTGGATTGCG GATCGTCGCC 180  
 GGTTTGGCTT TCGTATTGGG CCTTTATGCT CTGCGCGCA GTGTGCTCA GCTACGCCGC 240  
 40 TCTCAGCTT CGGTGACTGT GACCGGTATG GCGAGCGSTA ATTTCAAATC CGATCTGATC 300  
 GTTTGGACTG CTTGTAACCA GCTCCAGATG ATGGATCTCG AATCGGCCTA CAAGGCTTTG 360  
 AAGGAAAAAC AGATATTGGT AGCAGACTAT TTGAAAAACA AGCAGCTGCC CGATTGCTCT 420  
 TATATCTTCT CAAGCGTAGC CATCTCTAAA GAATACAACT ACTATTACGA TCCTCGGCAG 480  
 GAACAAAACG TCAGGACCTT TGCCGGGTAT CTGCTCAGCC AGACAGTTAC GGTGACCTCA 540  
 45 CAGGACATCG AACATGTGGA GAAATATCT CGCGATATAA CGGAGCTGAT CAATCAGGGG 600  
 GTAGAGATTA CCTCCGACCG TCCGGCCTAT TACTACACCA AGCTCAATGA TCTGAAGGTC 660  
 GAGATGCTGC GCAATGCCCT CGAAGACGCT TTCAATCGTG CTTCCGTGAT TCGGAGGGGG 720  
 AGCGGTTCTT CCGTGGGTAA GATGCTATCT TCTTCGATGG GCGTGTCCA GATAGTGGGG 780  
 CTCAACTCGA ACGAAGATTA TAGCTGGGGA GCTTCGTICA ATACGTCTTC CAGATGAAG 840  
 50 ACGGCAAGCA TAACGGTTAA GGCTTCTTTC GCTTTGAAG 879

## (2) INFORMATION FOR SEQ ID NO:61

55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 840 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 60 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 65 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 70 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...840  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61  
 75

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PCT/AU98/01023

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5 GGGAACTCC AAATGAAAA AAGCAATTGCA ATTATCGCCT CAGCCCTCTT GGCTTTAGGA 60  
 GCCGTCGGCT GTAAGAAAA TGCTGACACT ACCGCTGTCA GTGAAAAGGA TAGCATAGCC 120  
 TTGTCATGG GTATTTTGTG CGGACAGGAT TTTGCCAATC AGTTCGAAAT GTCCCGCTTG 180  
 CAAGGCCAGC CGATTGATTC GGTAGCTTTC TTGGACGGTT TCAATATATG TATCGATACG 240  
 ACGGCTTCT CGTACAATCT GGGAGCCATC TATGCTTCCA ATATAGCTCG TCAGCTGGCT 300  
 CATGATTCGA TCGATATCGA CAAATTCTAT GCAGCCATGC GTGCGGCTCT TCTTAAAGAC 360  
 ACCGATCTTA TCGCCATGAA GCCTGCAGAT GCACAGGCTT TCATGCAACG AATCCAAGCC 420  
 AAAAAAGCAG GAGAAAAACA TATGAAGCAG TTTGGCCAGA ACATCGAAVA GGGTAATGAA 480  
 TACATCGATA CCTTAAAAA AGAAGATGGT GTAAGTCTTA CGCAACTGG TCTGGCATAC 540  
 10 AAGACTCTTC AGGAAGGTAC GGGAGCTACT CCTCTTTGG CCGATACTGT ACGTGTCAAG 600  
 TATGTGGGTA CTCTGGTCTG TGGTAAAGAG TTCGACAAA ACGAAGAGG AATCGAATTT 660  
 GCCGTACCG GTGTGATTAA AGGCTGGACG GAGATGCTCC AACTCATCAA GGTGGTTCAG 720  
 AAGTTTCGGG TGGTAATCCC ACAGGAGCTG GCTTATGGGG AGACCGGCAA CTATACCATC 780  
 15 GAACCGTTCT CTACCCCTGAC GTTCGAGATG GAACTTATCG GGATCAAGCC CGGAAAAAG 840

## (2) INFORMATION FOR SEQ ID NO:62

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2409 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 25 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 35 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2409

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62

40 TGTCGAAAGC AGAAGCTCTC AAACCCGAAG AGGAGCCGGT ATCCGTGCAG ACGGATATCA 60  
 TTCCGACAAA GCGATAAGAA TCCGATGAAA GTATTACGGC AAGTATTCCT CCCCATCCTT 120  
 TTTGTCCTAC TGACAGGTGC CTGCTCCACC ACAAGAATC TGGCGGAAGG CGAACAGCTG 180  
 TATATCGGAA TGGGCAAGAC ACAGATACTC CGGCAGGACA AGAGCCACGC CGGCCAACAG 240  
 GCTCTGACCG AAGTGGAGAG TACACTGAAA GTTACACCCA ATGGAGCTAT TTTCCGCAGT 300  
 45 GCAAGTGCCT CCTTACCCTA GATACCATTC GGGCTATGGC TATACAACAG CTTCGTGGGG 360  
 GATTCCACTG TCATTTCGAA ATGGATATTC GACAAGTTTG CAGCCAAGCC GGTTTTCATC 420  
 AGTCAGGTCA AATCCGATAG CCGGGCTAAG GTGGCGACGA ACATCTCCG CGAACACGGG 480  
 TACTTCGATG CTAAAGTAAA AAGCAGTGTG ACCACTCTGA AAAAGGACTC GCTCAAAGCC 540  
 AAAATCTCCT ATACGGTGGG TATGGCTCT CCTTATCATT ACGACAGCAT CATTCCTTTA 600  
 50 CCGATCAGCA CTTTCCCGCA CAGCATTCTG GCTTACAGGC AGACTCCGTC TTTGATCAGG 660  
 AAAGGAGACC AGTTCATTTT GGCAAGCTG CACGAAGAGC GTACAGCCAT CAGTGCCTGT 720  
 CTGAGAGACA ATGGTTACTA CTACTTCCGC CCACAGGATA TTATCTACGA AGCCGATACC 780  
 CTCCTCGTAA GAGGTGCCGT ATGCTTGGCA GCCAAGCTCT CGGAAGATAC TCCACCCCAA 840  
 GCCATGCGCC CGTGGAGGAT AGGGAAACGG ACAGCAGTCC TGCTCGGAAT GAACGGAGAA 900  
 55 AGCCCGACAG ACTCGCTCGA AGTGGAGGAT ATGAAAGTCC TTTACTATCG TAAAAATGCCG 960  
 GTTCGCCCCA AGATTTTGGC CAAACGCTTT GCTTCTTCT CCGGCAATCT GTATCGGCAG 1020  
 AAAGACGATG AGACGACACG CAAATCCTTG GCTCGTTTGG GAGCCTTCTC CGTTATCGAT 1080  
 CTCAATTTTT TGCAACGCGA TTCCATTTCC GGCCTTTTGG ATGTGCGACT GCTAACCCAC 1140  
 CTCGACAAAC CTTGGGATGC ATCATTAGAG ACCTTGTTCA CGAGCAAAAG CAATGACTTC 1200  
 60 ATCGGTCCCG GACTGAATTT TGCTCTTGCT CGGCGCAATG TATTGGGGGG AGGAGAAAAT 1260  
 CTTTCTTGGA ATATCGGTGG ATCGTATGAG TGGGAGACCG GCAATCGTCC CGAAAATAGC 1320  
 AGCAATCGGC TGATCGATAT AAATTGCTAC AACATGAATA CGGCCGTGAA CCTCTCGTTT 1380  
 CCCTCGATTG TATTTCCCGG TCTGCTGGAT AAATACTATT ACTACCCAC GACTACGACT 1440  
 TTTGAGGCTT CTGCCACCGC GCTGAACAGG GCACACTACT TTAGCATGTA CTCTTTCGGC 1500  
 65 TTTTCGACCA CTTACGAATT TCAGCCCTCC AAGGAACACU GGCATGCTAT TTTCCCGCTC 1560  
 AAGCTCAACT ACAACCTCCT GGGGCATCAG ACAGAACTT TCCAGGCCAT TACGGCGAAC 1620  
 AATCGGCCCC TGCTGCTCAG CCTTCAGAGT CAGTTCCTTG CTCAAATGGG GTATATCTAT 1680  
 ACGTTCAACA AATCCGTTTC AGAGAAAAGT CCTCATCATC TTTGGATGCA ATTCCGACTA 1740  
 70 TCCGAGCGAG GCAATCTCCT GAATCTGATC TATCTGGCAG CCGGCAAGAA GTACAGCGAC 1800  
 ACCAAGATTT TCGTGGCGGT CCCTTCTCT CAGTTCATCA AAGCCACGGG AGAAGTGGCG 1860  
 TATTCCTATA CCAATACCGC CAATCAGTCA CTGGCAACCC GTTTCGGGAG AGGCGTGATA 1920  
 TATAGCTATG GCAATATGCG AGTGGACCCC TATAGCGAGC AGTTCTATGT AGCGGTGACC 1980  
 AATAGTATCA GAGCTTTCAC CGTCCGTAGC ATCGGCCCGG GACGGTTCAA TCCGATTCC 2040  
 75 GACAATCAST ATTCTTATTT GGATCAGGTG GCGCAATTCA AACTCGAAGC CACAGTGGAA 2100  
 TATAGAGGCA AGCTTTTCGG GGATCTCCAC GCAGCCGTTT TCCTCGATGC GSGCAACGTT 2160

SUBSTITUTE SHEET (Rule 26) (RO/AU)

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TGGCTCTTGA GGGAGGATTC TTCCCGTCCG GCCGGTGCTC TGTCGGAAGT GGGATCGGTG 2220  
 AGCAATTTCC TGAATAGCAT CGCTCTCGGC ACCGGTGTCT GCCTTCGCTA CGATCTGGCA 2280  
 TTTCTCGTGG TTCGTGTGGA TGTCGGCTTC GGTCTCCACC TTCCTTACAA TACGGGTAAG 2340  
 AAAGGTTACT ACAATATCCC ACGCTTTAAG GATGCCATCG GTTTCATTG GGTGTCTGGC 2400  
 5 TATCCCTTC 2409

## (2) INFORMATION FOR SEQ ID NO:63

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2349 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 15 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 20 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 25 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2349  
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63

TCTCTCTCCG CGTATATCCG TTTTCTATG TCCTCCGATT CCGTTCGSTA TCTAATCGGC 60  
 ATTGCCGGCT GCTTGCTCCT CATGCTTGCT TCCTCCTGCT CGGTCAACCG TTATGTGCCG 120  
 GACGGTAGCA GACTATTAGA CAGGGTAACG ATCGCAAGCG AACCGGGCAG TATCGCTCTG 180  
 35 CCGGAAGATA TTCGGGACTA TACCCTCCAG CAACCCCAATT ACAGACTGTT CGGGATGACT 240  
 CGCTGGCTAC TGGCGCTCTA TAGCAGCTCG AATCCGAACA GCACAGCTG GTGGAACCGT 300  
 TCGCTCCGGA AATGGGCGA ACCGCTGTG CTCATCGATT CTGTCTCAC CGATCGTACT 360  
 GCCAACCGTC TGGCAAAGGC GATGGCCGGC GATGGCTTTC TCATGTCTAC TGCTCGTGCC 420  
 GTGGTAGACA CCGCTTGTG CAAGAAAGCT CGCATTACTT ATCTGATTCA GCCCGGAAGC 480  
 40 CGTTATTATA TAGCAATAT GSCCTTGGAT GTGAAGAATC CACTCCTTCC TCCCGTTGCG 540  
 CTTGGCAATT CGCTTCTTTC GGCATACAAG GTCCGGATCA GCGAGGGTTC TCCTTGTCTG 600  
 CCCATCGTAC TCGATGAAGA GAGAAAGGCG ATAGCTCGTC ATATGCGCAA CAACGGCTTC 660  
 TGGAGTTCT CCGCCGAGGA TGTTTATTAT GAAGCAGATA CTACCGTTTC AGGAGGATCG 720  
 GGTACGAAAT CTGCGGATCT GAAATTAGTG GTCAATGGCA TCGGGCGTTA TCCATATCGG 780  
 45 ATCGGCAGGG TATCTTTCA TGCCGATTAT GATCCTCTCG AATCGGACTT CAGAGTTTCA 840  
 GAGCTGCCAC GTATCGATT GATTCGCGT GCGGATTACA CTGTTTACTA TGGGAGTAGG 900  
 GAGCTTATA TCCGGGCATC GGCTCTCACG CGGTCCGTGT CCGTTACACC GGGAGCTTTT 960  
 TTCTSCGAGG ATGATGTGGA ACGCTCTTAT ATCAAGCTGA ATGGGCTCCC TATCGTTCCG 1020  
 AACGTGAATA TCCGATTGTG GGAGCACAAT GGTAAGGATG AGATTGCTCT GGCAGATAGC 1080  
 50 TCTCGCCTTG TGGACTGCTA TATCTTACC GTTCCGGCCA AGAGCAAATC GTTCGAAGCC 1140  
 GAAGTCTCTG GCACCAATTC CGCTGGAGAC TTCGGGGCGG CTTTGTCTCT CGGTTTCACC 1200  
 GATCGCAATT TGTTTCGTGG GCGCGAGATG TTCAATATCA AACTCAAGGG TGCTTACGAA 1260  
 GCCATTCCGA AGGGTTCGCA CAGCTTCTAT GAATATGGGG TGGAAAGCTC GCTCCGTTTC 1320  
 CCTCGTCTCC TCTTCCATT CATTTCTGAC GAAACGCGCC GCGGGCTACG GGCATCCACG 1380  
 55 GAATGGAAGA TCGGGTATAA TTACAGACA CGTCCGGAGT TTGATCGGGT GATTCTCTCC 1440  
 GCTCAACTCA ATTATTATG GCAGACCTAC CTGCACAATC GTCTGCGTCA TACGATCCGC 1500  
 CTGCTGGATG TCGATTATCT CCATCTCCCG TACATCGATC CCGACTTCCG CCAATCCCTT 1560  
 CCGCTACGA CTGCACTGTA TAATACACG GAGCAGTTTA TCCTCGGCTC GGCATATATA 1620  
 CTGAATATA CCACGGCTTC GTCCATGGAG CGTACCGTAT CCAATCCTTT TACGGCACGG 1680  
 60 TTCAGTATCC AGACAGCCGG GTCCATGGAG CGTACCGTAT CCAATCCTTT TACGGCACGG 1740  
 AAGACGAAC ACGGGTTGTA TAAATGTTC GGTCTGCACT ATGCTCAGTT CGTCAAGCTC 1800  
 GATCTCGATC TGGCTAAAC CGTCTTCTC GAAAGGACA ATACTTTGGC ACTGCATCTG 1860  
 GCTTTCCGAC TGGCTTTCCC TTATGGCAAT GCTCGCCATA TACCTTTGA GTTACGTTAC 1920  
 TTTCCCGAG GATCGAACAG CGTTCGGGCT TGGAGTGTCC GTACCTCGG CCCGGGAGT 1980  
 65 ATGAAGATGA CTCGGACAA GACCTTCTTC GATCAGATGG GTGATATTCG TCTGGATCTG 2040  
 AATGTCTGAT ACAGGACAAA GCTGTTCTGG AAGTTTCGCG CAGCAGCTTT TGTGATGCC 2100  
 GGCAATGTCT GGACGATAAA GGAGTATGAG AATCAGGAGG ACGCTCTCTT TCGTTTCGAT 2160  
 CGCTTCTACA AGGAAATAGC TTTGGCTTAC GGTCTGGGSC TTCGTCTCGA CTTCGATTAT 2220  
 TTCTTGTGTC GGCTGGATGC CGGACTGAAA GCCTACGATC CTCAGCAGAC AGGGCGTTAC 2280  
 70 AAATGGGCTA TCACACGCC AAACCTTTCT TCCAATTTG CTTGGACAT TGCAGTAGGC 2340  
 TATCCGTTT 2349

## (2) INFORMATION FOR SEQ ID NO:64

- 75 (i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (Rule 26) (RO/AU)



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(A) LENGTH: 2625 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

5 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

10 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

15 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...2625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64

20	GTGGAATCTA	AATTGTTATG	TCTTATGAGA	AAAAGAATTC	TACAACTTTT	CCTGACCGCA	60
	TTGCTGCTGG	CATTAGGCTC	CTCTCTCGCC	ATAGCGCAAA	CAGTGGTGAC	CGGTAAGGTG	120
	ATCGATTACG	AAACGTCGGA	ACCGCTCATC	GGTGTATCCG	TAAGCACCGG	TCAGGGAGCA	180
	TCCTCTCGCG	GTGTAACCA	CGATATGGAT	GGTGGCTTCC	GATTTCGAAGT	ACCGGCCAAA	240
25	TCTGCTCTGA	CTTTCGGTTG	CGTAGGTTAT	GCTACCGTAA	CTCGCTCTAT	AGGCAGAGGT	300
	TCTCAAGAA	ACCTCGGTAC	GATTCTCTCT	GATCCCCAGG	CCATCGGCTT	GGATGAGATT	360
	CAGTAAATAG	CCTCTGTGGT	GCCCAAAGAC	CGTATGACGC	CGGTACCGGT	TTCCAATATC	420
	CGTGTGGCTG	ATATTACGGC	AGCATCGTTG	AATGTCGAAT	TTCCCGAACI	GGTTAAATCC	480
	ACTCCCTCTA	CCTATACGAC	AAAAGGAAGC	GGAGGTTTCG	GTGATGGTCG	TACCAATGTG	540
30	CGTGGATTGG	ACACTTACAA	CTTCGGTGTG	CTCATCAACG	GAGTTCCTGT	CAATGGTATG	600
	GAAGACGGGA	AAGTATATTG	GAGCAATTGG	AGTGGTCTGA	TGAATCAAGC	CAGTACCATT	660
	CAGATTACGC	GCGGACTCGG	AGCCTCCAAG	CTCGGTATCA	GCTCGGTAGG	TGGTACGATG	720
	AACATTATCA	CGAAGACTAC	GGACGCCAAC	ACCGGAGGTT	CGGCTTATGT	CGGTATGGGT	780
	AATGATGGAT	TGCACAAAGA	ATCGTTCTCC	ATTTCATCGG	GTATGACGGA	CGGTTGGGCT	840
35	ATCACCATTG	CAGGCTCCCA	TATGACGGGT	CTGGGTTATG	TGAAGGGGCT	GAAGGGACGT	900
	GCATTCTCTT	ACTTCTTCAA	CGTTTCGAAG	AAGTTCAATG	AACGTCATAC	CCTCTCTCTT	960
	ACCGGATTGG	GTGCACCA	ATGGCACAAC	CAACGTTCTT	CCAAATATTC	TGTAGCCGAC	1020
	TATGACAAAT	ACGGCATCCG	TCACAATCAA	TCCTTCGGCT	ATCTGCGAGG	CGAAGTGAAT	1080
	CCTACGGCTT	ATGCTTACAA	TACGTACCA	AAGCCCCAGT	TCTGCTGAA	CCACTTCTGG	1140
40	AAGATGGATG	AAAATACCTC	TCTTTATACC	gCANCTACG	CATCTTTGGC	TACCGGTGGA	1200
	GGTCTCGCG	CTTATGGAAA	GAACAGTAAG	TGGGTATTGA	TCAACTACAA	CACCGGACAA	1260
	CCCTATGAAC	AAACAAAGGT	GACTCCCGAT	GGACTTATCG	ACTACGATGC	CGTACTGGCT	1320
	GCCATGCTG	CGGCGAGCAA	TGGCTCGGAA	GCAATTTTTC	CCCTTGGCTC	CAACTCTCAC	1380
	AAGTGGTTCG	GTCTACTCTC	TTCAATCAAG	AAGAAACTTA	ATAGTTGCGT	GACTTTGACA	1440
45	CCCGGATACG	ATGGGCGTTA	CTACCGTGGC	GACCACTATG	ACAAGATCAC	CGATCTGCTC	1500
	GGCGGTAGCT	ACTACATAGA	GGATCCCAAG	ACAAAGCTCG	CATACCATGC	GGAAAGGTGAG	1560
	CAACTGAAAG	TGGGTGACAT	TGTAAATCGG	GACTACACAG	GCGAAATCAT	GTGGCACGGC	1620
	CTCTTCGCAC	AGATGGAGCA	TTGCTCCGAA	TGGATCGATG	CATTCGTATC	AGGATCTATC	1680
	AACATACGAA	TATACCGCAA	TCACAACTAT	GGCGGTAGCA	AGTCCACCGG	CTACCTGCCC	1740
50	GGCGTATCGC	CGTGGAAAAG	CTTCCTTCGG	TGGAGTGCCA	AGGCAGGTCT	GAGCTACAAG	1800
	TTCCGACAGG	GACACAATGT	ATTGCGCAAT	GGCGGTTTCT	TCACACGTGC	ACCACTCTTT	1860
	GGCAATATCT	ATGCTGCGGG	GGCTATCATT	CCCAATGACA	AAGCCAATAT	GGAAAAGGTG	1920
	CTTACAGGAG	AGGTGCGCTA	TGGATTACCG	AATCACAAA	ACTTCGAGTT	CAATATCAAC	1980
	GGATACATA	CGAAGTGGAT	GGATCGCGTG	ACCTCGAAGA	GAATCGGAAA	CGAGTATGTT	2040
55	TATCTCAATG	GCGTTGATGC	TGTTCACTGT	GGGGTAGAGG	CTGAGGTGAG	CTATCGTCTT	2100
	ATTCTGTCAG	TCGACCTTCG	CGGTATGTTT	TCTCTCGGTG	ACTGGACTTG	GCAAAACAAT	2160
	GTAAATTACA	CTTCTTACGA	CGAAGCCGGC	AATGAGACAG	GGCAGGATAT	AACCTATATC	2220
	AAGGTCCTTC	ACGTGCGAGA	TGCAGCACAG	ATGACGGCTG	CTGTATCGGC	AGACATAGAG	2280
	CTGTTCAAGG	GTTCCTATGT	CATAGGTAAG	TACAACTTCC	TTGGCAAGAA	CTATGCAGGA	2340
60	TTCAACCCCG	CAACGCGTAA	TGCACAGCAG	TACGAAGCGG	ATGGCAAGAA	AATCGTGGAA	2400
	TCATGGAAGT	TGCCCCATGT	AGGTCTGTTT	GATCTGTCTG	CATCCTACAA	TTTCAAGCTT	2460
	GGTTCACTCA	GCACCACATT	CTATTTCAAC	ATGGACAACG	TAGCCGACAA	GCGATATGTG	2520
	AGCGATCCCG	ACGACAATAT	CATCGGTAAG	AAACACGATG	AGGCTTCGGC	TCTCGTATGG	2580
65	TACGGTTTCG	GCCGCACTTG	GTCTACCGGT	ATTCGTGTAA	ACTTC		2625

## (2) INFORMATION FOR SEQ ID NO:65

70 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1380 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

75 (ii) MOLECULE TYPE: DNA (genomic)

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
10 (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65

15	AACAGATGTA ATCCCTCGCG TCAATACTTC CACCTATCGC AGAATGACGT TGGAAGATCT	60
	CTCCGAGCTT TTCTAATCCA TCTATCTATG AAGTTTTCAG TCCGCTTTT CCTCTGCATC	120
	ATCTTTCTCC TCTCTGCATT TATCCTGCCT GCTCTCGGAC AAAATTCAG GCAGGTACAG	180
	CGACTTGAGA AGCAAGCTAA GGAGGCCCTC AAAGCCATCG AAAAAACCA TCGGGAACCTA	240
20	CGAAATACCA AGAAAGACAA GCAAGACAAA CAAAAGCATC TCAACCTCCT GAACAAGCAG	300
	GTTCGCTCAAC GCAAGCAGAT GGTACAATC TTGGACAATG AGGTCAAAGA GTTGCAATCC	360
	GACATTGATT CCATGACGGG TGTATGTCAT CAGCTCTCTG TAGAAGAGAA AGCCCGATCC	420
	GATGAATATG CCCAAGCTCT ACAGTCTATG CAAAAGCGGA AACGCTCGTT GCATCGCATC	480
	CTTTTCATT CTGCGGCCAA GAGCTTTGAC GAAGGCATGC GACGGATCGG TTTCTTGGAA	540
	CAATACGCTT CTGCATACAA GCTGGCATCT GTCCGGCTGC GCGATACAG TAGCAAGTTG	600
25	GAGACTGAAC GTGCGACTCT AGAAGACGCC AAAAAGSAGA AAGGACATCT CTTAGTCATC	660
	AGAGAAGAGG AAAAAAGAA ACTCGAAGGA CAGLAAGCGG AGCAAGCTCG GCAGGTGCAG	720
	GCTTTGGGAG CCAACAAAA AGACTTGGAA GCGCAGCTGC GAAAGCAGAA AAGCAAGCC	780
	GAAGCTCTGA ACAGAAAGAT CGAGAAACAG ATTGCCAAGG AATAGAGAG TGCCGAACGT	840
	CGTGCTCGAG AAGAACGTGA ACGGTTGGCA CGCGAAGCCA AAGCCAAGGG TAAGCCGGTT	900
30	CGTGCGAAGC CGGAACGGAA GCGGAGAGCC AAAGGCGGCT ATGCTATGGA TGCCCTCTGAG	960
	CGTGCTCTCT CGGCGAGCTT TGCACAGAAC AAAGGTGCGC TGCCCGGCCG CGTTCGCGGC	1020
	AGTATCCGAA TCGTAAGCGA CTTTGGCGTG CATCAGCACA GTGAGCTGAA AAAAGTACAA	1080
	GTTAATAATG GAGGTATCGA CATCGCTGTA GCAACAGGAT CCGATGCTAC CAGCGTATTC	1140
	GATGGTGTAG TGTCCAGTGT ATTGCTGATA CCCGGTTATA ATTCCGCCCT AATGTTTCGT	1200
35	CACGCTAACT ATATCAGGCT TTATGCGAAT CTGAGCAAGG TGTATGTAAA TTCCGGCACT	1260
	CGTGTTAAAA CGGGTCAGGC TCTTGCTCGT GCCTATACGG ATCCTTCCAA CAACGAGACC	1320
	ATTATTCATC TCGAAATCTG GAAAGAACGC AGCAACAAA ACCCAAGACT ATGATTACGA	1380

40 (2) INFORMATION FOR SEQ ID NO:66

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1026 base pairs  
(B) TYPE: nucleic acid  
45 (C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

50 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
55 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
60 (B) LOCATION 1...1026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66

	AGTTTTTATC AAGAAATACA CAGACTTATG AAAAAGTATT TGTATATGC CTCGTTGCTA	60
	ACGAGTGTTT TGCTCTTTTC CTGTTCAAAG AACAACTCTA ACGAGCCGGT GGAAGACAGA	120
65	TCCATCGAAA TTTCTATAAG GGTAGATGAT TTCACCAAAA CGGGTGAGGC AGTACGCTAT	180
	GAAAGGAATC AAGGAAGTGC TGCCGAAAGG CTCATTACCA ATCTTTACCT CTTGTTGTTT	240
	GATCAGTCAG GGGCGAATCC GCGGAAATAC TATATTACCG GTAACACTTT CACCGGAGGG	300
	AGCTGGCTTC CTGACGATAT GAAGGTGAAG TTGGATATGA CACAATCCGA GCGCGGAGAG	360
	CGCAAGATAT ATGTCGTAGC CAATGTTGAT AATGCGGTTA AAACGGCTCT TGTGCTGTC	420
70	GCTAACGAAA GCGATTGCA GACTGTAAAG AGGACGACTG CAATGCCGTG GTCGACCGAT	480
	ATAGCCTCTC CTTTCTGAT GTCCGGAAGC AAGACACAGC ACTTCTTGCC CAATCGTCTT	540
	TTGGACAATG TGCCCTTGT GCGTGCCATT GCCAAGGTGG AGCTGAATAT CTCGCTGAGT	600
	GAGAAATTTT AGATTGTGCC GATAATTGTC AATGTTGTTT TGAGTGAGTT CAAGTTCAGA	660
	TACGTAAGCT TCGACAAGGA GACCTACGTA GTGAAGCCAA CGACCAAGCC GGACAACTCT	720
75	ATTAGTTCTG CTAATGGTGT TTGGCTTCAG ATTACAGATT GGACTGTATG GGGTGCTTCC	780

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5 TTAATACTT CTCCTGCTCC GGATGCGGGC ACAGGTTATA CATTGGATGC AAATGGCAAG 840  
 GTAACGGCAC TACGGATTGT TACCTATCTG AATGAGCGCG ATAGCAAAGG GGCTACGGTA 900  
 GAGGTCGCAT TGCCTCGTGT GGATGATGGC ACCCTTCCTC CTCGGAATT CGGTCCGGAG 960  
 CTTTATCGTT TGCCTTTGCC GGACAAGATC CTGCGCAATC ATTGGTACAA GTATGAAGTC 1020  
 GAGATT 1026

## (2) INFORMATION FOR SEQ ID NO:67

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 987 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 15 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 20 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 25 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...987

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67

30 AACCTTAGGA CACAGCCTTT CTTTGGTA GATTGCAAT CTATGATCAG AACGATACTT 60  
 TCACGATATG TATCCTCGAA CTTTGGAGT CGGGGAGCTA CCTTTTTTTT CACGATTTTC 120  
 CCGGCTTCA TCCTCGCCGC TACTGCTTTG CCGGCTTGTG GAGGGGGTAC TGCTTCAGGC 180  
 35 TCCGATCGTA CGCTGGCTGT GACCATCGAG CCACAGAAAT ACTTCATCGA GTCCATTGCG 240  
 GATAAGTCGG TGCAGGTGGT GGCATTGGTA CCGGCCGGA GCAATCCGGA GGAATACGAC 300  
 CCTTCGCTTA CGTGATGAA GCGTTTGTCC GAAGCAGATG CCTACTTCTA TATAGGAGGA 360  
 CTGGGGTTTC AGCAAAGAAA TCTCGCTGCC ATTCCGGACA ATAACCCCTAA GCTCCCTCTT 420  
 40 TTCGAAATGG GCAAAGCCTT GGCGGATGCC GGAAGTGAG ATCTCCACGG CTCCTGCACA 480  
 GATCATTCTC ATACAGACCT GCATGCCCAT GATCCGCACT ATTGGAGCAG TGTGGTAGGG 540  
 GCAAAGGCAC ACMAAGGGCA CGACCGTCTC AACGGAGCTA TCGACAGCGT GAAGAGACTC 600  
 GTCGATACCA TGTITGCCAA TGGCAAAGCA GACAAAGCCT TCGTCATATA TCACCCATCG 660  
 CTCAGCTTTT TCGCCCAAGA GTTCGGCTG CCGCAGATCG TCATAGAGGA AGATGGGAAA 720  
 45 ATCGTATTTA TCCAACCGA ATTTGAAACG CGTCAGGCGG AGGACATCGC ACGCGAGATC 780  
 GGTGCTCGTC CGGTAAGCAT CAATCCTCTG CGCAGCTCGT GGGACGAGGA AATTTTACAT 840  
 ATTGCTCGCG CTTTGGCTCA TGAACGG 900  
 987

## (2) INFORMATION FOR SEQ ID NO:68

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2634 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 55 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 60 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 65 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2634  
 70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68

75 GCAGATTCTA TTCGATATCC TCTTACTTT TTTGGGCGGA ATCGGAAGAA ATGCTTTAGG 60  
 GAACCTATTG CCACCTTATA CAATAAAAC ATGATCGGAA AAAAAATCTT TTTATCCTG 120  
 CTGGCGCTCA TTGCGTTTCA TGGGCTGAAC GCAGCGACAG AACTGAGTT CAAGTACCCG 180

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ACCGATGCCA ATATCATCGG TCACGTCAAA GACAGCAAGA CGGGTGAACA CCTTGTGGT 240  
 ATCACTATTG CTATCAAAGG CACTACCTTT GGTACATCTA CAGATGCAAC GGGGCACTAC 300  
 TATCTTCGTA ACTTGCCTCC GGGTGAGATC ACTTTGATTA TGGGTGGCAT GGGCTATAAG 360  
 AGCCAGGAGC GCGTAGTCCG CGTAGAAAAG GACAAGACTA TCGAGGTGAA TTTGGAAGCA 420  
 GAAGAGGATG CCATCAATCT GGACGAAATC GTGATTTCCG CCAACCCGGA ACTGACGCTT 480  
 CGCCGCTCTG CTCCCTACTCT GGTAAATGTA TTGAACGAAA AAGTCTTCTC GCAAGTCAAT 540  
 GCTTCTAACC TGCGTCAAGG CTGTGTCATT CAGCCGGGAG TTGCTGTAGA GAACAACTGT 600  
 CAGAAGCTGT GTTTCATCA AGTTCGTATC AATGGACTGG ATGGTCTGTA TGCACAGATC 660  
 CTATCGACA GCGTCCCAT CATGAGTGCC CTGCGCGGTG TTTACGGTCT GGAGCAGATC 720  
 CCTGCCAATA TGATCGAAGC TGTGGAGGTA GTACGTGGTG GAGGATCGGC CTGTAGGGT 780  
 TCTTCTGCTA TTGCCGGAGT GGTGAATATC ATCACCAGG AACCTTCTCA CAATTCTTTC 840  
 ACATTTCAATG AATCTCTGAG CTTTACCGGT TTCAGCAAGC TGGATAACAA CACGAACTTC 900  
 AATGCCCTCCA TCGTCAGCGA TGACAACCGT GCCGGTGCCA TGGTATTCCG GCAGGCTCGT 960  
 TACCGCAACU ATGCGGATGC TAACAATGAC GGTATTTCGG AATTGGGTAA AATAGATGCC 1020  
 CGCTCGCTGG GAGCGCATTC TTATTGCGC TTGAGCGACT ACAGCAAAAT GACGGGAGAG 1080  
 TTTCAACGGA TCAGTGAATT CCGCGGTGGT GGCATCGTA TCGATTGGCC TCCTCACGTA 1140  
 TGGGGTGTAG CTGAACAAAC TGACCATAGC GTATTTAGCG GAAACTTGAA ATACGATCTC 1200  
 TTCTCTTCCA ACTATAAACA CCACCTCCAG GCTTATACTT CCGGACAGAT CGTAAATCGC 1260  
 AAGAGCTATT ACGGAGGTAT CCGAGAGATT GACGTCAATG GCCACCCCGG TGGTACGGAA 1320  
 GGCTACCTCCA TCCTCAAGA TCAATACGGC AATAATTATG GCGTGACCAA AGGCAAGACA 1380  
 TATATGGGCG GTATCCAGTA CAGCTACGAC TTGGACAAAT TCCTCTCAT GCCTTCGCAA 1440  
 CTTTTGTTCC GAGCCGAATA TACGCGTGAT GAACTCAATG AAGTGATGCC CATCCTTCA 1500  
 TGGCAGACCG GCGAGGATGC CAATGGGAAT ACCATTCCCC TCTATCCGGA ATTGGATCAG 1560  
 AATATCAACA ACTACAGCCT ATTCGGTCAG AACGAATGGA AAAATGACAG ATGGAGCATC 1620  
 CTGTGTGGCG CTCGCTTGGG CAAGCATAGC GAAGTCAAGG ATATGATTCT GAGTCTCTGT 1680  
 ACCACACTGC GTTTCACCGT GAATCCGGAC ATCAACCTGC GCGCTACATA TGCAAAAGGG 1740  
 TTCCGCGCAC CCGAGGTATT CGATGAGAGC TTGCACGTAG GGGTTGAGG CGGTGAGGCA 1800  
 CAGAAATATG TCAACGATCC GAACCTCAAG CCTGAAATTT CTATGCAATT CAGTTTGAGT 1860  
 GCCGATATGT ATCATCGTTT CGGTAACTGC CAGACCAACT TCCTTGTGGA AGGCTTCTAT 1920  
 ACTCGTTTGC TGGATGTATT CACCAACGAG GAGCAGCGTG ATCAGCAAGA TGGCATCAAA 1980  
 CGCTACACCG CTATCAACGG TAGCGGAGCC AAAGTATTCG GTCTCAATCT GGAAGGTAAG 2040  
 GTGCGATACA AGTCCTTCCA GCTCCAGGCC GGTCTTACCC TGGCCAGCAA CAATACGAC 2100  
 GAAGCAGAGG AGTGGGTCTT GAATACGGTG AAAGACACCA ACGGAGCTTT TGTATCCGAG 2160  
 GCCAATGCAA ATGGACAACA GGAATACAAG AACGAATCCA TGACGGATAC GCAGATCACC 2220  
 CGTACCCCCA GCGTATACGG TTATTTTACT TTGGCCTACA ATCCTGCTCA CTCATGGAAC 2280  
 ATAGCCCTTA CGGAGACATA TACCGGTGAG ATGTATGTAC CCAACGCTAT CGAATATGGT 2340  
 GTGAAGTCTG CCGAAGTGGG TATTATGCGG AACAACTCTG AGATTACCGA CGAAACCGGA 2400  
 AAGGCTCCCC GTATTGATGA GCTGAAGAAG ACACCTGCAAT TCTTCGATTT GGGCTTGAAA 2460  
 GTGGGTTATG ACTTCCAGCT ATTCCAGGCT ACTGAGGTTT AACTCTATGT AGGTATGAAC 2520  
 AATATCTTCA ACTCTTCCA GAAGGACTTC GATCGTGGAG CTGCACGTGA CAGCGGATAT 2580  
 ATCTATGGTC CTACGCAGCC GCGTACAGGC TACATGGGCT TGGTAGTGAA GTTC 2634

## (2) INFORMATION FOR SEQ ID NO:69

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 618 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...618  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69

AAACAGATAG TTATGACAGT AAAGCGCGCA GTGCGAATAG CACTTCTCAC GCTGATAGGC 60  
 ATTCTTTTTT CCTCACCTTC TCTTGTTCGG GCGCAAAATC TTTTCAGCAC CGAATCATGC 120  
 TTGCAACTAT ACAACAAGAT ACTCTATGGA GAGTCGGCGG CGGATACCGT CGCAGAGAAA 180  
 ACGGCAGGTG AGTCGGCATT TCCTTTTATA GACAAATCCA TCAATCTCGG CCGCACTTTC 240  
 CTCGGCAAAAC CATATCGCTA TCGCGGTCCCT TCCCCATGGC CGATGGAGTG CTCGGGCTAT 300  
 GTGTCTTACC TCTACTCCAA ATTCCGACAT AACCTCCAC GTGGTGGCGG AGCAGAGAGC 360  
 CAATATACGA ATCTTATCGA GCGCGAGGAT GTTCGTCCGG GCGACCTCCT TTTTTCAAA 420  
 GCGCGCAATG CAGCGAGCAA CCGTATCGGG CATGTAGCTT TGGTGGTATC TGTCGATGAA 480  
 GATGATATTA CCATGATGCA CAGCGGCAAT TCGCGAGGGA TCGTGTATGA AAAACTCAAT 540

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CGCAGTGCAT ACTTCTCCCG TCGCTTGGTG AGCTATGGCA GGGTACCCGG AGCCAAGAGA 600  
GTGATCCAC GAAAAAGT 618

## 5 (2) INFORMATION FOR SEQ ID NO:70

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1401 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

15 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
25 (B) LOCATION 1...1401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70

AAAGGTACGT GGAAATAGAAA AAACCGAAGA GAAGAAATGA AACGGACAA CTTCTGACG 50  
GCACTGACCG TCCTATCTTC GCTCTCCTTG CTTCGTGCAC AAAATGAATC CGAAGCATCA 120  
30 ACCAATCCGA TGTCAGGCCT CTCCCTGGAA GACTGTATCC GGATAGCCAA GGAGCGCAAC 180  
CTGAATCTCG GCAGACAGGA GATCGAACAA GAAACCGAA TCATTAGTCT CGATGCAGCA 240  
CGACACAGTT TCCTGCCCTC GGTCAATGCA GGCATCGGAC ACAACTATAG CTTCCGACGT 300  
TCGAAAGACA AAACGGGAGT AACCGTAGAT CACTCTCTGA TGAATACCAA TCTCAGCATC 360  
GGAGCTTCGG TGGAAATATT CAGCGGCACA CGTCGTCTGC ACGACCTCAA GCAGCAAAAG 420  
35 TACAACGTGG AGGATGGTAT AGCCCGACTT CAAAAGCGC GTGAAGACCT CAGCCTGCAA 480  
ATCGCGGCTC TCTATATCAA TTTCCTCTTC CGTCAGGAAA TGACTCGTAC GGCAGAAACA 540  
CAGTTGGCAC TGATTCGCGA GCAACGCAAT CGCACGGCCG AATGGTTCG CGTAGGTAAA 600  
TGGGCGAGAG GTAAGCTCCT CGACATAAAT GCCCAGATGG CCAAGGACGA ACAACTTCTC 660  
GTACAATATC GTTCGGAGGA GGAGCTGGCT CGTCTGGACT TGGGGCAGC CCTCGAACTG 720  
40 GAGCAGCCCG AAAGCATTGC AGTCAAGGCT CCGGACACAG ACGTTCTCGT AGCAGAAAGG 780  
TTGGGATCTC TCCTTGCTCC CGAAGAGATC TATCGCACGG CTCTCGGCTT GAAACCGGCA 840  
CTCATTCGA GCGAGCTGCA AATAGCTTCG GCACGCGAAG GTCTGGCCTC GGCTCGTGCG 900  
GCATACITCC CGAGCTCAG CCTCTCTGCC GGATACAGCA AUGGTTACTT CCGCGACCTC 960  
GGCAAGGAGT ATGCCGCCAT CAACCCCTCC TTCTCCGAAC AGTGGAGAA CACGGGCGAG 1020  
45 TACAGTATCG GACTCTCTT GAATATCCCC ATCTTCTCTG CCATGCAAC GCAAGATCGC 1080  
GTTCGGAGCA GTCCCTGCA AATAGCTCA AGCGAGCTTC GACTCGTGA AGAGAAAAAA 1140  
GCCCTGTATA AAGAGATCAG GCAAGCATA AGCAATGCCG TGGCAGCCGA TAAGGCCATC 1200  
GCAGCAGCCG AAAACAGCAA GGCCGCTACG CTCAGGCAT ACGAATACCG TCCGACAGC 1260  
TTGAGGCGAG GGCGCTTGTC TGCTACGAA TATGCGAGG CAAAACAAA ATAGCCCTC 1320  
50 AGCCAAGTGG AAGAACTCG TGCCAAGTAT GACTTCATAT ACAAAGCCAA AGTTTTGGAT 1380  
TTCTATCAGG GCAAAGACTT C 1401

## 55 (2) INFORMATION FOR SEQ ID NO:71

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1353 base pairs  
(B) TYPE: nucleic acid  
60 (C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

65 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

70 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
75 (B) LOCATION 1...1353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71

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5 AAAACATCAT ATCGGAATAA TATGCGTTTC CAACATTATC TCATCTGTAC GGCTGCCGTA 60  
 GCGGCTTTGG CTGCGAATCC CCTTACGGGC CAATCGAATA TGACCTCGA AGAGTGCATA 120  
 GACTATGCAC GCGGCGACAG TTCGGCCGTG GCGCTGTCCG CTGCGGAAC TGGAGCAGTCC 180  
 AAGGCCGATT ACCTTCAGGC CGTCCGCAAT TTTCTGCCCT GTGTATCGGC CGGAACCGGT 240  
 GCTTCGTGGA ATTTCCGACG CGGATTGGAT GCCGAGACGA ATACCTACAC CGACATCAAC 300  
 AGCTTCAACA ATTCGTACAG CATACATGCC ACGATGACCC TTTTCGACGG TTTCGAGAT 360  
 GTCTATCGAC TGGCGATGGC GCATGCACGC CGGAGGGCTT CGCGCCTCTC CGTTCGCGAG 420  
 CAGCAGGAGC TGGCAGCTCT CGGCACCACG GAGGCCCTACT ACGACCTCGT CTATGCGCGC 480  
 10 CAAATGCAAG AGCTGGCCTAT GCAGAAGTAC GAGGAGAGCA GCCGCTCCA CCGGCAGACG 540  
 GCTCGAATGG AAGAGCTGGG GATGAAGAGT CGTCCCGATG TCCTCGAGAT CGAGTCCGGA 600  
 ATGGCCCGTG ACCGTTTGGC CCTGACTCAA GCGGACAATC AGTGCATCAT CGCTCTGATC 660  
 CGGCTCAAG AAAAATGAA CTTCGCCATC GATGACGAAC TCCTCGTAGA CGATATGCGG 720  
 GCTGACAGTC TCTCCGCGA CATGGCCGAA TCGGACAGCT CGGCGCGGT CTTCGCCCGT 780  
 15 GCTGCCCATC ATCATCCGT CTCTCTCCGT GCCAAACTCG ACGAGCAGGC TGCCACCCGAC 840  
 CGTTTCCGAG CGCGCGGAGG TGCAATTCCT CCGAGTGTGT CGGTATCCGG AGGATGGAAC 900  
 ACGGGATTCT CACGCTTTT GAATGGATCG GACTATACGC CTTTCAGCGA CGAGTTTCGG 960  
 AACGTCGGG GGAATACGT CAGTCTGAAT CTGAGTATCC CCATCTTTTC GGGATTCAGC 1020  
 CTGTGTAGCC ATCTCGCTCA GCGCGGTGCC GAACGCAAGG CGGCAATCGT CCGACGCGGC 1080  
 20 GAAGCGGAGC GCAGGCTCTA CAGCGAGATC GCCCAAGCCA TGGCCGACCG GGTATGCCGT 1140  
 CTGGCTTCTT ACCGCGAGGC GAAGGAGCAT ACCGAGGCCA TGCAAAACCG TTACGAAGCC 1200  
 GTCTTGACGC GTTATGAGCA GGGGCTGAAT ACGGCCATCG ACCTGACCAC TCAGGCCAAT 1260  
 CGGCTCCTGG ATGCCCGGT GCAGCGACTG AGAGCGGCCA TGACCTACCG GCTCAATATG 1320  
 25 AACTCATAG CCTATTACGG CTGCTTTTCG GAC 1353

## (2) INFORMATION FOR SEQ ID NO:72

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2886 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 35 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 40 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2886  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72

50 GCCATTTTGT TCGTATCATT GCAAAATTGA AAAATAACAG AGAATAAGTA TAATTCAGAC 60  
 AAGAGCATGA ACAAAATTTA CAAATCACTT TTGCAATCAG GACTGGCTGC CTTCGTGTCC 120  
 ATGGCAACTG CACTGACCGC TTCTGCACAG ATTTCTGTTC GAGGGGAACC CTTCAGTTTC 180  
 TCTTCAAGAT CCGCCGGAAC GCATTCATTG GACGATGCAA TGACTATCCG CCTTACTCCG 240  
 GATTTCAATC CGGAAGACCT GATCGCACAG AGCCGTTGGC AATCGCAAG AGATGGCCGG 300  
 55 CCGTCCGGA TAGGACAAGT AATACCGGTG GATGTGGACT TTGCATCAA GGCTTCGCAC 360  
 ATCTCTTCCA TCGGAGACGT AGATGTATAT CGCCTGCAAT TCAAGTTGGA AGGAGCCAAA 420  
 GCCATTAGCG TTTATTACGA TGCAATCAAT ATTCCGGAGG GCGAGCGCT CTATATCTAT 480  
 ACCCCGAGC ATGAAATGT GTTGGGAGCA TATACGAAC CCACTCATCG CCGCAAGGA 540  
 GCTTTTGCCA CAGAGCCGT ACCGGGGAGT GAGCTTATTA TGGATTATGA AGTGTCTCGC 600  
 60 GGAGGGACTT TGCTGACAT CAAGATCTCC GGTGCGGGT ATATATTGCA CAAAGTCGGC 660  
 GGAGCGCCCG TAACGGATAA CCATTACGGG ATCGGTGAGG ACGATTCCGA TTCGATTGTC 720  
 GAGATCAACA TCAATTGTCC TGAAGGTGCA GACTGGCAGG CAGAGAAGAA CGGTGTGGTG 780  
 CAAATGATCA TGGTAAAAGG ACAGTATATC TCAATGTGCT CAGGCAACCT GCTCAATAAT 840  
 ACGTAAGGAG ACTTTACTCC GCTGATCATT TCTGCCGAC ACTGTGCTTC CATAACAACC 900  
 65 AATTTCCGTG TAACGAATC CGAGTTGGAT AAGTGGATCT TCACTTTCCA CTATGAAAAA 960  
 AGAGGATGCA CCAATGTATC ATTGGCCATC TTCCGTGSCA ACGATATCAT CGGAGCTTCC 1020  
 ATGAAGGCTT TCCTCCCGAT CAAAGGTAAA TCCGATGGTC TCTGTCTGCA ACTCAACGAT 1080  
 GAGTCCCTC TCGCTATCG TGTCTATTAC AATGGATGGG ACGTACGCC CGATATTCCC 1140  
 TCGAGCGGTG CCGGTATTCA TCATCCGGCC GGAGATGCCA TGAAGATTTC CATCTTAAAG 1200  
 70 AAGACTCCGG CTCTGAATAC ATGGATCTCC TCCAGTGGTT CCGGAGGAGC TGACGATCAC 1260  
 TTCTATTCCA AATACGATCA AGGTGGTACG GAAGGAGGAT CGTCCGGTTC TTCTCTCTTC 1320  
 AATCAGAATA AGCAGTGGT CGGCACACTG ACCGAGGGTG CCGCAATTG TGGCGGAGC 1380  
 GAGTTCTACG GCAGACTGAA CAGTCATTGG AACGAGTATG CATCCGATGG CAATACGAGC 1440  
 75 CGCATGAGCA TCTATCTGGA TCCCAAAAC AATGGCCAGA CGACCATCCT CAACGGAACG 1500  
 TATCGTGACG GTTATAAGCC TTGCCCCCTC GTGCCCGGC TATTGTTGCA GTCTACAGGC 1560

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5 GATCAGGTCG AATTGAATTG GACGGCTGTT CCTGCCGATC AATATCCATC ATCTTATCAG 1620  
 GTCGAATACC ACATATTCGG AAATGGAAAG GAAATAGCTA CGACAAAGGA GTTGCTCTAT 1680  
 TCGGATGCCA TCGACGAAAG TATTATCGGT AGCGGTATCA TTCGATACGA AGTAAGCGCA 1740  
 CGCTTCATTT ATCCCTCGCC GTTGGATGGA GTGGAATCTT ATAAGGATAC GGACAAGACT 1800  
 TCTGCGGACC TTGCCATAGG AGACATTGAG ACCAAGCTGA AGCGGAGCT AACACCTCTC 1860  
 CCCGGAGGAG GAGTATCATT AAGCTGGAAA GTTCCTTTCT TAAGCCAGTT GGTTCGCCGA 1920  
 TTTCGAGAAA GCCCAATCC TGTGTTCAAA ACCTTTGAAG TGCCCTATGT TTCTGCCGCA 1980  
 GCCGCACAAA CCCCAATCC TCCCGTTGGC GTAGTCATTG CAGACAAGTT TATGGCCGGT 2040  
 ACATATCCCG AAAGAGCTGC TATCGCTGCC GTTATGTAA TGCCATCCGC TCCGGACTCT 2100  
 10 ACTTTCCACC TCTTCTCAA GAGCAACACA AACAGAAGAT TGCAGAAGGT GACAACTCCC 2160  
 TCCGATTGGC AGGCCGGAAC ATGGTTGAGG ATCAATTGG ATAAGCGGTT CCCGGTGAAT 2220  
 AATGACCATTA TGCTTTTTCG CGGTATCAGA ATGCCTAATA AGTACAAGCT CAATCGTGCT 2280  
 ATCGGTTATG TAAGAAATCC GGATAACCTT TTCTCCATTA CCGGTAAGAA GATTTCATAT 2340  
 15 AACACGAGG TCTCTTTGGA AGGCTACGGA ATACCTCGC TCTTGGGCTA TATGGCTATC 2400  
 AAATATCTGG TGGTAAATAC CGATGCTCCG AAGATCGATA TGTGCTTGT ACAGGAGCCT 2460  
 TATGCTAAGG GAACGAATGT GGCTCCATTG CCGGAATTGG TCGGCATATA TGTCTATAAG 2520  
 AACGGAACAT TTATCGGCAC ACAGGATCCA TCCGTCACAA CTTATTCGGT TTCAGACGGA 2580  
 ACAGAGAGCG ATGAATACGA AATAAACTG GTATATAAGG GATCGGGCAT TTCGAATGGC 2640  
 GTTGCTCAGA TTGAGAAATA CAATGCTGTC GTTGCTATAT CGTCTGTTGT AACAGATCGT 2700  
 20 TTCAGCATTA AGAACGCTCA TATGGTTAC GCTGCCGCC TCTACTCATT GGATGGCAAG 2760  
 CAGGTTCTGT CTTGGAACAA CCTCGCAAT GGGGTGACAT TCAGTGTTC AAGACTTAGC 2820  
 GCGGTACTT ATATGCTCGT TATGCAGAGC GCAACGSGC CTGTGAGCCA AAAGATCGTG 2880  
 AAGCAG 2886

25 (2) INFORMATION FOR SEQ ID NO:73  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2106 base pairs  
 30 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 35 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 40 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 45 (B) LOCATION 1...2106  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73

50 TGGAAAAA GTAATCTCA ATACCGGGG AGGACAGCAA ATTACCGAGA TCATTATAT 60  
 ACAGAAAGCT ATTTAAGCCT AAGGAGGAAT CAAACAATGA AATATCTTAT CAGACTCTTC 120  
 TTATCATTGA TGTACTCTC TCTCTGGACG GGCTGTACAC ACGAGGAGCT CTCTATTTCG 180  
 GATGGCGAGA ATACGCTTGT TTACCGGTA GAGACCGGTA AAGCCCCAA TTGCTCGTGCC 240  
 ACAGAACCCG GTCAGGGCAT ATACAAATGAG AATAAAGTAG GCTCCATTTC TGTGCTCTTC 300  
 TATTACAGG GACAACCTCG TTGGCAGGTG AAGTCTACAG ACTATCAAT CCATGAAGGG 360  
 55 GCCTATATCA TTCCGGTCAA AGAGCAAATG CGACCATAT TCAATGGCAA CAACAATTC 420  
 AGCATCTATG TAGTGGCCAA TCTCGATTTC AATGCTCCGG CCACAGAGC TGGCTTTCT 480  
 CAATTGTGG TAGAGAAATC TATTGAAGTC TCTTCTACGA CAGCCCTGCG CGATTTCGTA 540  
 ATGCTTGCTC ATGGCAATAA GCAGATCAAT ATGGCTACGA CAGAGGGGAA ACTGTTGGGG 600  
 GATTATAAAC TCAACAGAGT GGCAGCAAAG ATTGCGATGA TAAACCCAC CATCAATGTG 660  
 CAAGGATATG AAGTGGTCGG AAATATACAG GCAAAGTTTC GCAATTGGGT AACGAAGGGG 720  
 60 TTCTTACCA CAGAAGCTCA AGAGATCCCA GCTGCTGCAT CCTATAAGAC ATCGGAATAT 780  
 CTTGATATTG CAGAGTCGGC ACCTGCCAAT TCTATCCATT TCTATTCTTA CTATAACAAA 840  
 TGGACACTCT CCACACCGGA GAAGCGACCG GAATCTTCA TCATGGTCAA ATTCAAAAAG 900  
 ACAGGACAGC CGGACAAAC AGCCAAACCG TACTACTACA GAGTGCCCT CGAATCTCAG 960  
 65 GACAATCAGG TCAAGAGCAA TGTCTCTAT AATCTGAATG TGAATATCGA AATCTTGGGT 1020  
 TCTTACAAAG AGCCGGAAGC TGTCTCTGTA AACGGCACAC TCGCAATAGA AGAATGGATT 1080  
 CTCGATCAGG ATGCATTCAA TCTGCCTGCC ACCAATTACT TGATAGTGA ACAGCACGAA 1140  
 ATCTTACATG ATAACGTGAA CACATACTCG GTGAAATATC AAATTCGCA GAACCAATC 1200  
 AGCATTAGCA TACATCAGT TACCTTTAGC TACGCTCTTT CTGATGGCAC TCAGCACATC 1260  
 70 CATCTTGTAG CAAGTAGTAG CGACCAGTAT CCTACGATTA CAAGCGATAA TACAAGCATC 1320  
 ATAATCACTT CCAAGATACC GGTAAATAAC GTACCAAGA AGATCGTTTT TGAGGTAAC 1380  
 AATGGGGTAG CCGGTTTGA AGAGACTGTC ACAGTACTCC AATATCCTG ACAATTTATT 1440  
 GTCAATACAC TTGGCACAGC ATCGGCATGG AGACCAGAGC GATCTTTGGC TCCGGGGCTT 1500  
 AACATAAAG CGATTACCA TGTGTAAGTA CTGCTTCCAC CCGAGAATTT ATTTGAAGAT 1560  
 75 GGGACACAGA CAATCATCGG TTATCCCCC ACTGAACAA TTTCTTTTCA TAAGAAAGAG 1620

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5 AACAATACCT ATCCGATAGT ATGGTCTGAC ACAAATACGA CAAACAGGA CCTTGAGACA 1680  
 TCAAGAATGA TTTCACCTTC CTTTGAGTTA GCCTCCCAAC TTGGGGCTAC TCTCCCGATG 1740  
 CCCTATCTCG AGTATTGGCC AGGGACATCA TATCTCCTTG ACTATTCGGG AACTATAAT 1800  
 AATAAGAGAT ACCGCTTGTT TAATTGCGCT TTTTACTGGG AGAAAAGAAA AGTTAATAAC 1860  
 GAAGAAATTA AATTCGATGA CTGGCGTTTG CCGACAGAA CTGAGATCAA ATTGATAGAT 1920  
 AAGCTGCAAC ATAATGAGCA GAGTGTCTGC CAAGCTATCA TGACAGGGAA TTATTATTGG 1980  
 GATAGTTACT CTGCAATGG GTCTTATAAA ATGCAAGGAG GAGGGGGCCA AGGAAATTC 2040  
 TCCAAAGCCT ATGTTCTGTT CGTGCGGGAT GTGAAAAAGC CGATTCTGA CAAGAAGTCA 2100  
 CGTAA 2106

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## (2) INFORMATION FOR SEQ ID NO:74

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3936 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

20 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...3936

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74

35 AAGAGGGTAG ATAGCTATGA ATGCAGACAA AAAGCTTGCA AATGTGCAAT TTGTGTGATA 60  
 CAAAATTTTA CTAATGTAAA ACTAAATGAT ATGCGAAAAA TTTTGAGCTT TTTGATGATG 120  
 TGCTCTCTGC ATTTAGGCTCT ACAATCTCAG ACTTGGCATG GAGATCCGGA CTCAGTGGCA 180  
 GGCCTACGCTT CTATCGGTAT TCAAGAGTCA AGTTGTACCC GAATCACGTT CGAGGTTGTT 240  
 TTCCCGGAT TTTATAGTGT GGA AAAACGA GAAGGCAACC AAGTCTTTCA GCGCATTTCC 300  
 40 ATGCGCGGTT GTGGCTCGTT TGGGAATCTG GCGGAAGCTG AATTGCCTGT TTTGAAAAG 360  
 ATGATAGCCG TTCCGGAAAT TTCAACAGCT AACGTTGCTG TAAAAATCAA AGAGACGGAG 420  
 ACATTGACAA ATTATAATAT CTATCCTAAT CCTACCTATG TCGTAGAGGA GTTGCCCTGAG 480  
 GGGGGGACTT ATCTGGTAGA GGCTTTGCGG ATAAACAATG ACTATTATAG CCAAAATGTA 540  
 AGCCTCCCTT CTACTCACTA TGCTATTCT CAAGACGGGT ATTTCCGCTC ACAAAGATT 600  
 45 ATCGAAGTTA CCTGTATCC TTTTCGATAC AACCTGTCC GACAGAAAT TCTATTGCA 660  
 AAAAAATCG AGGTTACAAT AACTTTGAT AATCTCAGC CACCTTTACA AAAAACACC 720  
 GGCATATTTA ACAAGTAGC CTCCTCTCCA TTTATTAAAT ATGAAGCTGA TGGCAATCG 780  
 GCGATAGAAA ATGATATGGT GTTCAGTCGT GGTACAAACA CGTACATAAG CGGAAATGTT 840  
 GCGAGCAACC TCCTCAGAA CTGTGACTAC TTGGTTATTT ACGATGATAT GTTCAACGTA 900  
 50 AATCAACAAC CACACGACGA AATCAACGG CTGTGCGAAC ATAGAGCCTT CTACAACGGC 960  
 TTTGATGTAG CTGCTGTAG TATAAGGAC GTATTGAATA GCTTCCATC AAATGCCACC 1020  
 TCATACATCA ACGAACTAA ACTGAANAAT TTCATTGCT CAGTTTACAA CCAAGCAAT 1080  
 GCGAAGAGGA CTTTAGATGG CAACTGGGA TACGTGCTAC TGATCGGAAA ACCAATGAGC 1140  
 AAATATTGG CTGACACTGA TAATACAAA GTCCCAACCT CTTTATTACA TAATGTCTCC 1200  
 55 TTAATTCCAA GTCATCCAAC TTTTGTTCC ATAATGCGCT CCGACTATT TTTTAGTTCT 1260  
 GTTTCGCCCC TTGATACTGT GCGCGATTG TTTATCGGTC GATTTAGCGT CACCAATGCT 1320  
 CATGAATTGC ACAATCTGAT TGAAAAGACT ATCAACAAAG AAATCTCTA TAATCCTATT 1380  
 GCACACAAAA ATATTCTTTA CGCAGAAGGG AAAGGCTGCG ATGCTCCAAT CTACGTTTA 1440  
 TTCTTAAAG AAATCGCCTC TGGTTACACA GTCAACTCTA TCTTAAATC TAATCAGGTC 1500  
 60 TCTGCAATAG ACTCGATATT TGAATGCTT AATAATGTT OCCATCATTT TTATTTTAAC 1560  
 ACTCATGGAA TGCCGACTGT TTGGGGGATA GGGCAGGGAC TCGAGCTCAA TACTCTAACA 1620  
 GCCCATTGA ACAATACATC TPCGAGGGA TTATGTACGA GTCTATCATG TAGTTGGGCT 1680  
 GTAGCAGATT CAATATTAG ATCGCTTGGA GAAGTCTGA CCACATACGC ACCTAACAG 1740  
 GGATTCTCGG CTTTCTTAG AGGAAGCAGA GCCACCCAAT ATGCCGTTTA TTTAGAAGGC 1800  
 65 CCTGTCTC CGTCAGAAAT TTATGAATAT TACCTTATT CTTTATATCA CAATCTCTCG 1860  
 ACTGTTGTTG GCGAAATGTT GCTATCATCC ATTATCAATA CTAATTCTGT TGATACGTAT 1920  
 TCGAAATCA ACTTCAATTT CTTGGCGAC CCTGCACTAA ACATTATGGC TCATGGCATG 1980  
 GAGGTTAGTA ATTGTATTAC ACTACCAAA AACACCAATTA TAAGCAGTCC GATAACAATA 2040  
 70 AAAATGCTG GCTGCCTAAA AATACCGGAA AAAGGAGTTT TGCAATTTAC TAATATGGC 2100  
 TCCATACAAG TCATGTCCGG AGGAACCTCT GAAATAGGCA ATCAGGCTAA AATATCCGGA 2160  
 GAGACCGGCT CTAACCCAC CTTTATTACC GTTTACGGCG ATGGCTCTGC GATTAACAAG 2220  
 CAGGTAGAGA TAGACAATAT AGACCGACT AACTTGTTTT CTACGCATTC GGTATGCCU 2280  
 AAATTTTATT TTGACAGTGT GAAATTCAC AGTGCCCGCG TGTATACAAC GAACTGTATT 2340  
 GTGGAGATAA GCAATTGCGA ATTTACCAAT CGAAGTGACA TTTATTCAAA GAATTGTGAC 2400  
 75 CTAAGCGTTG AAAACAGTAT GTTTAGCAGT TCGGGGATAA CGGTATTCAA GCCTATGGCT 2460



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	ACAAGCTCCA	TCACCGGATT	ATCTACAAA	GCAAAGAITA	CCGACAATAC	TTTTTTTGGG	2520
	ACAGGAAACT	TGCGCTACCA	TATCACAAAC	ACGCCAGGCT	TAACAGCAAC	CTCCAATGCT	2580
	GCCATCAAGT	TAGACAATAT	TCCTGAGTAT	TACATTTCCG	GTAATAAAAT	AGTCAATGTC	2640
	GATGAGGCTC	TTGTACTAAA	TAATAGTGGC	AACAGAAGCA	ACAGACTCCA	CAATATCACA	2700
5	CGGAATGTGA	TAAAAAAGTG	TAGGATTGGG	AGCACGCTTT	ATAATTCCTA	TGGTATTTAC	2760
	AACCGAAATA	AGATCAGTAA	CAATCATATA	GGAGTACGTC	TCCTCAACAA	CAGTTGTTTT	2820
	TATTTCCGATA	ATGCTCCTGT	AATCAATGAA	GAAGATAAGC	AGACGTTTAT	TTCTAATAGG	2880
	ACTTGGGCAGC	TCTATTATC	AAACGGTACA	TTCCCTCTCA	ACTTCATTA	CAACAGCTTG	2940
	CAGGCGGGGAG	ATACAGATAC	ATGGATTTAC	AACGACACGT	ATACGAATCG	CTATATTGAC	3000
10	GGTTCAAAATA	ATCACTGGGG	CAACATGAT	TTGTTTGATC	CGAATCAGGT	TTTCAATACG	3060
	CCAGACTTGT	TCATTGGGAT	ACCTTTTGGG	GATGGATTGC	CAAAATGGGAG	ATCGGGCAAT	3120
	AGCTCTGCTG	AAGCAGTAGA	ATTCCAAACA	GCATTGAGCT	GTATTGGCNA	TAGCGATTAT	3180
	CTTTCGGCAA	AAGTGGCTCT	CAAGATGATG	GTTGAAACCT	ACCCGGAATC	CGACTTTGCA	3240
	ATAGCTGCTT	TGAAGGAATT	GTTGAGGATA	GAGAAAATGT	CAGGCAACGA	TTACGAAGGC	3300
15	TTGAAAGATT	ATTTAGATC	CAATCCAACC	ATCATCTCTT	CCAGAACTT	GTTCCCGACA	3360
	GCTGATTTC	TGCTGCGCG	ATGCGATATT	GTGTGTGAAA	ACTATCAGTC	TGCCATCGAT	3420
	TGCTACGAAA	ATCGCTTGAA	TAGTGAAATC	TCTATCAGG	ACAGTGTTTT	TGCAGTCATT	3480
	GACCTTGGTG	ACATTTATTG	GAATATGCAG	TTAGACTCAC	TCAGAGGGAG	TGGTATAGAT	3540
	TTGACATATC	TTTCTGTGA	ACAAAGGAAA	TCGCTCGAAA	GCCATCAAAA	TGTAAAAAAT	3600
20	TATTTGTTGT	CAACTCTTCC	CGAATCAACA	GGTACTCTCC	TGCCCTCCAT	AGAATGCAAC	3660
	AAATCAAGCC	TTGATAAATC	CAAGATAATC	TCTATTTCCG	CCAATCCGGC	GAAAGCTGTT	3720
	GTAACATAAA	TCTACTATAC	CGATAACCCCT	TCTGTCTTCT	TAATAAAAAAT	ATATGGAATA	3780
	AATGAGCCCT	CGGCTGATAT	AACCGGGTTG	CCCAACATC	TATCCGAAGG	TTATTACAGC	3840
	ATACAGTTCA	ATACATCCAA	CTTTGATCCC	GGTTTCTACC	TGGTAACGCT	AAATGTTGAT	3900
25	CAGAAAATTA	TAGATACGGA	AAAATTACGA	ATCAAA			3936

## (2) INFORMATION FOR SEQ ID NO:75

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2814 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

35 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

40 (iv) ANTI-SENSE: NO

(v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

45 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2814

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75

	TCAGAAAATT	ATAGATACGG	AAAATTACG	AATCAAATAA	TGGCTATCAT	GATGAAAAGT	60
	ATTGTTTTTA	GAGCATTCTT	AACGATTTTG	CTCTCGTGGG	CAGCGATCAC	GAATCCGACT	120
	GCTCAAGAGA	TCTCAGGCAT	GAATGCATCC	TGTCTGGCTG	CTCCGGCTCA	ACCGGATACT	180
	ATCTTATATG	AAAGTTTTGA	GAATGGACCT	GTTCCTCAATG	GCTGGCTTGA	GATAGATGCT	240
55	GATGCTGATG	GTGCCACTTG	GGGAAGCCCA	TCAGGCTCTT	TCTCTGTACC	TTACGGACAC	300
	AATGGCCTTT	GCACCTACTC	CCATATACGT	TCCGGTATCT	CAACAGCGGG	CAACTATCTG	360
	ATTACACCCA	ATATAGAAGG	AGCCAAACGG	GTCAAGTACT	GGGTATGCAA	TCAGTATAGT	420
	ACCAATCCGG	AACATTAAGC	AGTAATGGTA	TCGACAACGG	GGACTGCCAT	TGAAGACTTT	480
	GTTTGTGTTG	TTGATGATTC	CATAACAGGG	AAACCGACTC	CTCTGTATG	GCGTAGACGA	540
60	ATCGTGGACT	TACCGGAAGG	GACCAATAT	ATTGCTATGG	GACATTACAA	AGTCACCGAC	600
	TCACACACAG	AATTCCTTGA	ATTGGATGAT	GTCACTGTGT	ATAGGTCGAT	CGAAGGGGCC	660
	GAACCTGCTA	CCGACTTCAC	AGTAATCAAT	ATTGGTCAGA	ATGTGGGACG	ATTGACTTGG	720
	AACTATCCGG	AGGATTATCA	ACCGGAAGGA	AAGGGGAATG	AAGAGTTGCA	GCTTAGCGGC	780
	TACACATCTT	ATGCGAACGG	TACACTACTG	GCACAAATAA	AAGATGTCTC	CATACTGGAG	840
65	TATGTGGACA	GCACCTACTC	TTTGCGAGAC	AATCCCTTSC	AAGTGGAGTA	CTGCGTTACA	900
	GCCGTTTACG	ATGAAAGCAT	AGAACTTTCG	ACCGTATGTG	CCACGCTGCA	TTACGCCACG	960
	GATGCCATCC	TTTATGAAAA	TTTTGAGAAT	GGACCTGTTC	CCAATGGTTG	GCTTGTGATA	1020
	GACGCTGATG	GAGATGGATT	TAGCTGGGGA	CACTATTTGA	ATGCATACGA	CGCTTTTCCC	1080
	GGCCATATAG	GAGGCCATTG	CTCCTTGTCC	GCTTCTTATG	TTCCGGGTAT	AGGCCCGGTG	1140
70	ACTCCCTACA	ACTATCTGAT	TACCCCAAG	GTGGAAGGAG	CCAAACGTGT	CAAGTACTGG	1200
	GTAAGSCAGC	AGGATGCCAA	TTGGGCAGCG	GAACATTACG	CGGTGATGGC	TTGCACAACG	1260
	GGGACTGCTG	TCGGAGATTT	CGTCATATTG	TTCCGAAGAA	CCATGACAGC	GAAGCCGACC	1320
	GGCGCATGGT	ATGAAAGAAC	CATCAACTTA	CCTGAAGGGA	CTAAATACAT	CGCATGCGCG	1380
	CATTACAAC	GTACCGATAT	ATATTCTTTC	AAGTTGGACG	ATATCACTGT	ATTCGGGACT	1440
75	CCTGCATCAG	AGCCCGAACC	TGTTACCGAT	TTGCTGTCTT	CGCTTATTGA	AAACAACAAG	1500

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	GGACCATTAAGTGGGAATTA TCCTAACGGC TACGAACCCG ATAAGACTGA TGATAAAGAC	1560
	CCATTGCGAGC TTGCCGGCTA CAATATCTAT GCAAACGGCT CGCTCCTTGT TCACATACAA	1620
	GACCCGACTG TTTTGGAGTA TATCGATGAG ACTTATCTT CACGAGACGA TCAGGTGGAA	1680
5	GTGGAATATT GTGTCACTGC CGTTATAAC GACAATATCG AGTCCCAATC GGTTCGCGAT	1740
	AAGCTGATTT ATGATTCTCA ATCGGACATT ATCTTATATG AAGGCTTTGA GGCCGGAAGT	1800
	ATTCTGGAAG GCTGGTTGTT GATTGATGCT GATGGCGACA ATGTTAATTG GGACTATTAT	1860
	CCTTGGACTA TGTATGGACA TGACAGTGAG AAGTGATTG CATCCCTTC GTACTTACCG	1920
	ATGATTGGCG TTTTAACCTCC GGATAACTAT TTGGTTACAC CCAGACTCGA AGGAGCCAAG	1980
10	CTGTCAAGT ATTGGGTAAG TGGCAAGAT GCTGTTTATT CGGCTGAGCA TTATGCTGTG	2040
	ATGGTTCTTA CTACGGGAAC TGCTGTTGAA GATTTTGTCC TCTTGTTCGA AGAGACAATG	2100
	ACCGCTAAGG CTAACGGTGC ATGGTATGAG CGAACTATTA CATTTGCTGC AGGAACAAAA	2160
	TATATTGCTT GCGCGCATTA TGATTGCACC GATATGTTT TCTTGTCTCT GGATGACATT	2220
	ACGGTTTATC GTTCTACTGA GACTGTTCCC GAGCCTGTTA CTGATTTCGT TGTCTCGCTT	2280
15	ATTGAGAATA ACAAGGGTCG CCTGAAATGG AATTATCCTA ACGGCTACGA ACCCGATAAG	2340
	ACTGATGATA AAAAACCACT GCAGCTTACC GGCTACAACA TCTATGCAAA TGGCTCGCTC	2400
	CTTGTTCACA TACAAGACCC GACTGTTTTG GAGTATATCG ATGAGACTTA TTCTTCACGA	2460
	GACGGTCAGG TGGAAATGGA ATATTGTGTC ACTGCCGTTT ATAACGACAA TATCGAGTCC	2520
	CAATCGTTTT GCGATAAGCT GAACATATACT ATCAGATCCT TGGATAATAT TCAATCTGAT	2580
20	ACAAGCTTGA AATATATATCC TAATCGGGCA TCGTATGTGG TAAGGATAGA GGGATTGAGT	2640
	CGGAGCAAGT CGACAATCGA GTTGTATAT GCGCTGGGAA TTTGCATATT AAGGGAAGAG	2700
	ACTCATTTCAG AGAAAACGGA AATCGATGTT TCACGTCTCA ATCAGCGAGT CTACTTGATT	2760
	AAAGTAGTCG GTGGAATATA AACACAACC GAAAAGGTAG AGATAAAGAG GCCG	2814
25	(2) INFORMATION FOR SEQ ID NO:76	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1818 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: circular	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(iii) HYPOTHETICAL: NO	
	(iv) ANTI-SENSE: NO	
	(vi) ORIGINAL SOURCE:	
40	(A) ORGANISM: PORPHYROMONAS GINGIVALIS	
	(ix) FEATURE:	
	(A) NAME/KEY: misc feature	
45	(B) LOCATION 1...1818	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76	
	ATAATCTTCT GTACGATTCA TCACTCTGAG TTGGAATATA TGAACAGCAT CATGAAATAT	60
50	CAATATATA CCGGCGTCAT AATGGCTCTC TCTGTATCAT CCGTTTGGCG TCAAAACCCCA	120
	CGAATAACAG AAACCAACG CCCCGACACG CTGCGCAGGG AGCTTACTAT CGTTAATGAC	180
	CAGACTGTGG AGATGGAGCA TGCGGATCCG CTTCGGGCTG CATACAAAGC CATCGAACCT	240
	CGATTAAAC CTTCGGTCC GGAATATAAC AAGCGTACAT TCGGATTGTT CCTGGAAGTT	300
	TCCTCTTCA GCGAGAACAA TCTTCCGAAT ATCCTGCCGA CGGAAGGTCA TATGAAGCAC	360
55	CGGGGGTACC TGAATATCGG TATCGGCCAT ACGCTAAACC AGCGAATGGA TCGCGGCTAT	420
	CGTCTGATAG ATGCAGAGCA GGAGAGACTG AATCTTTTCC TCTCCTATCG TGGGATGAAA	480
	TCGGCTTCA ATACCGGTGA CTTCGAGCGG GACAGAAAGG ATAGACGAAT GATGGCAGGA	540
	GTGGACTACG AGCAGCGCAG GCCTTCCTTT GTGCTTGCTA CCGGCTTSTA TTATTCGAAC	600
	CATTATTCA ATAACTACGG ACGGGGAGCT ACCACCAATG TGGGCAGCAT CCTCAGCTA	660
60	TCGACACCTG TTACTCTCA GATGGACAAC GGGACCCACA ACGTCCGTGT ATACTTGGGT	720
	GCAAAAATG ATGTGATCGA TGCCAGGATC GACTATCGTT TCTTCCGTTT TATTCCTAT	780
	CTGGGTACCG ATCCGATGAA GGCTCTCACA GAACATACGC CTGAACGTGA CGTGACGATG	840
	AGTAATGAGT TGTCGGATGA TATTAAGCTC GGTGTGGAAG TTCGTACGGG AGGATTGTTT	900
	TTTGCCAAA ACAGCGAAAT GATTCAAACG GCGTTCTGT CCGAAACCGA CCGCAACCTG	960
65	TATTATGTGG AGGGCGCGCC CACAATCGGA TTGTGCGAG ACTCGGACAA TATGCAATGG	1020
	AACATACAG CCGAGTAGG GATTTCTTCC CATTTGCGAG CCAAAGGGAG GTTGTTTTTC	1080
	TGGCTTAAC TGGATGCTTC GCTTAGTATC TTCCCTTCAT GCGGTGTGTA TCGGAAAGCC	1140
	TTGCGCGGTG TGATTGGAAT TGTCTCGCC GATGTTATGC AAGAGGAGAT GCCCTACCTG	1200
	ATGCCCCAAT CGATTGTACT CCTTCGCGC AATGCTTGA CCGCCCAATT AGGGGTGAAG	1260
70	GGGAATATAG CCGATGTGT ACGTATGGAG GTTATGGCG ACTTCTCCAA GCTGACAGGT	1320
	GTGCTTTCT ATACTCCGAC TCTACCTTA TATAATCCAT CGACTTGA TCAGTATAAT	1380
	GTGAGTTCT TGCCGATATA TGCCGACGGC AGCGCTGCG GCGCAGGTGG TAAGCTGGAA	1440
	TACTCTTATC GCGATATGCT CCGCTTTCTG GTAGACGCAT CCTATGGCAA GTGGAATTG	1500
	GATGGAGGAC TTGTGCGCTC CATGCAGCCC GATCTTATAT TGAAGGCAGA AGTAGGTGTT	1560
75	CATCCCATGG CCCCATTGGA TGTGAGACTC CGGTATACAC AGCTGAACGG ACGGTATCGG	1620
	TATTCTTTCC GCTCGGCTGG CTGGAAGGCC TTGGGTATCG GTAATGTACA TCTTCTTAGT	1680

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GCGGATGTTT CATACAAGCT GAAAAAGAAC TTGAGCCTTT ATCTCAAAAT CGATAATATG 1740  
 CTGGCGGAAA CGACAGAGCT TATCGGTTAT TATCCTATGC AGCCGTTCCA TTGTTTCGCC 1800  
 GGTTTTAGCT GGACTTTC 1818

5

(2) INFORMATION FOR SEQ ID NO:77

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1071 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1071
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77

30 AACTCCCATG CAACAGTCTC CGTTATATGT TCAATGATGG AAAAATGTAT CTTTGCTCAC 60  
 TATCCACATA ACCTTGTGTT CATGATTTCG AAGCATTTCG GTATCATTTT GGGATTTCCT 120  
 TCTCTTGTGT TTTCGGCAGG TGCTCAACAA GAGAAGCAGG TGTTTCATT TCTGAACCTT 180  
 CCGGCTACTG CACAGGCTTT GGCTGCCGGA GGCAAAGCTA TCACCATCGT AGACGACAA 240  
 UCCGGACTGG CTTTGTAGAA TCCGGCTCTG CTGGGATATG AATCCGGTGG CCGCGCCTTT 300  
 CTTTCCTATT TATATTATAT GAGTGGTTCG CATATGGGCA ATGCCTGTTA TGCCTCGTCC 360  
 35 GTCGGAGAGC GTGGCAITGG GGGTGTGGC ATGCGTTTCC TGAAGTACGG GTCTATGCAA 420  
 GGATACGATC AGAATGCGAT TGGCAGCGGC TCTTTTAGTG CTTGGGATAT AGCTGTACAA 480  
 GGATTTTACA GCCATGAAC T GAGCAACCA TCCCGCGGTG GAGTCAGCCT AAAAGCATTG 540  
 TATTCTCTTA TCGAGACGTA TAGTTCCCTT GGCCTTGGTG TGGATGTCGG TATCAGTTAT 600  
 TACGACGATG ACAAAGGATA TTCCGCTTCC GCTCTGTTCA AGAACGTAGG GGCAGCACTG 660  
 40 AAAGGCTATA ATGAAGAAGC GGAACCGCTC GATTGGGATT TCCAGCTCGG CTTTCCCGC 720  
 AGTTTATCA ATGCTCGGT TCGCTTGAC ATCAGCTGTG TCAATCTGAA TCCGCACTAT 780  
 TTCAAGCGTC TTGTACCACG CGATCTGTCC AAGATGCAAA AGTTCCTCCG ACACCTTCTG 840  
 ATAGGAGCAG AATTACTCC TTCCGAGAGG TTTGGGTGCG GGCTGGGATA TACGCCACAG 900  
 ATTGCACAGG ATTTCGAGGT GGAAGGCGGC AACAAATGGG GAGGTCTTTC GGCGGCGCTC 960  
 45 GGTTCACACT CAGGTGTAGT ACGTGTAGGC GTATCTGCTG CCACCTATCA TCCTGCAGCT 1020  
 CTTTCGTTCA TGTGTTCGGT AGGTATCCGT TTGGACGATA AGAGCATCTT C 1071

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(2) INFORMATION FOR SEQ ID NO:78

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1011 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1011
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78

70 CCTCAGCCCG TCGGCCTTAA AGAATAACU ATTAACCCCA TGTGCCTCGA ACCATAAT 60  
 GCTCCGATTT CATCGAGTT GCTCGAGCAG GAGCTGACTG CCGATCGTTT TCTGCGGATG 120  
 75 ACAACAAAG CCGCAATGA GATCTATGTT TTTACGGCCG AAGAAGCTCC GCATTGCATG 180  
 AAAGAAGTAG GCCGACTGCG AGAAGAAGCC TTTCCGCATT ATGCGGAGG TACTGGCAAG 240

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5 GCGATCGATA TAGACGAGTT CGACACCATG CCCGGGAGCT ACAACAGCT GATCGTATGG 300  
 GATCCGCAAA ACAAGGCTAT ACTCGGAGGC TACCGCTTTA TCTATGGGGG GGACGTTGCT 360  
 TTCGATACCG ATGGCAAGCC TTTGCTGGCA ACGGCAGAGA TGTTCGCTT CAGTGATGCT 420  
 TTTTGGCAGG ATTATCTCCG CTACACAGTC GAATTGGGAC GTTCGTTTCGT GTCGCTCCAG 480  
 10 TACCAATCGA CACGGATGGG CACAAAGGCC ATTTTGTGTC TGGACAATCT TTGGGACGGT 540  
 ATCGGAGCAC TCAGTGTAGT CAATCCAGAG GCACTCTATT TCTATGGCAA GGTGACCATG 600  
 TACAAGACT ATGATCGGCG AGCTCGCAAT CTGATCCTGT ATTTTCTTCG CAAGCACTTC 660  
 TCCGATCCGG AAGGCTTGGT CAAGCCTATT CATCCCTAC CGATAGAGAT CAGTGGGGAG 720  
 15 GACGAAGCCT TGTCTCTCTC ATCCGACTTT SACACCAATT ACAAGACTCT CAATATAGAA 780  
 GTGGCGAAGC TGGGTATCAA TATCCCTCCT CTCGTGAGTG CATATATAGC TTTGTCTCCG 840  
 GAGATGCGTG TTTTCGGCAC TGCAGTGAAT GAGTCTTTTG GAGAGGTGGA GGAAACCGGC 900  
 ATATTCTTGG CTGTGGGTAA GATCCTGGAA GAGAAAAAC AACGGCACAT AGAGAGCTTC 960  
 ATCCTCAGCC GGAACGAAAA AAAAGGTCTC GACAGTAGCA ATGGCCGATC A 1011

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(2) INFORMATION FOR SEQ ID NO:79

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1698 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

25

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

35

(ix) FEATURE:

- (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79

40 TACCACGGAG CGAGACTGGT CTATACCTTA TTTCCGAATA GAAACGACAT TCACCCTATG 60  
 AAAACCATTT TAAGATACAG CCGCTTCCG GTCCGCTCTT TCTTTTGCTT TTTGGGAGCT 120  
 GTGCACTTGT CTGTCGAGGC GCAGATGCTC AATACTCCTT TCGAGCTGTC GGATCAGATC 180  
 GTCCCTGTCT CCACCGAAAG GCAATACAGG GAGATTGTGT TGCAAACGAA AGAAAAAAGG 240  
 GGGGCCGATC TTTTCCCGTT GAGCGATAAG CTGCGCGATT CGGCCTATGT TCGTTTCGGC 300  
 TCGGCCTATG GCGATATTGC GGGCGACTAT CTTCCTTACA ACGGCATATA CTACTCCTCG 360  
 45 CTCTCGCTCG AATCGGGTGG TCGCATCAGT GTCCGTAAT ATGGCACATT GCAGGGCAGT 420  
 GCTTCTACT CACGTGCCAT GCACAAACGC ATCGGCTGGA ATGCTCTGCG CAACGCCGAA 480  
 GCTTACTATC CCTATTGGT GTCCGATTCG ACGGGCGGAG ACTATCATT CSAAGACTAT 540  
 CGGCTTGCCG GCTACTATTG TTTTCGGCGC GGCCGCTTGC CCTCGGTAT AGGCTTCTCA 600  
 TACAGGGGCG AAGTTGCTTA TCGGCTGACC GATCCGCGTA CGACCAATAC GACCGGTGCA 660  
 50 TTGGAGCTTT CTTGTGCTAC CTCTTTGACG CTGCCTCGAG AGAACAGGCT ATCGCTTTCG 720  
 GCTCGGTATC TCTATCATAG ACAACACCTC ACACAGTACA ACTGGGCTCC CGGGCAGCAG 780  
 GACAAATTCT TCGTCAGCTA CGGTTTCGGT CAGGTGGATG TCAGCAACAG CCCTATCTGG 840  
 TTCGGTATCT CCAGAATGAA CTACGTCAAC GGATGGAAGC TTAGCTCCCG TCTGGATACC 900  
 CGTAGGGGCG ATGCCATCGG TCTCGACTAC AGCGGCTACT TCCTCGATAC CGAAGAGAGG 960  
 55 TCGTCCATCA ATCTCTTTCG TTTGCTTTAC AATCGCCTGC GACTCTATGG TAGCTGGCAT 1020  
 CTGTGCGACT TCGATTTTTC ATTTTCAGCC GACTATGCTC TGGCGCAAGG GATAGAGCGG 1080  
 ATATACGAAG ACTACAAGCC GGATGATAAT TATCATATCT ACGACCTCCG TATCTTGGCC 1140  
 ATTCGCGGCT GGTATATGCT CAATGAGTTT TCTGCCCAAG CCCAAGCCTC CTACGATATT 1200  
 CGCACGGATA GAGGTTGTGC COTGAGAGTG AGTCCCGATA GTGATTCTA CGGCTATGAT 1260  
 60 GAGACGTATC GCAAGCATGG ACATCATACC ATGAGCGGAA TGCTACGTCC TTTTCCCGGT 1320  
 ATAGCCTATG ACCATGCCGG ATCCAATTG GATTTTGGAC TTTTCGTTTC GGCTGCTTAT 1380  
 CGAATGGTGC TGACGCATTC GTATAAGATT CGTACCATCC AGAAAGAGCA GCTCGACTAT 1440  
 CAGCTGCGCT ATTTGCCCTA TGCCTATCGT AATAGAGAAG GCGTGGAGGT GCGTTCCTCT 1500  
 CTGTACGTCT CGATTCCGAT GCAGAAATACC CACCGCCTGA TGACAGAGCT GCGGTTGTAT 1560  
 65 GGCGACCTGA TGAAGAGAAA GGACGGTATA GCCTATGGCA AAACGCCCGG TGTATCTTCA 1620  
 CATATCCTGT CCGATCCGCA AGCCGAACGA ACGTCCGCTC ATACCATCGG GCCTATCTGC 1680  
 AATATCTCCT ACCTCTTC 1698

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(2) INFORMATION FOR SEQ ID NO:80

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2457 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

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(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

5 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

10 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...2457

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80

AGGACGAACG	TTTTCTTATC	1TTGTCCCAT	AAAAATGGGA	GAAGGGGTGC	TTCTGTAGC	60
AATCGGAATG	CGTGGATGGC	TGAGAACAAA	CCCTCATCAC	CTGAACCGGA	TAATACCGGC	120
GTAGGAAACT	CTCCGCTGGA	CTATCTTCAC	GGCGAAGCAA	TCATTCCGCC	TCTCTCTTCT	180
TTGTCCAACT	TCAATGATAA	GAGATTTATG	AAAAAANTTC	ACATGATTGC	CGCCTTAGCC	240
GTCTGCTT	TCTGCTGAC	GGCACAAGCA	CCCGTCTCCA	ACAGCGAGAT	AGATAGTCTT	300
AGCAATGTGC	AGCTCCAGAC	CGTACAGGTC	GTAGCTACTC	GGCCACGGC	GAANACCCCT	360
GTCCGCTTGA	CCAACGTTTC	CAAGGCGGAA	CTTTCCAAAT	CCAATTATGG	TCGTGACATC	420
CCCTATCTGC	TGATGCTGAC	TCCCTCCGTG	GTAGCCACCA	GGGATGCCGG	TACGGGTATC	480
GGATATTCGG	GCTTTCCGCT	GCGTGCCACC	GATGCCAATC	GCATCAACAT	AACTACCAAT	540
GGAGTACCCC	TCAACGACTC	CGAATCTCAG	TCCGTCTTTT	GGGTGAATAT	GCCCGACTTC	600
GCTCTTTCCA	TGCAAGACCT	TCAGGTGCAG	CGAGGTGTGG	GTACTTCCAC	CAATGGTSCC	660
GGAGCTTTTC	GGGCAAGTGT	CAATATGCGT	ACGGATAATT	TGGGACTGGC	TCCCTATGGC	720
CGTGTGCAAT	TGAGCGGAGG	TTGTTCCGGC	ACATTCGGCC	GATCGGTCAA	ACTCGGTAGC	780
GGACGCATCG	GTCCGCAATTG	GGCAGTGGAT	GCCCGCCTGT	CCAAAATCGG	TTCCGACGGC	840
TACGTGGATA	GAGGAAGCGT	GGATCTGAAA	TCCTATTTCG	CACAGGTGGG	CTATTTCGGT	900
AGCAACACGG	CTCTCAGGTT	CATCACTTTC	GGAGGAAAAG	AAGTTACGGG	TATCGCATGG	960
ACCGGTCTTT	CCAAGGAGGA	TGAAGCCAAA	TATGGCCGCC	GATACACAG	TGCCGCTCTT	1020
ATGTACGTGG	ACGCCGAAGG	AGTACCGCAC	TACTACCACA	ATACCGACAA	TTACGAGCAG	1080
CGTCACTACC	ATGCCATCAT	GACGCACAGC	TTCTCTCCTT	CCGTTATCCT	CAACCTCACG	1140
GCACACTACA	CGGCCGGATA	TGGCTATACG	GACGAATATC	GTACCGGACG	TAAACTAAAG	1200
GAATATGCAC	TGCAGCCCTA	TGTGGAAAAC	AGTGTGACCG	TGAAGAAAAC	GGATCTCATC	1260
CGTCAGAAAT	ATCTGGACAA	TGACTTCCGA	GGACTCATCG	GTTCCGTTAA	CTGGCACACC	1320
GGTGCATGGG	ATTTGCAGTT	CGGGGCCCTCG	GGCAATATCT	ATAAAGGAGA	CCACTTCGGC	1380
CGTATCACTT	ACATCAAAAA	GTACAATCAG	CCCTTAGCTC	CCGACTTCGA	ATATTATCGG	1440
AAACAGGGCAG	ACAAAAGAGA	AGGTGCAGCC	TTTGCCAAAG	CCAACCTCGA	GATCACTCCG	1500
GAAGTGAACA	TCTATGCCGA	CCTCCAGTAT	CGTACCATCG	GCTACACGAT	AAACGGCATC	1560
ACGGAGCAAT	ATGATGAGGT	ACAGGGGAAT	ATGCAGCACA	TCGATTTGGA	CAAGACCTTC	1620
CCCTTCCCTA	ATCCGAAGGC	CGGTCTTACC	TATAGTTTCG	ACGATGCTCA	TACTGCCTAT	1680
GCTTCTGTTG	CGGTAGCACA	CCGCGAGCCT	AACAGAACCA	ATTACACCGA	AGCCGGAATA	1740
GGACAGTATC	CTACGCTGGA	GCGACTGATC	GACTATGAGC	TGGGCTACCG	CTATGCTTCG	1800
CCCTCTTGT	CGGCCGGAGT	AGGTCTCTAT	TATATGCAAT	ACAAGGACCA	ACTCGTGCTG	1860
GATGGCCGTT	TGAGCGATGT	GGGACAGATG	CTCACAAACA	ACGTCCCCGA	CAGCTACCGT	1920
ATGGGACTGG	AGCTGACTCT	CGGTTGGCAG	ATCCTTCCCT	GTTTGCTGCG	TGGGATGCT	1980
TCTTTCACCTA	TGAGTCCGAA	CAAAATCGAC	CGCTACGTAC	AATATACATC	CGTATATGAT	2040
GGGACTACA	ACTGGCTCGA	ACTCAAGGAG	GAGACCCTCG	AAAGCACGGA	TATAGCCTAC	2100
TGCCCCAATG	TCATTGCCGG	CAGCATGCTT	ACCCCTCTCT	ATGCCGGTTT	CGAAATGGCT	2160
TGGACGAGCC	GCTTCGTGAG	CAAGCAATAT	CTGGACAATA	CACAGCGCAG	CGATCGCATG	2220
CTTCTCTCTT	ATTGGGTGAA	CGACCTCCGC	CTCGGCTATG	TGCTGCCGGT	TCACTTCGTT	2280
AAGAGAGTGG	CACTGGGCGT	ACAGCTCAAT	AATCTCTTCA	ACCTCATGTA	TGCGTCCAAT	2340
GCCTACATCT	ACGATGCCGG	TTACGTACAG	GCATCCGGAG	AACTAAGTGC	ATATGCCGAT	2400
CTGCGTTATT	ATCCTCAGGC	CGGATTTAAT	GCATGGGTA	GTCTGACAA	CGATTTTC	2457

(2) INFORMATION FOR SEQ ID NO:81

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1596 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81

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10 TACAGGCGAT CGGGAAGGGT TGTCTCTCGT ATCCTCCGGA ACAAACGTTT CTACGCAGAT 60
   ACTCGGTTAC AGCCGAGAAAG AGCGGTTTGA CTACGAGCCG GCACCAGAAC AAAGATGAAA 120
   AGAAGGTTTC TATCGCTGTT ACTGCTGTAC ATACTCTCTT CCAICAGCCT TTCTGCTCAG 180
   CGGTTTCCGA TGGTGCAGGG AATCGAGTTG GATACCGATT CGCTTTTCTC TGTGCCCAAG 240
   CGTCTTTGGC GCGCCATCGG TAAACGATA GGCCTCAATC TGGCCGTATG GGGCTTCGAT 300
15 CATTTTCATCA TGAACGAGGA CTTTGCAGAC ATCAGTTGGC AGACTATCAA GAGCAATTC 360
   CAAACAGGCT TGGCTGGGA CAATGACAAG TTTGTCACCA ACCTCTTCGC ACATCCTTAT 420
   CACGATCGC TCTATTTCAA TGCAGCGAGG TCGAACGTTT TGAGCTTCAG GCACTCTGCT 480
   CCGTTTGCTT TCTTTGGCAG TCTCATGTGG GAGCTGCTTA TGGAAAACGA GCCACCAGAT 540
   ATCAACGACC TCTGTGCCAC CACCATAGGC GGTATAGCTT TGGGGGAGAT GGGGCACAGG 600
   CTGTCCGACC TGCTCATCGA CAATCGTACC ACAGGGTGGG AAGTATGGG GCGCGAGGTG 660
20 GCTATCGCTC TGATCAATCC GATGCGCTTT CTCAACCGTC TGACAGCAGG AGAGGTGACT 720
   TCTGTCCGGA GTCCGAGCGG ACAGATATTT CAGTCTGTCC CCATAAACAT AGTCGTGAT 780
   GCGGCTTTT GCTTTTGGC AGACAAGCGG CATGCCCGAA CCGGTGCCAC GGCTCTGACC 840
   CTGAATCTGA GATTGAGTCA CGGCGATCCA TTCCGAAGCG AGACTTTCTC TCCATACGAT 900
   TTCTTCCAA TCAAAGCCGG ATTGAGTTTC TCCGAATCGC AACCTCTGCT GAGCCAGATC 960
25 AATCTGATCG GAATCCTAAG CGGATGCCAA CTGCTCGCAC ACGAACGAAC GGTTTTGGTG 1020
   GGAGGTCTCT TTCAGCACTT CGACTACTAC AATTCCGAAA AACGAATAAG CAAAATTCG 1080
   GAGGAGGTAC TCGTCACCCC ATACCGTATC TCGCAAGTGG CAGCTCTGGG AGGCGGTCTT 1140
   ATCTTCCAGC ACCACGGAAA ATTTGACGGA CGTCTCTGG AGCTATATGC CGAGACCTAC 1200
30 CTGAATGTGC TCCCGATGGG AGCCAGTCTG TCGGATCACT ACAACGTGGA CAATCGGGAC 1260
   TATAACCTCG GCAGCGGATT GAGCGGCAAG CTATACCTTG GTGCTACGTA CAATGATCTG 1320
   TGGAGCTGGC TCTTGGGAGT CGAAAGCTAT CGGCTCTACA CATGGATCGG GTATGAAGAG 1380
   CCGCACCAGA AAAATACCGA TGTCACTCT TTTATGGTGC AGGGGGACGA AAGCAAGCGC 1440
   CGCTACTGG TGACGAGTTC CGAGTTCGCA TTTCATCTG GCCCTGGCA TGTAGCCATC 1500
35 GTCTCTGCC GTTTCATCG CAAAACAGCC TATCAATTCT ACCCTAACGT ATCATTGAT 1560
   ACCGGCGACA TACAGCTGCG TGTCGGATT CACTTC 1596

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(2) INFORMATION FOR SEQ ID NO:82

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40 (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 900 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: double
   (D) TOPOLOGY: circular
45 (ii) MOLECULE TYPE: DNA (genomic)
   (iii) HYPOTHETICAL: NO
50 (iv) ANTI-SENSE: NO
   (vi) ORIGINAL SOURCE:
   (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
55 (ix) FEATURE:
   (A) NAME/KEY: misc_feature
   (B) LOCATION 1...900

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82

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60 AAAAGAAGAA AAAACAGAT GAAACGACTG ATTGTTTTTC TGGCAATGGG TGGCTTGCTG 60
   TTCACCCCTG CGAACGCACA AGAAGCAAAC ACTGCATCTG ACACTCCCAA AAAGGACTGG 120
   ACTATAAAAG GTGTACCGG ACTAAATGCC TCTCAGACTT CTCTGACCAA CTGGGCTGCC 180
65 GGTGGAGAAA ACACGGTGGC AGGTAACCTC TATTTGAACA TAGATGCCAA CTACCTGAAA 240
   GATAAATGGA GTTGGGACAA CGGTTTGGCT ACAGACTTCG GTCTGACCTA CACAACAGCC 300
   AACAAAGTGA ACRAAAGTGT AGACAAGATC GAACCTCTCA CGAAGGCCGG CTATGAGATC 360
   GGAACACATT GTTACGGAAG TGCGCTTTTC ACTTTCCTCT CACACTATGC CAAAGGATAT 420
   GAGAAGCCCT CGGATCACTT GACAGGAGTC AAGCATATCT CTAATTTCTT CGCTCTGCA 480
70 TATCTCACTC TCGGTATTGG TCGGCACTAT AAGCCCAATG AGAAGTTCTC TCTCTACCTC 540
   TCTCCTACAA CGGGCAAGCT GACTGTAGTA GCAGACGACT ACCTCTCAAG TTTGGGAGCC 600
   TTCGGGGTGA AAGTTGGTGA AAAGACAATG TTCGAACCTG GTGCTTTGGT AGTGGGTTGG 660
   GCCAATATAA ATCTGATGGA GAATGTCAAT TTGATAACCA AGGCTTCATT CTCTCGGCT 720
   TATACGCACG ACTTTGGCAA CATTGACATC AATTGGGAGG CTATGCTGGC CATGAAGATC 780
75 AACAAATTCC TCACGGCTAC GATAGCCACC AATCTTATCT ACGACGATGA TGTGAAGATC 840
   AACGATGGCC CGAAAATCCA GTTCAAAGAA GTTGTGGGCG TGGGTGTTGC GTACACTTTC 900

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## (2) INFORMATION FOR SEQ ID NO:83

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 663 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 20 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...663

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83

25 ACGAGAGAGA GTGTGTTACA TTGTAGRACA AAACCTCAAAA AAGAACGAAA AATGAAGAAA 60  
 ATGATTTTGG CAGCTACTAT GCTGCTCGCA ACAATCGGTT TTGCAAATGC TCAGAGTCGT 120  
 CCTGCTCTTA GACTGGATGC TAACTTTGTC GGTAGTAACT TAATGCAAAA AGTCGCAAAAC 180  
 ACGAGCGTGA ACAATAAGAT GATCGTAGGC TTACGTGTTG GTGCTGCTGC TGAGTTGCT 240  
 30 CTTAGCAATG ATGGATTCTA TCTCGCCCCC GGATTGGCCT ATACGATGAG AGGTGCTAAG 300  
 ATGGAAATCAC TAAGTGAAAC GACAACTCGC TTGCATTATC TGCAAATACC GGTGAATGCC 360  
 GGTATGAGAT TTAGCTTTGC TGACAACATG GCTATTTTCT TGGGAAGCAGG TCCTATTTTC 420  
 GCATATGGTG TCGCCGGAAC GATTAAGACT AAAGTTGCAG GCGTTACGGC TTCTGTAGAT 480  
 GCCCTTGGTG ATAACGGATA TAACCGTTTC GACTTGGGCT TGGGCTTGTG TGCTGCCCTG 540  
 35 AGCTACGACC GTTATTACGT ACAAATTGGA TATGAGCATG GATTGCTTAA TATGTTGAAG 600  
 GATGCTCCGG ATAAGACTTC TTTGCGTAAT CATGACTTCT TTGTGGGTCT CGGTGTTCCG 660  
 TTC 663

## (2) INFORMATION FOR SEQ ID NO:84

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 744 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 45 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 50 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 55 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...744

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84

65 ATCAACGAA TAGAAATGAA AAGGATTTT ACTGTAGCCC TTGTGCTACT TGCTTCGGTC 60  
 ACTATGGCCA TCGGACAAAG CCGCCCCGCA CTTGCGCTAG ATGCCAACTT CGTAGGCAGC 120  
 AATCAGAGCA TGAAAAGAGA CGGATATGTG TGGGACACCA AAATGAATGT CGGCCTGCGG 180  
 GTCGGTGCCG CTCGCGAATT CATGATCGGA TCAAGAGGAT TCTACTTGGC TCCGGGTCTG 240  
 AACTATACGA TGAAGGGCTC CAAAACCGAA TGGGATATAC CCGAAATGGT TCCTGGTACC 300  
 TATATTACGA TGGTTTCCAC TCGCTTGCAC TATCTGCAAC TGCCGATCAA TGCCGGCATG 360  
 70 CGSTTCGACC TGATGAATGA CATGGCGGTT TCGATCGAAG CGGGTCCTTT CCTTGCATAC 420  
 GGTATATATG GTACATATCG GCAGAACTTG GAAGGATGGA AGCCGAACAA CTACAGCACA 480  
 GAGTTTTTTT GCCCAACGCT TGGTGGCCCA ACAAAATATCC GCTGGGACAT CGGGGCAAAAC 540  
 ATAATAGCCG CATTCACCTA TAAGCGTTAT TATATACAGA TAGGCTATGA ACATGGATTT 600  
 GTGGATATTG TGTCAGGTGG AGGTTCTGAT ATTCCCGAC TGAACGACAA TAGGCAATCC 660  
 75 TCTTCGACGA CCGCTCTAAG AGAAAAGGGA AATAACGAAT ACGCTTATAA TCGTGACTTC 720  
 TTCGTGGGCA TAGGTTACCG CTCT 744

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(2) INFORMATION FOR SEQ ID NO:85

(1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 633 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85

AAAAAGAAAGA	GTATGAAAAG	AATGCTGCTG	CTTCTCGTTG	TATTATTATA	TGGAATTGCA	60
GGCCGATTGG	CTGCACAAGA	CGTTATCAGA	CCATGGTCAT	TGCAGGTCGG	AGCGGGATAC	120
TCCGATACCG	AGAACATCCC	GGGAGGATTC	ACCTATGGTT	TCTATTGGG	AAAGCGTATG	180
GGGAGCTTTC	TGGAAGTGGG	GCTGTCCATG	TACAACTCCA	CACGTCAAAC	AGCCAACAAT	240
GCAGACTCCT	TTGCATCGAA	CGAAGGAGAC	GGATCTTTTC	AGGTAAATAT	GTCTTCTCCG	300
AATGAGAAGT	GGTCATTCTT	CGATGCAGGC	AGTGCCAACT	GCTATATGAT	CGTCGTCCGA	360
GTCAATCCTC	TCCATCTGTT	TTGGCAGAAT	AGCCGGCACA	ATTGTTTCT	GGCAGTACAA	420
GCCGGCCTGT	CCAATAAGCA	CAATATTCAT	TTCATCTATG	GAGACAAGGG	AGCCAAAGTC	480
AGTATCTACA	CAAATTCGAA	TACCTACATC	GGTTACGGAG	CACGTGTAGC	CTACGAATAT	540
CAAATTCATA	AAAACGTGGG	GGCGGGTGCC	GCTGTAATGT	ACGACCACGG	CAATAAGATG	600
CTTACGGCCA	TGGCCACGCT	CTCCACTCAT	TTT			633

(2) INFORMATION FOR SEQ ID NO:86

(1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2859 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2859

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86

ATCCGAATGA	GAGTATCCGA	TCTCTGTTCC	AGACTTTCAT	GGTTATTACC	CGTAATCCTT	60
GTCCGATTGC	TCTGTGCTAC	TTTGGTGCCT	GCGGAACGTC	CTATGGCCGG	AGCAGTCGGA	120
TTGCACCACC	GTCCGGCATGC	TGCGCTGTCT	GATTCTACAG	CGAAAGACAC	GGTGCTCTC	180
GCAAAACCTA	TTCTTGACAG	TGCTTTTCGA	GATTCCCTTC	CTGCCGATTC	CACCGGATCG	240
ATGCGGCAAG	ATAGCGTGTA	TGACGATGAA	TTGGAATTGG	AAGATATAGT	GGAGTACGAA	300
GCTGCCGATT	CCATCGTTTT	GCTCGGACAG	AATCGTGCCT	ATCITTTTCGG	CAAGAGCTAT	360
GTGAGCTATC	AAAAGAGTCG	CTTGGAGGCA	AACTTCATGT	ATCTCAATAC	CGACAGCAGT	420
ACGGTTTATA	CTCGCTATGT	CCTCGATACG	GCCGGTTATC	CGATGGCCTT	TCCTGTTTTT	480
AAGGATGGAG	AGCAGTCGTT	CGAAGCCAAG	AACTTTACCT	ACAACTTCCG	CACGGAGAAG	540
GGGATTATCA	CGGGAGTGAT	CACGCAGCAG	GGCGAAGGCT	ATCTGACTGC	CGGTAAGACC	600
AAGAAGATGC	CCGACAATAT	CATGTTTATG	CAAGGAGGGC	GTATACGAC	CTGCGACAAT	660
CACGATCATC	CTCACTTCTA	TATCAATCTT	TCCAAGGCAA	AGGTGCATCC	GGAGAAAGAC	720
ATCGTCACAG	GTCCGGTCAA	TCTGGTTATC	GCCGATATGC	CGCTGCCGAT	AGGTCTTCCT	780
TTCCGGTATT	TTCCCTTTTC	CAACAAATAC	TCTTCCGGTA	TATTGATGCC	CACGTACGGA	840

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5 GAUGACAATC GCTATGGATT TTATTTGAGG AATGGTGGAT ATTATTTTGC CTTACGCGAC 900  
 TATATCGATT TGGCATTGCG TGGGGAGATC TTTTCCAAAG GGTGATGGGG CATTTCAGCC 960  
 CAATCGAAAT ATAAGAAGAG GTATAAGTAC AACGGCTCGT TCGAAGCCAA TTATCTGGTA 1020  
 TCGAAGTCCG GCGACAAATA CGTGCCCGGA GACTACAGCA AGACCCACAG TCTGAATATC 1080  
 CGATGGACAC ACAGTCAGGA TCCGAAGGCC AATCCTTTGC AAACGTTGTC GGCCAAATGC 1140  
 AATTTTGCCA CUGGGAGCTA TTTCAGAAAT TCGCTGAATA CCACCTATGA TGTCAATGCC 1200  
 CGTACTGCTA CGACACGAAG TTCGGCCGTG AGCTATTTCG GCAAGTTTCC GGGTACTCCT 1260  
 TTTTCGATTA CCGGTAGCAT GGATATCAGC CAGAACATGC GCGATACGAC GGTGAGCCTT 1320  
 ACCTTGCCGA ATCTTTTCGAT TAATATGTCC ACGCGTTATC CTITCAAGCG GAAGACCCGT 1380  
 10 GTAGGACCGG AGCGATGGTA CGAGAAGTTG AGTGTGGGCI ATTCCGGTCA GCTTCGCAAT 1440  
 AGTATCTTGA CAAAGAGAA AGATTTGCTC CAGAGCAATC TCGTGGCGCA TTGGAAGAAT 1500  
 GGTATGGCTC ATTCGTACC GATCAGTTTG ACTGTCCCTT TGTGGGATTA TATCAATCTG 1560  
 ACTATGGGGG TTAACATCAA TGAGTGGTGG TACACGAAAG GCATACGGAA GTCGTGGAAT 1620  
 GAGGATAAGA AACCATTCCT GCCTTCGGAC ACGACCTATA AATTCCGCGAG ACTGTACGAT 1680  
 15 TACAGTCTGT CGGCAGGCTT ATCTACCACA TTGTACGGTA TGTTCAGGCC TTGGAAACCT 1740  
 TTTTCTTCG GAGGCAATCT CATTATGATC CGTCATCGCT TCACGCCCAC TGTCACTTTC 1800  
 TCCTATATGC CGGACTTAC GAAACGCGCA TATGGCTTTT GGGAGCTTCT TGAGCATACG 1860  
 GATCAGAACG GCAAGCTGCA TACGCTGCTC TACTCTCCTT ATTCGAGCA GATATTCGCT 1920  
 20 GCTCCCTCCA TGGGCAATGC AGGATCTGTC AATTTCTCTT TTGACACAA CTTAGAGGCC 1980  
 AAGATCAAA CCAATCGGA TTCGACAGGG ATCAAGAAGA TCAGCCTGAT AGATCAGTTC 2040  
 ACATGGTCTA CATCCTATAA TATGTTTGGC GATTTCGATC GATGGAGCAA TATCTCGGCT 2100  
 TCGCTGGCAC TTGCGCTCTC CAAGAGCTTT ACCTTGCGCT TGTCCGGTCT GTTCGATCCC 2160  
 TATTGACGA AGTATTATGA GGGAGAAGAT GGGGAAGATCA TTCCCTATAA GAGCAACGAC 2220  
 CTGCGCATTT TTAACGCGAA GGGATTGGCA CGCCTGATCA GTACGGGTAC TTCTTTCAGC 2280  
 25 TATACGCTCA ACAAGAGTC GCTCAGCGGA TTGATAGCTC TTTTCAGTGG CAAAAAGGAG 2340  
 CGGAGAGATG AAAAGAAAAA CACAGGGGCT ACTCCTCATG AAGGAGACGA TGCTGCCGAT 2400  
 ATACTTGAGG GAGGAAGACC GCAAAATGAA AGTGGGGGGT CGCTCCTCGA GCGCAACCGT 2460  
 CAGGGCGGAG CAGTGGATCA GGATGGTTAC TTCGCATATT CGATCCCATG GAGCCTGTCC 2520  
 30 TTCGACTATA GTTGAATAT TGCTACCGAC TACAATAGGT ACAATGTCAA TAAGATGGAG 2580  
 CACTACTACC GGGTAACGCA GAATCTGAGC TTTCGCGCCA ATATCCAGCC TACACCGAAC 2640  
 TGGAGCTTCG GATTCAATGC GAACTACAAT TTGAGCTTGA AGAAAAATAAC ATCGCTTACC 2700  
 TGCAACGTCA CTCGCGACAT GCACGTGCTGG GCTATCTCGG CCAATTTCTAT CCCTATAGGA 2760  
 GCATACAAAT CCTATAATTT CGTCATATCG GTGAAGAGTT CACTCTTGCA GGATCTGAAG 2820  
 35 TATCAGCAGA GCAATCGTCC CATCACGAAT ACTTGGTAT 2859

## (2) INFORMATION FOR SEQ ID NO:87

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3753 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...3753
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87

60 AAATGGAAT TGGCATGCGC TTTTGATTGC GCGTGTGTT TCGATCCATT TGTAGTAAC 60  
 AACGAGGTAA TAATAATGAT GAAACGATAT ACAATAATTC TTGCAGTTTT TCTTTTATTC 120  
 TGCACGGTAT TTACCTTTCA AATAAAGACT CGCCCTTATG AAAGATTTGC AGATGTAGAG 180  
 AAGCCTTGGG TTCAGAAACA TTCAATGGAT TCTAAATTGG TGCCCTGAAA TAAGGGTAAC 240  
 TTAATTCAAG CTGAAATGT ATACCAATCT GTTTCTGAAC ATAGTGACTT AGTTATTTCA 300  
 65 CCTGTGAACG AAATAAGGCC TGCAAAATCGT TTCCCTTCGC ATAGGAAGTC TTTTTTGGCA 360  
 GAAATCTAC GGGCATCTCC CCCCAGTAGT CCGGTTGCCG TCGACAACTA TGCGGTACCG 420  
 GTTGCCATC CAATGGATCC TGAAATCCC AATGCCCTGG ATGTGACCGT AAAATCACT 480  
 ACTAAAGCGG TAACAGTACC TGTGATGTG GTGATGGTTA TCGACCAATC TTCGTCAATG 540  
 GGAGGGGAAA ACATTGCCAG ATTAAAGTCT GCCATTGCAT CGGGACAGCG TTTTGTGAAA 600  
 70 AAAATGTTGC CTAAGGGGAC GGCTACAGAA GGGGTGCGTA TCGCTCTTGT GAGTTATGAC 660  
 CATGAGCCTC ATGCTTATC TGATTTTACC AAAGACACTG CTTTCTCTG TCAAAAAATC 720  
 CGGGCTTTGA CTCCTATTG GGGAAACAT ACCCAGGGGG GGCTTAAAT GCGGAGAAAC 780  
 ATTATGGCCA CTCTACTGC TGTGGATAAG CATATCATAT TGATGTCTGA CGGGTTAGCG 840  
 ACGGAGCAGT ATCTGTAA AAATGTAAC ACTGCAGACT TCATTGGCAA AACTGAAAT 900  
 75 GCGAATGATC CCATTGATTT GGTATACAA GGAGCAATTA ATTCCTCTAC AAATTATGTT 960

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TCCACAATC CATCTACACC TCTTACCCCA AATTATCCAA CTCATTCTTC TAAAGTTGGA 1020  
 CGGAGAAATC TGCCGGAATC CAAATTCGAT TATAGTAATC TGAGTGCAAG GATTACTTTT 1080  
 GATGGTGTGT CTGGCGCATT GGTCTATGAA CCGAGGTTTC CTCATCCCTA TTATTATTAT 1140  
 TTCCCTTGTA ACCTGTCTAT CAATGAGGCT CAGTTTGCGA AAAACTCTGG TTATACAATC 1200  
 5 CATACTATTG GCTATGACCT GGGAGATTTT GCCTTGCGCA ACAATTCGTT GAAACTAACC 1260  
 GCTACAGACG AGAATCACTT CTTTACGGCG ACACCGGCCA ATTTAGCTGC AGCGTTTGAT 1320  
 AATATTGCCC AAACATTTAA TATAGGTATA CAGAGGGGGG AGGTGACGGA CTTTGTAGCT 1380  
 CCTGGTTTCA TCGTTAAAAA TCTGACGCAA TCGGGAGATG TTACTCATTT GCTAAATGTT 1440  
 10 TCAAAATGGA CGGTGCACTA TGATGTCTCT ACTAAAAAAC TGACATGGAC TACTGGTACT 1500  
 ATCCTGAGCT CATCAGAAGC TACCATAACT TATCGTATTT ATGCCGATTG GGTATATATA 1560  
 CAGAACAATG ATATTCCGGT AAATACTACT TCTGCTATCG GCCCGGATCT TGGTGGATTC 1620  
 GATACCAATA CCGAGGCAAA ATTGACCTAT ACCAATTCCTA ATGGCGAACC GAATCAGCAG 1680  
 TTAATTTTCC CACGTCCGAC GGTAAAGTTA GGTATGCTG TTATTAAGCG GCACTATGTA 1740  
 15 TTGGTAATA AAGACGGTCA ACCCATACAG GCAAAATGGA CAGTTCTCAG TTCCCTAAGC 1800  
 GAGGCTCATG TTCTACATGC ACAAGATTTT TTTTTCGCTT CAGGTGGAGG TCATATTGTT 1860  
 CCCAAATGGA TAAAGTTGGA CAAAACGACC GAAGCATTAC AGTACTATTC CGTACCGCCG 1920  
 ACTAACACGG TCATCACTAC TGCCGATGGT AAACGTTATC GTTTTGTGCA AGTCCAGGGC 1980  
 TCCACGCCCA ATCCGGGGCA AATCGGTATC AGTTGGAAAA AACCGGACAG AAAGCTTAC 2040  
 20 TTGCTTACA AGCTCCTCAA TTATTGGATG GGAGGAACAA CAGACCAACA GAGTGAATGG 2100  
 GATGTGACGT CCAATTGGAC AGGAGCCCAA GTACCGTCA CAGGAGAAGA TGTAGAGTTT 2160  
 GCAACGACAG AAAATTTCCG TTCTCCGGCG GTAGCCGATT TGCTGTCCC GACAACCAAC 2220  
 CCCAAATTA TCGGTAACTT TATCAATAAT TCCGACAAGG ATTTAGTTGT TACCACAAGC 2280  
 AGTCAATTGA CGATCAACGG CGTGGTTGAG GATAACAATC CGAATGCTGG TACGATCGTC 2340  
 25 GTGAAGTCGT CGAAGACAA TCCTACGGGG ACATTGCTTT TTGCCAATCC GGGCTATAT 2400  
 CAAATGTAG GGGGACCGT CGAGTTTAC AATCAGGAT ATGATTGTGC CGATTGTGGT 2460  
 ATGTATCGCA GGAAGTCGCA GTATTTCGGT ATCCCTGTCA ATGAATCAGG TTTTCCAATT 2520  
 AATGATGTGG GCGGAACGA GACCGTCAAC CAATGGGTTG AGCCTTTCAA TGGCGATAAG 2580  
 TGGCGGCCAG CACCTTATGC ACCTGATACA GAGCTTCAAA AATTCAGGGG CTACCGATC 2640  
 30 ACGAATGAUG TGCAGGCACA GCCTACGGGA GTTTACAGCT TCAAGGATAT GATTGTGTG 2700  
 TGCGATGCC TCTGAACTT GACACGCACG TCCGGTGTCA ACTACTCGGG CGCCAACTTG 2760  
 ATCGGAACT CATACACTGG AGCCATCGAC ATCAAGCAGG GTATTGCTTT CCCGCCGGA 2820  
 TCGAGCAGA CGGTGTATCT GTTCAACACG GGAACACGCG ACCAGTGGCG TAAGCTTAAT 2880  
 GGAAGCAGG TTTCAGGCTA TCGAGCCGGT CAGTACCTCT CTGTACTTAA GAATACAGCG 2940  
 35 GGTACAGACA ATCTCCGGA TCGATTCCA TCGATGCATT CCTTCTTGGT GAAGATGCAG 3000  
 AACGGAGCGT CTTGTACGTT GCATATCTTG TACGATAAGC TGCTCAAGAA CACGACTGTA 3060  
 AACACCGGTA ATGGTACGCA SATCACATGG CGATCCGGCA ACTCCGGATC GCGAATATG 3120  
 CGGTCACTTG TGATGGATGT TCTTGGTAAC GAGTCGGCCG ACCGTTTGTG GATCTTTACC 3180  
 40 GATGGGGGTC TTTCTTTCGG ATTCGACAAC GGCTGGGATG GTCGCAAGCT GACTGAAAA 3240  
 GGTTTGTAC AACTTTATGC GATGCTGAC ATCGGTAATG ATAAATTTCCA GGTTCAGGG 3300  
 GTTCCCGAGT TGAATAACCT GCTGATCGGC TTGATGCGG ATAAGGATGG TCAATACAG 3360  
 45 TTGGAGTTTG TCTTTTCGGA TCATTTTCGG AAAGGGGCTG TTTACTGCA CGATCTTCAG 3420  
 TCAGGAGCCA AACACCGTAT TACGAATCT ACCTCGTATT CATTCGATGC CAAGCGGGGA 3480  
 GATTCGGGG CTCGTTTCCG CTGTGTCAT GGAIGTGATG AGAACGTAGA TGATTGCGAT 3540  
 TCGTGAAGTA CAAATGGCCG TGAATTTATA ATTCTGAATC AAGATGCTCT TGACTGCACT 3600  
 50 GTAACCTTAT TCACAATAGA AGGTAAGCTT CTTCGCCGCT TGAAGATATT AGCTGTCAT 3660  
 AGAGAAGTCA TGAAGTGCA GACCGGAGGG GCCTATATTG TGCACTTCA AAATGCTTTC 3720  
 ACTAATGATG TGCATAAGGT GCTTGTGAG TAT 3753

50 (2) INFORMATION FOR SEQ ID NO:88

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1278 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

60 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

65 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...1278

70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88

ACTATGGAG TGAAGAAAA CACAGTGGTG CTACGCCCTC TGATTGGTT CGTGGCCATT 60  
 CTCTCTTCC ACTCTCACG GCTGTGGGGA CAGGAAGGGG AGGGGAGTGC CCGATACAGA 120  
 75 TTCAAAGGAT TCGTGGATAC CTACCATGCC GTACGCAGCT CTCTCTCTT TGATTTCATG 180

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5 AGCTCGCGTA CGAGAGTGAG AGGTGAGCTG GAGAGGTCGT TCGGTAATTC GAAAGTAGCC 240  
 GTATCGGTCA ATGCCACCTA CAATGCTCTA CTGAAAGACG AGACCGGCTT ACGTTTACGT 300  
 GAAGCCTTCT TCGAGCATCA GGAAGAGCAT TGGGGCTTGC GCCTCGGACG ACAGATTGTC 360  
 ATTTGGGGGG CTGCGGACGG TGTGCGCATC ACGGATCTGA TCTCCCGGAT GGATATGACC 420  
 GAGTTTCTGG CACAGGATTA CGATGATATT CGTATGCCGG TCAATGCATT GCGTTTCTCT 480  
 GTCTTCAACG AATCGATGAA AGTGGAAATC GTGGTACTGC CTGTATTGCA GGGGTACCGT 540  
 CTGCTGTGG ATCTCTGCAA TCCTTGAAT ATCTTCTCCC TTTCGCCCAT TGCTCAGGGG 600  
 ATGAATATCG TCTGGAAAGA AGAAGCCGGC AAACCGGCTT TCAAGGTTGC CAATATCGAG 660  
 TACGGTGCGC GATGGAGCAC TACGCTCTCC GGTATCGACT TCGCTTTGGC TGCAATGCAT 720  
 10 ACATGGAACA AGATGCCCGT CATCGAAGTA CAGGGCATTG TGCCGACGGA AATCATCGTT 780  
 AGCCCTCGCT ATTATCGTAT GGGATTGTCT GCGGCGGACC TCTCGTACC CGTCGGACAG 840  
 TTGTGTTTCA GGGGAGAGGC TGGTTTCAAT ATCGACAAAC ACTTCACCTA TAAGAGTCAT 900  
 GCCGAGCAAG AGGGTTTCCA AACAAATCAAT TGGTTGGCCG GAGCCGATTG GTATGCTCCC 960  
 GGTGAATGGA TGATCTCAGG ACAATTCTCA ATGGAAGACA TATTCAGGTA TAGGGATTTC 1020  
 15 ATCTCCCAAA GACAACATTC TACCCTGATT ACTCTCAATG TTCCAAGAA ATTCTTCGGC 1080  
 AGTACACTCC AACTTTCCGA CTTCACCTAC TACGACCTTA CCGGCAAGG ATGGTTCAGT 1140  
 CGCTTTGCAG CTGACTATGC CTGGAACGAT CAGATACATC TGATGGCCGG ATATGACTGG 1200  
 TTCAGTAGTA AGGGCAGCGG TATATTCGAT CGGTACAAAG ACAATTCCGA ACTCTGGTTC 1260  
 20 AAAGCCCGCT ACAGCTTC 1278

## (2) INFORMATION FOR SEQ ID NO:89

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1392 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 30 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 40 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1392  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89

45 TACGGCAAAA GAAGAAAGCT CGGAACCTCC GTCCGACCTT CCGTTCTAAC CCAATCAGA 60  
 TTTATTTTGG ACTTACACCT TATTACTGAT TTTTGAAG GGCTTCGGGT CAATCCTATC 120  
 GGTGCAGAGC CCATAGTGGC TTCTATTATC GACCTGCTTC TTCTTTGCTG TTCGGCTTTT 180  
 ATGTCTCCT GTGAGGTGCG TTATTTTTC CTAAGCCGA TCGATCTGCA GAACATCCGC 240  
 GAACGGAATC ACTCTCCGA CATCGCGCTT TCCAAITTAI TAGACAATTC GAATCAGCTA 300  
 50 TTAGTACTIA TTCTGATCGG GAATAATGTG ATTAATGTAG CCATCGTAT COTTTCCAT 360  
 TATGCCATCG AGCAGACATT CGTTTCTCT TCTCCGATCA TTGGATTCTT GATCCAGAGC 420  
 ATACTCCTGA CCACTGTTCT TTGCTGTTT GGAGAGATTG TGCCGAAAGT GTATGCGGGG 480  
 AAGAATCCCG TGCAATACTC GCGCTTTTCT GCTGCAGCTA TGTCGGTAT CTATAAGATA 540  
 TTGTCAACGT TTTCAAAATT GCTGGTCAAA AGTACCGGCA TCGTTAACCAG AGGTATCAGC 600  
 55 AAGAAGAAAT ACGATAATGC CGTGGATGAG CTCTCGAAAG CCGTAGCCCT CACCACTACG 660  
 GAGGAGAGGC CGGAGGAGAA AGAAATGATT AACGAAATCA TCAAAITCTA TAATAAGACA 720  
 GCCTGCGAAA TCATGGTTCC GCGTATCGAT ATTGTGGATG TGGATCTGAG CTGGCCATT 780  
 CGTAAGATGC TTGACTTCGT TGTTCGTCG GGTATTCCA GACTTCCCGT TTCAGAGGGG 840  
 TCAGAAGACA ATATCAAAGG GGTGATTAC ATCAAAGATC TAATCCACA CATGGATAAA 900  
 60 GCGCATGAAT TCGACTGGCA TCCTCTGATT CGTAAAGCAT ATTTTGTCCC CGAAAACAAG 960  
 CGCATAGATG ATTTGCTCGA GGAGTTCAGA GCCAATAAGG TGCATGTCIC CATCGTTGTG 1020  
 GATGAGTTCG GTGGCACTTG CGGACTGATC ACAATGGAGG ACATATTGGA AGAGATCGTC 1080  
 GCGCAGATTA CGGACGAGTA CGATGAGGAA GAATCCCTT TTAAGGTTT GGGGGATGGC 1140  
 AGTTATCTTT TCGAAGGAAA AACGTCTCTC TCCGATGTT GACACTATCT TGACCTTCGG 1200  
 65 GAAATGCTT TCGGTGAAT GGGGACGAG GTAGATACTC TAAGTGGGCT CTCTTGGAA 1260  
 ATCAAGCAGG AACTCCCCCA TGTGGGCGAT ACAGCAGTGT ACGAGCCATT CCGCTTCAA 1320  
 GTGACCCAAA TGGACRAGCG CCGAATCATC GAAATCAAGA TTTTCCCTTT CGAGCGCACT 1380  
 70 TGGGAGTCCG AA 1392

## (2) INFORMATION FOR SEQ ID NO:90

75 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 798 base pairs  
 (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90

20	ATAATTTATA GATCAACAAT GAAACTATTA CTTTATCTCC TATTGGTCTT GTCGACTCTA	60
	TCCCGGATGT ATTGCGCAAAT GCTCTTCTCA GAGAATCTCA CAATGAATAT AGACAGCACC	120
	AAACCCATAC AAGGAACGAT ATTGCCCCGA CTGGATTICA AAACCGAAAA GGAAATGTG	180
	TTACCCCTCA AAAATACTGC CAATCTCAAT CTGCTGATAA AGCACGGTCA AGTAATCAAC	240
	TTAATTAATA AGCTTGAGTT TTCTACCTAT GGCAATAAAG TAACCGTAAG TGGAGGATAT	300
25	TCGCAATGGG CAGAAAGTAG AGGAATGAAA TATAAGGTTT CTACGGGATT ACAGTCGCGT	360
	TATCGGCTGG TAAATAGTGA TAACTGTCTC ATGTTTGCAA CATTGGGGGT ATTITTCGAA	420
	TTCGAAAAGT GGAACAGGCC AGCCACTAGC CTCTTTGCAG GAACCTATGC ATACAGCCGA	480
	AGTATCAAAA GCCACCTGTC TATCAGTTTC AGACATCGGT TGGGTGAACA TTGGGAATTT	540
30	ACAATACGG CTATTACCA GGGAAAGCCT GACAGTTATT TTAAGAAGGC ACGTTTGGGA	600
	GGAGCTATCG ACCTCAAATA CCATATCACA CCTACGATAG GAATACGGGG GGCCTATCGG	660
	ATCATCTACG ATACTGCCCC TATTGTACCT GTGCGGAAAG ATTACAACAC CGTTGATGTT	720
	GGTATCGATA TTTCGTTT	780
		798

(2) INFORMATION FOR SEQ ID NO:91

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2721 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...2721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91

60	ACTATATGCG TTGCCTTCTT ATCCGCTCCC GTTGGCGCAT TGCGGAGTGC GCCGCCAATG	60
	GGGGCGGAGC GGAAGACTCC CTCTCTCCTA CCCCTTCTTT TCGAGCATTG TGATAAAGGA	120
	AAGGGGTTTC ACTACAGACT ATTCAACAGC AATAAACTTA AAGTGTGTC CACAGGTAAC	180
	AGCCGATACA TACACAATAA ACCAACAATC ATCCAAGCAA TGAACGAAT CGTTTTATCA	240
	TCCTTCTCTG TCGTTCTGTC CATACTTTCT TTGATGGCAC AGAACAATAC CCTCGATGTA	300
	CACATATCCG GTACGATCAA GGATGCTCC TCCGGCGAAC CAGTGCCCTA TGCCACTGTA	360
65	AGCATCCGGC TGACAGGAGC AGATACCACA CAGGTGTTCC GACAAGTGAC TGACGGCAAC	420
	GGCTACTTCG TCATAGGCCT GCCGGCAGCT CCCTCCTATC ACCTGACAGC TTGTTTCGTA	480
	GGTATGAAAA CCCATACCAT GCAGATTAGT CGGGGAAATG GACAGCACGA CATCAATCC	540
	ATCGACATT CTCTCGAATC CGAGGACAAA CAACTCTCCA CCGTCACCGT ATCGGCAGCA	600
	CGACCACTGG TGAAGATGGA GATAGACCGC CTGTCTCTATA ATATGAAGA TGACCCGCCA	660
70	GCCAAGACGA ACAACCTGCT CGAAATGCTG CGCAACGTTT CTITGGTAAC GGTGGATGGT	720
	CAGGGCAATA TCCAGGTGAA AGGATCTTCC AACTTCAAAA TCCACCTCAA TGGCAGGCC	780
	TCGACCATGG TGAGCAGCAA CCGAAGGAG GTCTTTGCT CCATTCTGTC CCATACGATC	840
	AAACGGGTGG AGGTATCAC CGATCCGGGT GTAAAGTACG ATGCGGAAGG CACAAGTGCC	900
	ATCCTGGACA TCGTCACGGA AGAAGGTAA GAGCTGGAAG GATATTGAGG TTCCATCAGG	960
75	GCCAGTGTA GCAACAATCC CACAGCCAAC GGTAGTATCT TTCTGACGGC AAAGTCCGGC	1020
	AAAGTCGGGC TGACTACCAA CTATAACTAC TACGGTGSCA AAAACAAGGG CTCCTGCTAC	1080

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	TTTACCGAAC	GTA	CTACATC	CAT	GCTCCAA	ACG	ATAGAAG	AAG	GCAAAGG	GCA	AGAAACC	1140
	TTTGGCGGAC	ACT	TCGGCAA	TGC	CTCCTC	TCAT	TCGAGA	TAG	ATTCGCT	CAAT	CTCTTT	1200
	ACGGTGGGCG	GCA	ATGTACG	CCT	TTGGGAG	ATG	ACCACCG	ACC	GGAACAG	CGT	AGAAAAA	1260
	AGCTTTGGCG	GCAG	CAACCT	CAT	GTCTAC	ATAG	CAGAA	AACT	CAAAAC	ACAG	ATGGAT	1320
5	GCCGGATCAT	ACG	AGCTCAA	TGCC	GACTAT	CAG	CACAGCA	CTC	GCTGCC	GGG	CGAATTG	1380
	CTCACCGTTT	CCT	ACGCTT	CAC	TCACAAT	CCT	AATAATA	GCG	AGACCTT	CATT	GACCAA	1440
	TGGAAGCGCG	ATC	CGCTCAA	CAC	AGCTAAT	ACG	ATCCAGT	ACG	CCGGCCA	GCAT	CCCAA	1500
	TCCGATGCGG	GCAT	GGACGA	ACAT	ACGGCA	CAAG	TGGACT	ATAC	ACGTCC	CTTA	GGACAA	1560
	GCACATTCTT	TGGA	AGCAGG	GCT	GAAGTAC	ATCT	ATCGTC	ATG	CCACGAG	CGAT	CTCTC	1620
10	TATGAGATAC	GACCA	TCCGA	AGAT	GCTCCG	TGG	CAGCCG	GCT	CTCTATA	TGC	CAGAAAT	1680
	CCGTGGAACG	GAA	AGTTCCG	CCAC	GATCAA	TAC	ATCGGAG	CAG	CCATATG	CGG	CTACAA	1740
	TATCGTAAGG	ATC	AGTATTC	TTT	GCAAACC	GGC	CTCCGAG	TGG	AAAGCAG	CAGG	CTGAAA	1800
	GCACCTTTTC	CCG	AAAACGC	AGC	AGCAGAT	TTCT	CCCA	ACT	CGTTCSA	CTGG	TGCCA	1860
	CAGCTCACGC	TCGG	CTATAC	CCC	CTCGCC	ATGA	AGCAGC	TTA	AGCTGGC	CTAT	AACTTC	1920
15	CGAATCCAAC	GTCT	TGCAAT	CGG	CCAACTG	AAT	CCCTACC	GGC	TACAGAC	CAAC	GATTAT	1980
	CAAGTACAGT	ATGG	TAAATCC	CGAC	CTAAAG	TCGG	GAGAAGC	GTCA	CCACGT	CGGT	CTCTCC	2040
	TATAATCAAT	ACG	GAGCCAA	GST	CATGCTT	ACAG	CATGCG	TCG	ACTACGA	CTT	CTGCAAC	2100
	AACGGCATCC	AGA	AATACAC	CTT	CTCCGAC	CCG	GCCAATC	CCA	ATCTGTT	CCAC	CAGACC	2160
20	TATGGCANAT	TCGG	ACGAGA	GCAT	TCTTTC	AGCT	TGAATA	CCT	ATGCCAT	GTAC	ACGCCG	2220
	GCCGTATGGG	TCAG	GATTAT	GCT	CAACGGA	AATAT	CGATC	GCAC	ATTCCA	AAAG	AGCGAA	2280
	GCATCGGCA	TTAT	GTCAA	TTCA	TGGTCC	GGCA	TGGTAT	ACT	CAGGCT	GAT	GTCAAC	2340
	CTGCCGAAGG	ATT	GACTGT	GAAT	CTCTTC	GGAG	GTTATT	ATCA	TGGGGG	AAGA	AGCTAC	2400
	CAGACGAAGT	ATGA	TGGCAA	TGT	ATTCAAC	AATAT	CGGTA	TAG	CCAAACA	GCTT	TTGAC	2460
	AAAAAATTGA	GAGT	CTCGCT	GAG	CGCAAAC	AACAT	TCTATG	CGA	AGTATTC	GACAT	GGAAG	2520
25	AGCCGGACCA	TCGG	CATGG	ATT	TACTATT	TATT	CGGAAA	ATG	CCGGTAT	ACA	ACGGAGT	2580
	GTTTCCCTCA	GCCT	CACCTA	CAG	CTTCGGT	AAGAT	GAAATA	CACA	AGTGGC	CAAG	GTAGAG	2640
	CGTAGATCG	TCA	ACGACGA	CCT	CAAGCAA	ACCT	CATCCC	AAGG	ACAGCA	GGGT	GCGGA	2700
	CAAGGAAATC	CTAC	CGGCAA	T								2721
30	(2) INFORMATION FOR SEQ ID NO:92											
	(i) SEQUENCE CHARACTERISTICS:											
	(A) LENGTH: 1350 base pairs											
35	(B) TYPE: nucleic acid											
	(C) STRANDEDNESS: double											
	(D) TOPOLOGY: circular											
40	(ii) MOLECULE TYPE: DNA (genomic)											
	(iii) HYPOTHETICAL: NO											
	(iv) ANTI-SENSE: NO											
45	(vi) ORIGINAL SOURCE:											
	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS											
	(ix) FEATURE:											
50	(A) NAME/KEY: misc feature											
	(B) LOCATION 1...1350											
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92											
55	TGGTGCCAAAT	CCG	ACCCAAT	ACCT	CATTGC	CAT	GCAATAT	ATC	GAAACGC	TCA	AGGACAT	60
	CAACAAGGGC	GAT	CAGACCA	AGAC	CGTTTA	CCT	CCCCTTC	GAG	GCTACCG	GTAT	GCTCGG	120
	TGCCTTGGGC	GGT	ATGAAGG	ATT	TGGTGAA	AGG	ATGAGAC	TCT	CTGCCAT	TCT	TATCGCT	180
	TTGATTGTGA	TGCT	GCCTGC	TGT	GCTTAGC	GGG	CAGCATT	ATT	TATCCAT	GGC	GGGAGAG	240
	CGACTGGAGA	CGG	ACAGCAT	TCGT	CCGAAC	GAA	CTCTCGS	CAT	CGATCCG	AAG	TGCGCTT	300
	TTCTTTCGGA	ACA	ATGAATA	CAAT	GCAAGT	TCGT	CAAAAG	GTT	TATAGTT	GCG	GGTGCA	360
60	CGGGTTTCCG	CTTT	TGCCTC	TTAC	TGCTG	CCG	CAGCAC	ATGG	TGTGAA	GCTT	TCGCTC	420
	GGAGTATCTA	CCCT	GAACTA	CTGG	GGGGCA	AGT	CGCTATC	CGG	CCGGTAT	CGCT	TATTCC	480
	GATTTACCTT	ATT	GGACGGA	CTAT	AACGAC	TAT	GTACGCT	TGG	TATCCT	GCT	TATGTA	540
	CAGGCCATGC	TGA	AGCCGAC	GGCC	CAGACT	GCT	CTCATGC	TGG	GCAATAT	AGC	CGGTGCT	600
	ACGGCTCACG	GACT	GATCGA	ACCG	ATCTAC	AAT	CCTGAGT	TGG	ATTGAC	GGC	TGATCCT	660
65	GAAGCCSGTG	TGCA	ATTTCG	GGGT	GATTGG	ACAG	CTTCC	GAAT	TGGATGT	TTGG	GTCAT	720
	TGGATGAGCA	TGAT	TTTCAA	AAAT	GACAAT	CAT	CAGGAGT	CGT	TTGTCTT	TGG	CTTGTCC	780
	ACTACTTCGA	AATT	GTTATC	GGGT	GAAAGC	AAAT	TGGGAC	TCGA	ACTGCC	CTT	GACGGCT	840
	ATTGCCACGC	ATCG	CGGCGG	GGA	ATACAA	TGGG	CGCAGC	AGG	ATACCGT	GCAT	ACATGG	900
	GTCAATGGAG	CTGT	CGGACT	TAAG	CTTTCC	TAT	CGCCCTC	GTAC	CGACAA	ACCC	ATGCAG	960
70	ATTTGGGGAT	CTG	CTTATGG	TGT	GCGAGCC	TTGT	CAAGCG	GAGG	ATACTT	CCCT	TACGAA	1020
	AGAGGGTGGG	GCG	GTTATCT	TTCT	CTCGGA	ATGG	AGCTTGG	AGCA	CTTCGC	TTT	TCGTACC	1080
	GACTATTGGT	ACGG	CAGGCA	TTAC	GTTTCT	CCCT	TTGCTG	CAC	CTTTCGC	CAAT	TCCTTG	1140
	ACGTATGACA	AAC	AGCCTCT	TAC	GAACGGT	TGGG	CGGATT	ATAT	TCGTCT	CTAT	GCGGAC	1200
	TATTCGTGGC	GGAT	GGCACG	AAG	TGTTTCG	TTGG	CGGCTG	TTGT	CTCGGT	ATGG	TCCAG	1260
75	CCTTCGGATC	GTTT	TGCGAT	GAG	CCACGCC	TTGG	AACTGA	CGAT	GCGTAT	CGAT	CCCCAAA	1320

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TTCCCAATAG CTTTCTGAA AGGCAATCAT

1350

## (2) INFORMATION FOR SEQ ID NO:93

5

## (i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 1341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

15

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

20

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...1341

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93

CGGTTTTCAC CGCCATGGGT ATGTGCTGGA GCGGCTTCCT CAGTACGCAC ACGGCCATGC 60  
 TCGACAGTCT CAAGTACCGC CGCCTCATCA CACAGGCGAT CGGAGCACAT GCGATCGGCG 120  
 GACTCGTGGC CGGCATATTC GCCCATTTGGC TCTTTGTCTT CATCTCACTC ATTTGATTCT 180  
 ATACCCGACC AACGTATGAA CAAATCGCTA TTATCATTGG CATCCCTCAT CCTGTGCGGT 240  
 ATGCCGGCCA TCGCCCAACA GACAGGACCG GCGAAGCGCA GCGGCGAGCC TTCTCTGGCC 300  
 GAACGTGTAT TCGGTCTGGA GCAGAAGCAG AAAAAGCTGA AGGTGTACTT AGGCATACAG 360  
 TCGTTCTACG ACCAGCGGCT TGTGATGAC GAATCCATA TCGGACACTT CAAGGTACAG 420  
 GAGCTGCGGA TGTCTGCTCA TGGCGAACTG AACCGCCACC TCAGGTTTGA CTGGCGACAA 480  
 CGTCTCAACC GTGCGGCGGA CGGCACTTCG TTTGCCGACA ATCTCTCCAA TGCCATCGAC 540  
 ATCGCAGGTG TGGACTGGCA CCCGAACGAC AAGGTGTCTT TCTCTTCGG ACCTCAGTAC 600  
 GCGGTTTTCG GAGGGATAGA ATACGACATG AACCCGCTAG AGATCTACCA GTACAGCGAC 660  
 CTTGTGGATT ACATGACCTG CTATCTTCG GCGTGAACT TCGCATGGAA CTTCCACCCC 720  
 GAACAGCAGC TGCAGCTACA GGTACTCAAT GCTTACAACA ACCGCTTCGC CGACCGCTAC 780  
 CACGTGACAC CCGATGTGCG TACCGCCACG AGCTACCCGC TCCTCTACTC GGCACAGTGG 840  
 AACGTATCCC TCCTCGGAGG AGCACTGCAT ATGCGTTACG CCGTGTGAT GGCTCATCAG 900  
 GCCCAAGAGC GTAATATGTG GTACTTCACT GCGGGCAACC TGTTCATCC GGGCAAACGG 960  
 ATCAACGGAT ACCTCGACCT CACCTACTCG ATCGAGGGAT TGGACGACAA AGGCATTATG 1020  
 ACTGCTCGCT ACGGCAAGGG CAAGACCCTC ACGGACGTCA AGTACTATGC TCTGGTATCG 1080  
 AAGTGGAACT TCGCATTTT CGATCAGGTC AATCTCTCC TCAAAGGCAT GTACAGAAAC 1140  
 GGCTATGCGC CTGCCCAATA CGGCGAGAGC AGCCACAGCG GCCACTCCTA GGGCTATATG 1200  
 GGAGGCGTGG AATATTACCC TACGGAGACC AACTTCCGTC TGTTCGTAC CTACATAGGA 1260  
 CGGCATTACC GGTACAGTGC GACCGAGACG GAAAGCACCA ATGCTCTTCG CCGCGGTCTG 1320  
 ATCTATCAGA TACCTTTCTT A 1341

50

## (2) INFORMATION FOR SEQ ID NO:94

55

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

60

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

65

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

70

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...681

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94

75

TATAAGCAAG CTATAATGAA ACATTGTTT AAGTCGACAT TAGTACTTCT TTGTGCTCTT

60

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5 TCTTTTCCG GTACCTATAC CTTTGACAAA GAAAATAATA CAGAAAAGTC ACGATTGAT 120  
 TTTTCTGTTA GGCTGGGACA GGGATATATT GCAGGTTCAA CTACCAACCT GATGTATGGG 180  
 TATACATCTG CTAACGATAG ACTTTTGTCT GGTGCAATTT ATCTGGGCTT GACACCAAGT 240  
 AAGAAAGAAA ATGCAACCGG CGTAGCATT CTTTTCTTAT CCCCCCTCC GGGTTATTAT 300  
 10 GTCGATATAT CCGGCAAGA AAATACCTTG AATTATGCGT TTACGTTGT CGGAGCATAT 360  
 AATAGAATAG CCATTCCAT ACGCCCTATC AAAAATTTTA ATTTCTACTT CTCTACAGAA 420  
 GTCGGAATGG CTGGGATGAG TCGTCATGAG CAAATTTACA ATTCTACTTC GCAGACTTGG 480  
 GATAAGCAGC GCAAGTCGAG GTCGGGACTG GATTTTGGTC TCGGGATGCA TCTGCAATHC 540  
 CACATTAATA AGACCGTTTA CTTTATGGCA GGAACCGATC TTACGTTCTG CATGTTCCGA 600  
 15 AAAAGGATCA ATGACTACCA GCRAAAGGAT CGAACCTTCA TTGCACATAT CGCAACAGT 660  
 ATTGGCATAG GATTAAACCT C 681

## (2) INFORMATION FOR SEQ ID NO:95

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1218 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 25 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 30 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...1218

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95

35 ATATTCATAG ACCCCGATAA GAATACAAAA CAAAACGAAC GAAATATGAT TATCAAGAAA 60  
 ATGCTGAAAA ATAAATTGGC CCCCTTGGCC ATACTGTTCC TTTTGTCTCC AAAGGCTATG 120  
 40 AAGGCTCAGG AGCAACTGAA TGTGGTACAC ACCTCTGTGC CATCGCTGAA TATCAGTCCG 180  
 GATGCACGTG CGGCCGGTAT GGGGGATATA GGTGTGGCAA CGACGCCGGA TCGGTATTCA 240  
 CAGTATTGGA ATCCGAGTAA ATATGCTTTC ATGGATACGA AAGCCGGTAT TAGCTTCTCA 300  
 TATACACCTT GGCTGTCCAA GCTGGTCAAT GATATTGCC TGTGTCAGAT GACCGGTTTC 360  
 TACAAATTGG GAACAGACGA GAATCAGGCT ATTAGTGCTT CTCTGCGTTA TTTCACATTA 420  
 45 GGAAAGTTGG AGACTTTTCA CGAATTGGGC GAATCCATCG GAGAGGCCCA ACTTCTCCAT GGCTGTGCA 480  
 TTTGCTGTGC ATTTGGGCTA TAGCCGCCAG TTGTCCGAGA ACTTCTCCAT GGCTGTGCA 540  
 CTGCGTTACA TCGGCTCAGA CCAAGCACT CACAACCCG GAGAGATCA GGCCGGAAAT 600  
 GCCTTTGCGG CGGATATAGC CGGTTATTG CAGAAGTATG TGCTACTGGG TAATGCGGAG 660  
 AGCTTGTGGT CGTTGGGTTT CAACGTAAAG AATATCGGAA CGAAGATCTC CTATGACGGA 720  
 50 GGTGTACAGA GTTTTTTCAT CCTACTTCG TTGAATCTCG GGACGGGGCT GTTGATCCG 780  
 ATCGATGACT ATAACAGCAT CAATTTCAAC CTTGAACCTA GCAAGCTGCT TGTACCCACT 840  
 CCTCTATCA TGGATCAAAA CGATCAGGCC GGGTATGAGG CTGCACTCAA GAAATATCAG 900  
 GAAACTTCTT CGATCAGCGG TATATTCTCT TCTTTCGGTG ATGCGCCGGG AGGACTCAAG 960  
 GAAGATTCC GTGAGATTAC ATGGGGACTT GGGGCTGAAT ATAGCTATGA CGATAAAATT 1020  
 55 TTTGTTCGTG CCGGATATTC ATACCTGCAC CCCACCAVAG GCAATTGCA GACTTCACG 1080  
 GCCGGTCCG GCTTCAAAAT GAACATATTC CGTATCGATG CTTCTACTT GTTGCTACG 1140  
 ATCCAGAGTA ATCCGTTGGA TCAGACTCTG CGGTTTACGC TTGCTTTCGA TATGGATGGA 1200  
 TTGCACAATT TGTTCAC 1218

## (2) INFORMATION FOR SEQ ID NO:96

- 60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1356 base pairs  
 65 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 70 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 75 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

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## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1356

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96

```

CTAATAATCG AAAAGGAAAT GAAACAACA GTTCAACAAA TTATTCTGTG CCTGGCTTTA      60
ATGATGTCAG GTGTATTGGG CGGAAACGCA CAGAGCTTTT GGGAAAGAAAT AGCTCCTCCT      120
TTTATCAGTA ATGAGCCTAA CGTCAAGTAT ATAAITCCCA ATATGGGGAT TGATTCAAAG      180
GGAAACAATCT ATGTAACCGT GACAAAAAGG ATTACGCAGG GAGCAATTA TACTTCTGAG      240
CAATTGGCTA TGTACTATCG ACCATTAGGT GATAATGAAC AGTGGTGGAA ACATGATCCG      300
TATTTTGATG ACAAGATAGT TCGGGATATT CAGACAGATG CATATGGCAG AGTTTATGTA      360
TGTACGACTT CTTCCTCGAG TCAAGAGTAT CAACTTTATA TAAACGAGCA GAACGAATGG      420
AGGTGTATAT TCAAACTTC TGTGTCTACA TATGAGCATG GTATGGCTGT TTTTCGCTCT      480
TCGACAGGGG TGACTTATAT AGGTACCAGG CATCACATCT TCGCATCAGG TGTAATGAT      540
TTGAGTTTCA ACACTATCTA TGAAGACTCT ACACCTATGA GCTGTGCTT TGCAGAGGCT      600
ACGAATAGTG GCACCATCTA TCTGGCATTG ATGCATGAAA CCACATGTC TACGACTATC      660
CTTACTTATC AAAACGGTGA GTTCGTCGAT ATCTCGGAAA GTGAATTGAG TAACTCGATT      720
ATTGCATCCA TGTGCTCTAA TAAAGAAGGT GATATAATAG CTCTTGTAC TTCATATACA      780
CGATTATGA GTGGAACCTT TCGGATCACA AAAGCAGATG AAGGCAATG GCAACTTGT      840
GGCGGAGATA TACGAATGC GATCGTTCAA AATATATGCA TGATGGACGA CAACAGATT      900
GCTTGTGAAG TCTTCGGGAC TCCTAACGGA GTAGATGGTC GGACAAGGGT TTGTGTTCT      960
GACGATCTG TCTTTGATTT TGAGTGGTAT GAAGATGAAA TATACGGAGG CCTGATATTT      1020
GACACTTTCT TCTATAGCCC TTGGGACAAA CTTCTTTATG CGAAATTG3 TGGGATTATG      1080
CTCAGGAGTA AAGAGTCTT TATAACCTCT TTCATTTCTC CGACAGTTGT ACAAGGAGTG      1140
GATGTCATATA CTTTGGCCGG GAAGATAAGG ATCGAAAGTG AAACCTCCGT GTCTGAGGTG      1200
TTGCTTTTCC ACCTGGCTGG CAGGATGGTA CTTGCGCAAA CCATTGATAA TAAATCTAT      1260
TCGACATAG ATACTAACGG ACTAAGCGA AGCGGTAATT ACGTAGTCTC GGTGCGGCTC      1320
TCTCCGGAC AGGTATTGAG TCATAAGGTG CAGGTA      1356

```

## (2) INFORMATION FOR SEQ ID NO:97

35

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 993 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

40

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

45

(1v) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

50

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...993

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97

```

GGCGTGTACG GTATGCTGT TGIACCTATA ATAAITTTAT TTTGCGGTAT ATCAAATTAT      60
GCAAGACTCA TGATAATCCG GTGTCTTATC CGTCGTCCGA GAACCGTCTT GTTCGGGTTG      120
ATATTGCTGG TAGGTCTTTT CTCTGCGATG GCGCAAGAGA AAAAGGATAG TCTCTCTACG      180
GTTACGCCAG TGCCGAATAG CAGCATGGTG GAGCAGACCC CTCTCTCTC CATTGATCAC      240
CCGCTCCTGC CCGCTTCTTT TCAGAATACG CTTACACTGA AAAGGTTTAG AGACAAACAT      300
CTTTCCGATG CTTTCCTCAA TGGATTGAAG CCTCATCGCT CATCTTTGCA ATTGAATGAG      360
GAACCTCACT TCGCGGCAGA GCGTCGGGAT TCGTTTCTC CCCTCTTGCA TACTCGCCAC      420
GCTGCGGGTG TCCTTTTCATG GCGACCGACC GATAGGATGC ATTTTATAC ATCGGGCAAT      480
ATCGGTCTTG GCCATGATTT ATTGACCGGT GTGCGCAAGG ACTTCGGATG GAATGCTGGT      540
CCCGACTTCT TGCTGAGTCA AAATCTTACG GCACATGTCC AAGGCGGTTG GCAGCAGAA      600
TTGCGCTTTA TACCTATGAC GGCTGTCAAT G3CCCACTGC GTTGGCAAGC CACCGAGAGA      660
TTGAGTTTAA CCACCGGTAT CGATTATCGA CAGGTACAGT GGAATGCTTT CGATAATAGA      720
ACGTTCTCGC TTAAGGAAG TGCTCGATAC GAATGATG5 ACAATGTCTT TGTCAATGGA      780
TTTGGCAGCT ATCCTCTCTA CAGCAGTACG CGCTCAGGAC TCAATATGGC TGTTCGATG      840
CATGGATTG5 GCCCTCAGTA CGGTGGATCG CTTGAGCTGA AAGTCTCCGA GCGATTCCGC      900
TTTCCGCTCG GTATGGAGCG CGAATACAAT ATCTGGACTC GTCGGTGGGA AACGCATTAC      960
TTTGCTTATC CTGTATTCTA TGGCGATAAG AAG      993

```

75

## (2) INFORMATION FOR SEQ ID NO:98



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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 987 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98

5	GAGACGA	ACT	CTTGGGT	ATC	CAGCGAT	TGC	AATTCGA	CGA	CGATGAA	AAC	GAATAGAC	GA
	TACCGAT	TTG	TTTTGCC	GCT	TCTGCTA	CTC	ACCGGAT	TGT	TGGCATG	GGG	GCAGGAT	TCT
25	TCCACAG	GTA	GCAATAC	GAG	GTTTGCA	ACT	GATTCCT	CGA	GTAGAG	AGT	GCCCACG	GAG
	CAGTCCG	CCT	ACCGCAT	TCA	TTCTGCC	TAT	ATGGTC	GCG	TG	GGCGGA	AAG	CATAACG
	GACACCT	AAT	TGTCACG	CCT	TCGTTAT	GGA	GGATGG	ACAC	TGAATT	TGT	GGGAGAG	AAG
	ACGTTCC	CTC	TCAAAGC	CTC	CGATTCC	CGT	TGGATG	ATCC	GTACCG	GGCA	TGAGCT	GAT
30	TTTGCC	TGA	TGGACA	ATCC	GGCCAAT	AAT	GCTCAT	TTCT	ATTCCT	CTGT	GTATAAC	CGT
	TCCGCTG	CGG	CTCTTTA	CCG	CCTTGGC	GCT	AAGCAT	CTGC	GAGCCG	CGTG	GATGGAC	CAAT
	CTGCGCT	TGG	CAITCGG	CCC	GGGCTTG	GAA	ATCGGG	CTTG	GAGGAAT	TTA	TAGTACA	CGC
	AACGGCA	ATA	ATCTGCG	SAC	ATTGAAG	CTC	TACACCA	ATG	CCATCG	CCCA	AGCCTC	GATA
	GGATACT	ACG	TCCCCTC	CGA	AACTTTT	CCC	CTGTATT	TTT	GGTTG	CTCT	CCAGAT	CAAT
35	CTCTCG	GTA	TAGCCTA	TGG	AAATGGT	TTT	GGTGAG	AGCT	ATTACG	AGAA	TTTTTTG	CTC
	AAATAAC	GGCA	TTGCAGG	CTC	CCTGCAT	TTT	ACTTAT	CCGG	GCAAGT	TTAC	TCGGTT	CACG
	ACACTCA	TAA	CGGCGGA	TAT	TCCCAT	TCG	AACTCT	GTGA	CGCTTC	CGTG	CGGTTA	TCGC
	TATTCC	CATT	TGGGCTC	TTT	GCTTAA	CGCA	TTGGAT	ACTC	GAATCC	ACAG	TCATAC	GCGT
	TTTATCG	GTT	TCGTACG	GGA	GTTTTAC	CGA	TTCCGT	GGGC	GCAAGC	CCAT	GAATAC	CGGT
40	CGGAGA	AACCA	GTCTTTA	CTA	TCATG							987

(2) INFORMATION FOR SEQ ID NO:99

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 957 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99

65	TTTACGT	CCG	GTACGAT	ATT	CGTCCGT	ATA	GGCATAT	CCG	GCCGTGT	AGT	GTGCCGT	GAG
	GTTGAGG	ATA	ACGGAAG	GAG	AGAAGCT	GTG	CGTCATG	ATG	GCATGGT	AGT	GACGCTG	CTC
	GTAATTG	TCG	GTATTGT	GGT	AGTAGTG	CGG	TACTCCT	TGC	GCGTCC	ACGT	ACATAAG	ACC
	GGCACTG	TTG	TATCGGG	CGG	CATATTG	GGC	TTTCAT	CCTCC	TTGGAA	AGAC	CGTTCAT	GCC
70	GATACCG	ATA	ACTTCTT	TTT	CTCCGAA	AGT	GATGAAC	CTG	AGAGCG	GTGT	TGCTACC	GAA
	ATAGCCC	ACC	TGTGCGA	AAAT	AGGATT	TCAG	ATCCACG	GCTT	CCTCTAT	CCA	CGTAGCC	CTC
	CGAACCG	ATT	TTGGAC	AGGC	GGGCAT	CCAC	TGCCCA	TATG	CGACCG	ATGC	GTCCGCT	ACC
	GAGTTTG	ACC	GATCGCG	GGGA	ATGTGCC	GAA	CGAACCT	CCG	CTCAAT	CGA	CACGGCC	ATA
	AGGAGCC	AGT	CCCAAAT	TAT	CCGTACG	CAAT	ATTGAC	ACTT	GCCCCA	AAAG	CTCCGGC	CACC
75	ATTGGTG	GAA	GTACCC	CACAC	CTCGCTG	CAAC	CTGAAG	STCT	TCGATG	GGAAG	AGGCGA	AGTC
	GGGCAT	ATT	ACCCAAA	AGA	CGGACTG	GAGA	TTCCG	AGT	TCG	TGAGG	GGGA	CTCCAT
												660

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AGTTATGTTG ATGCGATTGG CATCGGTGCC ACGCACGCGA AAGCCGGAAT ATCCGATACC 720  
 CGTACCGGCA TCGCTGGTGG CTACCACGGA GGGAGTCAGC ATCAGCAGAT AGGGGATGTC 780  
 ACGACCATAA TTGGACTTGG AAAGTTCGGC CTTGCCGAACG TTGGTGTAG CGACAGGGGT 840  
 TTTCCCGGTG GCGCGAGTAG CTACGACCTG TACGGTCTGG AGCTGCACAT TGCTAAGACT 900  
 5 ATCTATCTCG CTGTTGGAGA CGGGTGTCTG TGCCGTCAGG CAGAAAGGCA GGACGGC 957

## (2) INFORMATION FOR SEQ ID NO:100

- 10 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1842 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:  
 (A) NAME/KEY: misc. feature  
 (B) LOCATION: 1...1842

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:100

CCATATAATG TCCAATCTAT TAGCAACAAG ACGATTAAAA AACAAATGGA AACTTAAAG 60  
 AACATTGAGC CCAGAGAGGA TTTCAACTGG GAAGAGTTTG AGGCCGGTGG CGTCCATGCT 120  
 GCGGTGAGTC GTCAGGAGCA GGAAGCTGCT TATGACAAAA CGCTCAATAC CATCAAGGAA 180  
 AAGGAAGTGG TAATGGGTAG GGTAACTGCT ATCAACAAGC GTGAAGTGGT TATCAATGTA 240  
 35 GGGTACAAAT CGGAAGGTGT GGTACCTGCA ACAGAATTCC GCTACAATCC CGAACTCAAA 300  
 GTGGGAGACG AAGTGGAAAT TTATATCGAG AATCAGGAAG ATAAGVAGGG CCAGCTCGTC 360  
 TTGTCTCACC GCAAGGGTGG TGCCGCTCGC TCTTGGGAGC GCGTGAACGA GGCTCTCGAA 420  
 AAGACGAAAT TCGTAAAGGG CTATGTGAAG TCTCGTACCA AGGGTGGTAT GATCGTCGAT 480  
 GTATTGCGTA TCGAGGCTTT CCTCCCGGGA TCACAGATCG ACGTGCAGCC CATTCGCGAC 540  
 40 TACGATGCAT TCGTTGAGAA GACGATGGAG TTCAAGATTG TGAAATCAA TCAAGAATAT 600  
 AAGAAATGTA TTGTTTCCCA CAAGGTGCTC ATCGAAGCAG AGCTCGAACA ACAGAAGAAA 660  
 GAAATCATCG GCAAGCTCGA AAAAGGGCAG GTACTCGAAG GTATCGTCAA GAATATTACT 720  
 TCTTACGGAG TATTTATCGA CCTCGGTGGA GTGGATGGTC TTATCCATAT CACTGACCTT 780  
 TCATGGGCTC GTGTGGCTCA TCCGGAAGAA ATCGTACAGC TGGATCAGAA GATCAATGTC 840  
 45 GTTATCCTCG ACTTTGATGA AGATCGCAAG CGTATCGCTC TCGGACTCAA ACAGCTGATG 900  
 CCTCATCTTT GGGATGCTCT CGACAGCGAG CTTAAGGTAG GCGATAAGGT GAAGGGTAAA 960  
 GTTGTGGTGA TGGCAGATTA CGGTGCTTTC GTTGAGATTG CACAGGGCGT TGAGGGTCTT 1020  
 ATCCACGTAA GCGAAATGTC ATGGACACAG CACTTGCCTT CTGCTCAGGA CTTCTGCAT 1080  
 GTAGGCGAGC AAGTGAAGC CGTGATCTG ACGCTCGACC GCGAAGAACG CAAATATGTC 1140  
 50 CTCGCTCTGA AGCAACTCAA GCCGGATCCT TGGGCTGATA TCGAAACTCG TTTCCCTGTA 1200  
 GGCTCTCTGC ACCATGCTCG TGTTCCGAAC TTCACCAATT TCGGTGTATT CGTTGAGATC 1260  
 GAAGAGGGCG TAGATGGCCT TATCCATATT TCCGACCTTT CTGGACGAA GAAGATCAAA 1320  
 CACCCGAGCG AGTTTACGGA AGTAGGTGCT GATATCGAAG TTCAGGTAAT CGAGATCGAC 1380  
 AAGGAAAACC GTCGTCTCAG CTTGGGTGAC AAACAGTTCG AAGAGAATCC TTGGGATGTA 1440  
 55 TCGAGACGGT TATTCACGTG AGGATCTATC CACGAAGGAA CGGTAATCGA AGTGATGGAC 1500  
 AAGGGTGTCT TCGTTTCTCT GCCTTACGGT GTGGAAGGTT TTGCCACTCC GAAGCACATG 1560  
 GTGAAGGAAG ATGGCTCACA GGCTGTACTC GAAGAGAAGT TACCTTTCAA GGTATTAGAG 1620  
 TTCAATAAGG ATGCCAAGCG AATCATTGTA TCTCATAGCC GTGTATTGTA AGATGAGCAG 1680  
 60 AAAATGGCTC AGCGTGAAGC CAATGCAGAG CGTAAGGCTG AAGCCAAAGC GGCTCAGAAA 1740  
 GAAGCTGCTG CCGAAGCTGC CAATCCTGCA CAGGCTGTAG AGAAAGCCAC TCTCGGAGAC 1800  
 CTCGGCGAGC TGGCCGCTTT GAAAGAAAAG CTTTCAGAAA AC 1842

## (2) INFORMATION FOR SEQ ID NO:101

- 65 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 729 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- 70 (iii) HYPOTHETICAL: NO
- 75

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- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...729
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101
- |             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| TCGACAATAA  | TGAAAAAAGC | TATTCCTTCC | GGAGCGGCCT | TGCTCCTCGG | CCTATGTGCC | 60  |
| AACGCACAAA  | ACGTGCAGTT | GCACTACGAT | TTCGGTCATT | CCATCTACGA | CGAACTAGAT | 120 |
| GGACGTCCCA  | AACTGACTAC | CACAGTGGAA | AACTTCACAC | CCGACAAATG | GGGAAGCACC | 180 |
| TTCTTCTTCA  | TCGACATGGA | TTACACGGGC | AAGGGTATCC | AGTCGGCCTA | TGGGAGATT  | 240 |
| TCGCGCGAAC  | TGAAGTTTTC | GCAAGCTCCC | GTTTCCATTC | ATTTGGAGTA | CAACGAGAGC | 300 |
| CTCTCCACAA  | GCTTTACTTT | CGGACACGAT | GCTCTAATCG | GTGCCACCTA | CACCTACAAC | 360 |
| AACCCCTCCT  | TTACACGTGG | ATTACGATC  | ACGCCCATGT | ACAAGCATCT | GGGTGCGCAC | 420 |
| GACTTCCACA  | CCTATCAGAT | CACCGGCCT  | TGGTACATGC | ACTTTCIGGA | CGSTCTGCTT | 480 |
| ACCTTCAACG  | GCTTCTCGA  | TCTTTGGGGT | TTCCCCAAG  | AGAACCCAA  | CGGGGGCCCT | 540 |
| GTGCTCAAAG  | AAGGGGATAA | GTTCGTAATC | CTGTCCGAAC | CGCAGTTCTG | GATCAACCTC | 600 |
| AAATCGCATCA | AAGGCATCGA | CAAGGATTTT | AATCTCAGCA | TAGGGACAGA | GATGGAAATC | 660 |
| AGCAGGAATC  | TCGCTCGCAT | GGACAAATTC | TCCTGCATCC | CTACTCTTGC | GGTCAAATGG | 720 |
| ACTTTCAAC   |            |            |            |            |            | 729 |
- (2) INFORMATION FOR SEQ ID NO:102
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 705 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...705
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102
- |             |             |             |            |            |            |     |
|-------------|-------------|-------------|------------|------------|------------|-----|
| ATGAAAAACAA | TTAGTAAGAA  | CCATGCGGCA  | CGGATCTGTG | CCGCCATTGC | TTTGTTTGCA | 60  |
| GTGTGTAACG  | GCCGGATAGC  | TGCTCAGGAT  | TTTCTCTATG | AAATAGGAGG | AGGTTTGGT  | 120 |
| GCTGCTCAGT  | ATTTTGGCGA  | TGCAAAACAGA | GGCTTGTTCG | GTTTCATCCG | AGTAGGTTTG | 180 |
| GAGTTGGTTC  | GACGTTACAA  | TTATAATTTT  | CGCTGGGCTT | TCAGTACCAT | GTTGGATTGG | 240 |
| CGTACATTGA  | GAGGCGATAC  | CGATAAGTCC  | GGGAATGTCT | TCCCCGATTI | TGCTCAAGCG | 300 |
| GATTTTAAGG  | TCGGGCTTGAC | TCAGCTCCAC  | GTTAGAAGCG | AAATTAACCT | TCTCCCTTAT | 360 |
| AGCGATGGCT  | ATAAGTATCT  | TGGTACAGCT  | CGGCTGTCTC | CTTATGTAGC | GGCCGGGTTG | 420 |
| TCTTTGGGTT  | TTGCTTCGGG  | TGCTAAAGCT  | TCGGCTTTTG | CTCCCGGGAT | TACTGCGGGA | 480 |
| ATGGGAGTGA  | AGTATAAGCT  | TAAACCGCGG  | ATCAATGTCT | GTATCGAGTA | TTCTTTCACG | 540 |
| GGGTTACTTA  | CCGATGCTTT  | GGATGCGCTG  | ACGGATAAAA | GTGTTTGGCT | CGAGGATCCA | 600 |
| TATAAGATCA  | ATGACTCCTG  | GGTCAAAAAC  | AAGGATGCTA | CAGGGGCCCT | AGTGCTTAGG | 660 |
| ATTACGTATG  | ACTTCGGCCT  | GCGTAAGACT  | TTTTGTAATA | AACAA      |            | 705 |
- (2) INFORMATION FOR SEQ ID NO:103
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1300 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103

AAATATAATGT	ATAAAGACTA	TAAAGGTTTG	TATCGCTCGC	TTCGGTGGTA	TGCCCTGATC	60
ATTGGGTTGC	TATTTCAGC	AGACGGTATA	CAGGCTCAGA	ACAACAACCT	TACCGAGTCG	120
CCTTACACIC	GCTTCGGCCT	TGGCGGTCCT	GGAGAACGGA	CGACTATTAG	TGGGCATTCC	180
ATGGGAGGAC	TCGGCGTCGG	TCTGCGTCAG	GGCACATACG	TCAATGCCGT	CAATCCTGCT	240
TCATACCTCG	CTGTGGATTC	GATGACGTTT	ATCTTCGATT	TCCGTGCATC	TACCGGAATT	300
ACGTGGTATG	CCGGAACCGG	GAAAAAGGAC	AATAGGAAAA	TGGGAAACAT	TGAGTATTTC	360
GCCATGGTTT	TTCCTATTTC	CAAAATCCAT	CCTATGAGTG	CGGGAGTGCT	TCCTTACTCC	420
GCATCCGGGT	ACCAAGTTCGG	ATCCGTTGAT	CAAGTGGAA	GAGGCAGCGT	CCAGTACACC	480
CGTAAATACT	TGGGACAGG	CAATCTGAAC	GATCTCTATG	TCGGTATAGG	TGCAACCCCG	540
TTCAAAAACT	TCTCAATAGG	AGCCAATGCT	TCATCCCTTT	TTGGGCGATT	CACACACAGC	600
AGGCAGGTAA	TCTTCCTCAC	GGAGGCTCCT	TACAATCCCG	TACATCTCTC	GACGCTGTAC	660
TTGAAGGCTG	CCAAGTTCGA	CTTCGGTATG	CAGTATCACC	TTCTTCTCAA	ATCAGATCGT	720
TCGCTCGTTA	TCGGTGCCGT	CTATTCTCCG	CGGGTGAAGA	TGCATAGCGA	GCTGACTCAG	780
ATAAAGATC	AGGTTTCAG	CGGTGTAGTA	GTGGAGAGCG	AAACCCCAAG	ATATATCAAG	840
GGAAATGACI	ATTATACCT	GCCTCATACA	TTGGGATAG	GTTTTCTTA	TGAAAAGAAA	900
GATAAATCTC	TCTTAGGAGC	AGACSTCCAA	TATAGTAAT	GGAAAGGCGA	GAAATTTTAT	960
AAATCCGATT	GCAAAATCCA	GGACAGAATA	CAGGTATCTC	TCGGCGGAGA	GATCATACCG	1020
GAATATAATG	CCGTTGGGAT	GTGCGCTAAA	GTTGCTATC	GCTTCGGTTT	ACATGGTGAA	1080
AATTCTTACC	TGAAAGTGCC	GACTAAAGGC	GGTGTATATC	AAGGATACCA	TATCGTAGGT	1140
GCTGTATTGG	GTATAGGAAT	CCCGCTCAAT	GACAGACGTT	CGTTCGTAAA	TGTCCTCTCT	1200
GAATATGACC	GATTGATCCC	GAAGGAGGGT	ATGATCAAA	AAATATGCTCT	GAAATTGACC	1260
TTGCGCTCA	CGTTCAACGA	GTATGTTT	AAAAAGCTGA	AACTGAAC		1308

(2) INFORMATION FOR SEQ ID NO:104

(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2835 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...2835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104

AAATACCATTT	CGGAGAATGG	GAACGATAGC	ACCTATTTTT	CTTTTCAAAC	TTTTCTTATG	60
CGATCGATTT	ATCAATTACT	GTGTCAATA	CTCCTTGCTT	CTCTTGGTTT	CGTCGGGCTG	120
GAAGCCCAAC	AAGCCGGAGT	AGCAGGTAGA	GTATTGGACG	AAGAAGGCAA	CCCCATGATT	180
CAAGCCCAAC	TACAGCTTGT	ACAGAGTACC	GGCCAAGTAG	CCGTTGCCGC	AGGTGCCACT	240
AATGAAAAAG	GGTTGTTTCA	CCTGAAAAAG	TCACAGGAGG	GTGACTACAT	TCTGCGCGTT	300
TCATATGTAG	GTACACTAC	CCACGACGAA	AAAATATCTC	TTAGAAACGG	GCAAAACATT	360
ACGCTCAAAG	ATATATCCAT	GAACGAAGAT	GCCCGTCTTC	TACAGAGTGT	GACGCTGCAG	420
GCTAAAGCGG	CAGAGGTCGT	GGTACGCAAC	GATACGCTCG	AATTCAATGC	CGGATCTCTAT	480
ACCGTAGCAC	AGGGAGCTTC	TATCGAGGAA	CTGATCAAGA	AGCTACCCGG	AGCAGAGATC	540
GGATCCGATG	GGAGATCAC	CATCAACGGC	AAGGACATTA	GCAAGATCCT	TGTCGATGGC	600
AAAGAGTTTT	TCTCCAAAGA	TCCACAGGTG	GCAATAAAGA	ATCTTCCGGC	CGATATGGTC	660
AATAAGTAC	AGGTAAGTAA	CAAACTGAGC	GAGCTCTCGC	GGATGAGCGG	TTTCGATGAT	720
GGAGAAGAGG	AGACCGTAAT	CAACCTGAGC	GTGAAGCCCG	AAAAAAGAAA	AGGCTCTCTC	780
GGAAACGCTC	AGGCGCGCTA	CGGTACCGAC	CAACGCTATA	TGGCCGGAGG	GAACGTCAT	840
CGGTTTCGATG	GAATAAGCA	ATGGACATTG	ATCGGTAGTG	CGAACAATAC	GAACAATATG	900
GGCTTTAGCG	AGATGGACAG	CGAGATGGGA	TCCATGACCT	TCTTCTCTCC	CCAAGCGCGT	960
GGTCGACGCG	GCTTCGGCAA	TAGTGGAGGT	GTACGTCCTT	CGTCGATGCT	GGGCGGCAAC	1020

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5 TTCAGTGTG AATTCTCTTC TGCCCTTAAT ACAGGAGGCG ATGCACGCTA CGGATACAAAC 1080  
 GACAAGGCCA TAGAGACGAC CAAACGCGTG GAAAATATCC TCGCCGAAGG GAATACTTAT 1140  
 ATGGACGAAA ATATATTGGA ACGCTCTTTC TCTCACAATG GTCAGGCGCG ATTTAGGATG 1200  
 CAATGGAAAC CGTCCGAACG TACCGAAGTG GTATTGAGC CGGATCTTTC GATATCCAAG 1260  
 ATCGATGGGT TCTTTAACGA CACATACGAG ACGAAAGATG CCACCGGAAT CTCTATCAAC 1320  
 AAAGGTTCTA TCCACCAAAC TACACAAGGA AACAACTTCA GACTGAACGG AGAATTGGAT 1380  
 ATCAGTCACA AGCTCAACGA CGAAGGCCGT ACGATCAGTG CCTCCGTGAG TGGCGGTCTG 1440  
 ACCGACGAAG ACGGAGATGG CATATATCAG GCTGTGCTCC AAAGCGTGGG GACGAATCAA 1500  
 AAGCAATTCA ACTACAATC CAACCTGCAA TATCGGCTTC GCCTCTCGTA TGTGGAACCG 1560  
 10 TTGGTAAAA CTACTTCGC ACAAGCGATT CTGAACAGAC GTTCTCTCCG TCGCAATTCTG 1620  
 GATCGTGAGG TGTACCGACT GGGCGATGAC GGGCAATACT CCATATTAGA CAGTCAGTAC 1680  
 GGACTCTCCT ACAGTAACGA GTTCACCCAG TATCGCATCG GACTCAACCT CAAGAAGATT 1740  
 GCCAAAACGT GGGACTACAC CGTAGGATT AATGTGGATC CCAACAGAAC TGTCAGCTAT 1800  
 CGGAGCGTAG CCGGAGTAGA GCAGGACAAA CTGGCTTTCA ATCGTGTCAA TCTCTCCCG 1860  
 15 ATGCTCCGAA TCAACTACAA ACCGAGCAGG ACTACCAACC TCCGAGTGGG CTACCGAGGA 1920  
 CGCACGACAC AACCATCCAT CAATCAGATC GCTCCCGTTC AGGACATCAC GAATCCGCTA 1980  
 TTCGTGACCG AAGGCAATCC CGGTCTGAAG CCGAGCTATT CCAACATGT GATGGCCATG 2040  
 TTCTCGGACT TCGATGCCAA AAGTCAGCGA GCTTTCACAA TTGTTTTCTT CGGCAACTAT 2100  
 20 ACATTCGACG ACATCGTCCC CAATACGCAC TACGATCCGT CTACAGGGAT CCGTACCACT 2160  
 CGTTACGAAA ACGCCTCCGG TACGTGGCAA GCGAATCTTC ATGGGACACT ATCGCTTCCA 2220  
 CTCAAGAACTA GGGCATTTTC TTTCAGGATG TCCTTGTTC ACAGGTTGGC CGAAGGACAA 2280  
 AGCTTCATCA ATGACGATAA GAACAAAGCT CTCTCTTTC GAACAGGGA ACGCTGACG 2340  
 CTCACCTATC GCAACAATTG GATCGATACG AGTATCGGTG GCAATATCGG ATTCTATATG 2400  
 GCGAATTAATA GTCTGAGCGG ACAGAAAGAT TCTCGCACAT ACGATTTTGG CGGCAATTAT 2460  
 25 CAAGTTGCCC TAACGCTTCC CTATGGATTG CGTATCGACA GCGATGTGA ATACAATACG 2520  
 AACTCCGGTT ACAGCGGAGG ATTCAGTCTG GACGAATGSC TTTGGAATGC TTCGCTTCA 2580  
 TACAGCTTCC TCCGTGACAA GGCCGGTACA CTGCGTGTCA ATGGCTATGA CATCTCGGT 2640  
 CAGCGTCAA GTATCAGCGG TTCTGCTTCG GCCATCAATA TAGAAGAGAG CATGTCCAAT 2700  
 30 ACGATCGGAC GCTACGTGAT GGTGGACTTT ATCTACCGAT TCAACGCCCT CAGTGGTGGT 2760  
 GGATCTCGCA CGGATCATCA GCGTGGCAAT ATGAATCGTC CGGCCCCACC TTTGCGCGGT 2820  
 GGCAGACGAC CGTCC 2835

## (2) INFORMATION FOR SEQ ID NO:105

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1236 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
  
 (ii) MOLECULE TYPE: DNA (genomic)  
  
 45 (iii) HYPOTHETICAL: NO  
  
 (iv) ANTI-SENSE: NO  
  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 50  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1236  
 55  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105

GGAGAGTATC CTGCAAAACG TAACGACAAA AAAGAGATGG TTATGAAGCT GATTAAAAGA 60  
 AGTTTGCTCC TGCTTGGAGC GGTACTGCTG ATTACGCTTC CTGCGTACTC GCAGAATGAT 120  
 60 GACATCTTCG AAGATGACAT CTATACATCG CGAAAAGAAA TACGTAAACA AAACCAAGTT 180  
 AAAGACTGGC AAAACCAAGA GGACGGATAC GGGCAGGATA CGGAATATAC AGTGGCTTCC 240  
 GATCGGGACA TTGACGCCCTA CAATCGTAGA GATGGCCAGT CCTACGATGG GAAAAAGTTG 300  
 TCCAAAGACA AGAAAAGAGA CTCCACTCGT TCTTCTGTTC CCGGTCTGCTA TAGTCGCCGC 360  
 TTGGCTCGAT TCTATAAGCC GAATACGATC GTCAATTCAG GTGCCGACAA TGTATATGTA 420  
 65 ACTGATGATG GTGAGTATTT CGTCTATGGA GACGAATACT ATGATGACGC GTCGTCTGTA 480  
 AACATTTACA TCAACAGTCC TTGGTGCGAT CCGTTCCTTT ATACGTATG GTATCCATCT 540  
 TTCTCGGGCT GGTACAACCTA TACGTGGAAC TATCCATGGT TCTACTACGG TAGCCATATC 600  
 GGATGGGGCG GTTATTACCC CGGATATAAT TGGTATTGGA GCTACTACTA TGATCCTTTC 660  
 TACAATCCCT ATGGAATCGG TATGGGTTGG GGATATCCTT ATGGCTGGGG CAGCTATTAC 720  
 70 GGTGGGGTGG GCTATCCGGG AGTGATACAT CACTACCAAC ACTACCCCAA GAAGACCTAT 780  
 TCCATGTGTC AGCATTCCGG AGCTTACTAT TCTTATGGCC GACCGAATCG TATCAAAGGT 840  
 GGAACGTCGG GTGCCAAACT TGGGACAGGA CGCTACGATA GAATTCAAAA TTCGTCTTCC 900  
 CAAAAAATA AGTTGGGATT GCAGTCGAAC AAACCCATA ATAATCTGCA AAATGTCAAG 960  
 TCGGACGCTA CCGGCCGAGC CAATAGAGAG CGAAATATAG AAACGGTAAC TCCAAACAAC 1020  
 75 GGGCAAAAGC AGAATCGTCC CGTATTCCAG CAGATCAGT CCGCAATGA CCGACCGACC 1080  
 GGACGGAATA TCCGACGCGA GAGACAGGGG GAAAATAACG ATAGGACATT TTCAGTCTCT 1140

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TCTCGTAGCA ATAGTAACGG TGGCTTCTCC ACGCCTTCTC GTCTTCTTC CGGCTCTATG 1200  
 ACGCGAGGTG GCGGACGTAG TGGCCGGGGA CGCAAT 1236

5 (2) INFORMATION FOR SEQ ID NO:106

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1803 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature  
 (B) LOCATION 1...1803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106

AGTAATAGCA GCTCCACAA GTGGTTAATT TATTATCATA TAGAAGAC TAAAGTATT 60  
 ATGATCCGCA AGTTGATCTT ACTGCTTGCT CTGATGCCGG TAGCCTCTGT GGCTTTTGGC 120  
 GTACCAACGG ACAGCACGGA ATCGAAGAC AATCGTATCC TTACAAGCAT GCAATCCTCC 180  
 TCTTTGAATA GGGATGATGC TCCGGATAAA TGGCAACCTA TGCATGCCAA TTTCAGTATT 240  
 CAGAGCGATA TGCTGCTTTC TACTGCCCAA AAGTCCAAAG ACACCTGGTT CGGCAACTCC 300  
 TATATCATGG GTATAATCAA GAACAATTAT CTGGAGTTTG GTGCCCGTTT CGAGGATCTC 360  
 TATAAGCCCC TGCCCGGACA TGAACCCGAG ATGGGGCGTG GCGTTCCTCA CATGTATGTG 420  
 AAGGGAAGCT ATCATTGGGC GGAGCTGACT ATGGGAGACT TCTACGATCA GTTCGGTAGC 480  
 GGTATGGTAT TCCGCACCTA TGAAGAGCGC AACCTCGGTA TAGACAACGC GGTTCGCGGC 540  
 GGACGTATAG TACTCACTCC TTTTGATGGA GTSCGTGTCA AGGGTATTGC AGGACACGAG 600  
 CGTAACACT TCGACCGCAC GGGCAAGGTA TTCATTCCG GCCGAGGCTA CCTACTGGGT 660  
 TCTGATCTGG AGCTGAATGT AGAGCGTTGG AGCAGTGCCA TGCCGACAA TGACTATCAT 720  
 TTGGCTATCG GGGGATCGTT CGTTTCCAAA CACGAAGCAG ACGAAGATAT ATTTGTGGGT 780  
 GTAGGCGAAG ATCGCAAGCG ACTCAACCTG CCGCTCAATG TCCCGATTAT GGGCCTGCGC 840  
 ACCAACTTTC AAAAAGGAGG TCTCGCCCTC TACGCAGAGT ATGGATACAA ATACAACGAT 900  
 CCCTCGGCAG ACAATGACTA TATCTACCAC GACGGACAGG CTGCACTCCT CTCTGCCCTCA 960  
 TACTCCAAAA AAGGGATGAG TATCCTGTTG CAGGCCAAC GTTGTGAGAA CTITGCTTTC 1020  
 CGCAGCAAGC GAAGTGCCCA GCTCACACCG CTTATGATCA ACTATATGCC GGCTTTTACC 1080  
 CAAGCTCACA CTTATACGCT GCGGCCATC TACCCCTATG CTACTCAGCC TCAGGGAGAA 1140  
 TGGGCTTTC AAGGTGAAC GCGTTACAC TTTGCTCGCC GGACAGCTCT CGGTGGACGC 1200  
 TACGGTACCG GCTTGGTAT CAACGTTTCG CATGTGCTG GTCTGGACAA AAAGATGCTC 1260  
 AAAGAGATC CCGACGAAC GATCGGAACG GATGGCTACA CCGTTTCTTT CTTCGGCATG 1320  
 GGCGACCTCT ATTATCGGA TATAGATGTG GAGATTACTA AAAAGGTAAG CCCAGGATTC 1380  
 AACTTTACGC TCACCTACTT GAATCAGATC TACAATAACA AGGTACTGCA CGGTGCAGCC 1440  
 GGAGAGAAGC CTGAGAAGAT CTATGCCAAT ATCTCGTCT ATGATGGTAA GTATAAGCTG 1500  
 AGTAATAAGG TAGCCCTCCG TACCGAAGT CAATATITGC ACACGAAGCA GGATCAGGGT 1560  
 GACTGGATCT ACGGCATGGC CGAGCTCTCT ATCCTGCCTT CTCTGATGCT TTCCTCTCG 1620  
 GAGCAGTATA ATATCGGAGA GACCAAGAAA CATTATGTCA TGGGGTCTGT CACCTATACT 1680  
 CACGGAGCAC ATCGAGTAGC TTTCTCTGCA GGCAAAACCC GTGCAGGGAT GAACTGCTCG 1740  
 GGAGGTGTAT GTCGTGTGGT CCTGAGACT CAGGGATTCT ACCTTCTTA TAGCACCAT 1800  
 CTG 1803

60 (2) INFORMATION FOR SEQ ID NO:107

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 756 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107

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10 AGGGGGTCGA GTTCGGGCAT TTCAGCCCGT GGACGCGACA TGCCTTCTTT ATTTTGTAGC      60
   GCGTTGCGCA GCTCCTCTCT CCATGGTTCA GAGCGACGCA GTCGGATAAG TTCTTCTGTA      120
   GTCATGTCAA TAAGGCAGAA AATAAGGTTA TTCCATCTCT CCGTATGCGC CCAAACGCAT      180
   GATCATCTCA TCGAAATCCA CTGGGTGTGC ATCGAATTCT GGGCCATCGA CACAGACGAA      240
   TTTCGTCTGT CCTCCACGCG TTATACGACA AGCCCCACAC ATACCGGTGC CATCCACCAT      300
   AATTGTATTG AGAGAAGCTA TGGTCGGTAT CTCGTAACGT TTGGTCAGGA GAGAAACGAA      360
   CTTCATCATC ACAGCGGGCC CGATCGTAAC GCAGAGGTCT ACCGTTTCCC GTTTGATAAC      420
   GCTTTCCACT CCATCGTTA CGAGGCCTTT CGTCCCATAA GACCATCTGT CTGTCTATGAT      480
   GATCACTTCA TCGCTATTGG CTCGCAATTG TTCTTCRAGG ATAACCAGAT CTTTAGTTCT      540
   GGCAGCCAAT ACGACAATTA CACCGTTGCC TGCTTTGTGG AAAGCCTCCA CGATCGGGAG      600
   CAAAGAGGCC ACACCCACAC CGCCTCCGGC ACAAACTACT GTGCCGACCT TTTCGATATG      660
   CGTACTCTGT CCCAGCGGAC CTACCACATC CGTGATATAG TCGCCGACTT CGAGTTCGGC      720
   CAATTCTTGT GAAGATTGTC CCACGGCCTG AACCAC      756

```

(2) INFORMATION FOR SEQ ID NO:108

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2370 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...2370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108

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CTCTGTGTTT CTCTCTCTTT ACCCGGAATG GATCGTCTTA AGCCTTCATA TATTGTTTGA      60
ATAGCAGCCA TTCTCTGCTT GTTTGTGCGG AGGCCTTTGT TTGCGCAGAG CTATGTGGAC      120
TACGTGATCG CGCTGATCGG GACGCTAAGT TCTTTTGAGC TGAGTGCGGG CAATACCTAT      180
CCGGTGATCG GTTTACCGTG GGGGAATGAAT AGCTGGACAC CGATGACCGG TGTACCCGGT      240
GACGGCTGGC AATATACCTA CTCGGCACAC AAGATTGCGG GATTCAAACA GACCCACCAA      300
CCGAGTCTCT GGATCAACGA CTACGGCCAA TTCTCCCTTC TTCCCTTAC GGCACCGCAG      360
AAGCCATCAT CGAACGACTC CATAGCTCTG ACTAATGGT GCAAGCACT CTTTTCGGAC      420
GAACAGACCT CGTGGTCTCT GCACAAAGCG GAGACGGCGA CGCCNACTA TTATAGTGTG      480
TATTTGGCCG ATTACGACAC ACGCGTGGAG ATGGCTCCGA CCGAGCGTGC AGCTATCTTT      540
CGCATACGTT ATTCCGGCAA TACCGAAAGT GGCTCCGGTC GATGGCTTGG TCTTGATGCC      600
TTTACCGGTG GTTCGGAGAT TAGCATCGTG GATCCTCACA CCGTAGTGGG CATATCTCGC      660
AAGAATAGCG GAGGTGTGCC GGCTAACTTC GCCTGTTATT TCATCTGCA GTCCGATACT      720
CCTATGGCCG ATGCTCTGCT TGAGACAGAT ACGGGCAAGT CAGACGAAGG CACAGGGGCA      780
TGGGCAGCCT GTGCTTCTGA TTGCGAAGAA GTTACCGTCC GGGTGGCATC TTCTTTTATC      840
AGTGTGAGCG AGGCCGAAAG AAATCTTGCG GAAGTCAAAG GGCAGAGTTT CGACCGGATC      900
AGACTTGCCG GTCGCGAAGC TTGGAATAAG GTGCTCGGAC GCATACATGT GGAAGGAGGA      960
ACGAAGGATG AGCGCACTAC ATTCTATTCC GCACTCTATC GCTCTCTGCT TTTTCCCGGT      1020
CGCTTCTATG AGGAGGATGC TTCCGCAAT TTTGTGCATT ACAGCCCCTA CAATGGAGAG      1080
GTACTTCCCG GTTATCTCTA TACCGATACC GGATTTTGGG AACTTTTTCG AGCCCTTTTC      1140
CCCCTGCTCA ATCTGCTGTA TCCCGATGAA AACATTAAAA TTCAGGAAGG TCTGCTGAAT      1200
GTATATCGCG AGAGTGGCTT TTTCCCGGAA TGGGCCAGTC CGGGCCATCG GGATGTGATG      1260
ATAGGCAACA ACTCTGCTTC TGTCTGGCG GATGCCTACC TCAAGGGTGT TCGGGTAGAA      1320
GATACCGGTA CACTGATGAA CGGACTCTTG CATGCTACGA AAGCCGTCCA TCCGAAATC      1380
TCCTCCACGG GTCGCAAGG TTGGGAGTGG TACAACCTCT TAGGTTATGT TCCGGCTGAT      1440
GCAGGCATCG ACGAAAGTGC TGCCCGTAGC CTCGAATATG CTTATAACGA TTGGTGATC      1500
CTCCGACTGG GGGGCACATT GGGTTGGGAT AGAGCTGCAT TGGACACGTT GGCTCATCGT      1560
TCGATGAAC ATCGTCATCT GTTCGATCCG GAAACCAAA TCATGCGCGG TAGAAATCAG      1620
GATGGTAGTT TCCGGACACC TTTTCCCGT TTCAATGGG GAGATGTATT CACGGAGGGC      1680
AATGCCTGGC ACTACACTTG GTCGGTCTTT CATSATGTG AGGGGCTTAT CGACCTGATG      1740

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5 GGAGGAGATC GCCCGTTTCGT GTCTATGCTC GATTGGGTAT TCAATACTCC TCCTATGTTT 1800  
 GATGAGAGCT ATTACGGATT TGTATCCAC GAAATCAGAG AGATGCAAT AGCGSATATG 1860  
 GGCAATTATG CTCATGGCAA TCAACCCATA CAGCATAIGA TATATCTGTA TAATCATGCC 1920  
 GGTATCCAT GGAAAGCTCA GGAGAGACTA CGCGAAGTGA TGGGGGGGCT CTATCGTCT 1980  
 ACTCCGGATG GGTATTGCGG CGATGAAGAC AACGGACAGA CTTCGGCTTG GTACGTTTTT 2040  
 TCTGCTTTAG GCTTCTATCC TGTACACCC GCTACGGATC AGTATGTGCT CGGTTCCGCG 2100  
 ATTTTTCUAA AGGTAACTCT CTCTTTTCCC GACGGACACA AACGGTGTG GCATGCTCCG 2160  
 10 GCCAACAGTG CCGATACGCC TTACATCCCG TCGATCAGCG TAGAAGGAAA AGAATGGAGC 2220  
 TGCAATTACC TGAATCAGCA ACAGCTTCGC TCTTCTGCAT CCAATCAATG GATGATGGAC 2280  
 ACGAAACCCA ATTATAATCG TGGTATGAAG GAAAGTGACA GACCTTATTC CTCTCCACG 2340  
 GAGCAACAGC GTCCGCTAA TCACAGTAAT 2370

## (2) INFORMATION FOR SEQ ID NO:109

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 858 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 25 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 30 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...858

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109

35 ATTTGTGGCA GTAAATGAA TCTATCGGGA TTACAATCTT TCACTATGAT GAAATCCATG 60  
 GCGAGCGTGC TGTGCTACT CTTCCATTG TCTTGATCA CTGCTTTGGG CTGTAGCAAT 120  
 AACAAAGCTG CGAATCGAA GTCTGTCTCT TTCGATTGGG CCTATCTCGA ACGCTACATC 180  
 40 CCTCTGCGGG CAGACATAGA TAGGCCATCG CTGCATGTGA TGATCAGCTA CGTCTATCCT 240  
 TCGGGAGATG ATATGCTCAC AGAGATTTTC AACGGTTTGC TCTTCGGCGA CAGCCTGATG 300  
 GATTCTCTTT CCGCGGAGAA TGCCATGGAA GGGCTATGCAC AGATGCTGGG AGAAGACTAT 360  
 CGCTCTAACA ATGCCGAAGC CAATCTGCAA GGGCTTCCTT CTGACCTTTT GGACTATATC 420  
 TACAAGCAGG AAAATACCAT CGCTTATTGC GATACGGGAT TGATCTCCAC GCGCATCAAT 480  
 45 ACATATACTT ACGAAGGCGG TGCACATACG GAGAATACAG TCGGTTTTC CAACATCCTT 540  
 CGCACCACCG GCAAGGTGCT CGAAGAGCGA GATATATTCA AGATCGACTA TSCGGAAGG 600  
 CTGYCCGCAC TCATCATAGG ACAATTTGGT CACGATTTCG GCAAGACCAC ACCTGCCGAA 660  
 TTGGATGCAA TAGGTTTCTT CAACGCAGAA GAAATACAGC CCAATGGCAA TTTTATGATC 720  
 50 GATGACAAAG GTCTCACATA CTGTTTCAAT GAGTATCAGA TAGCTGCTTA TGCCAGAGGT 780  
 GCTGTCTATG TCCGTCTCGG ATATGACGTA TTGGCTCCTT TGCTAAGGGA TGATTCCCCA 840  
 CTAAGCGT ACTTGCCG 858

## (2) INFORMATION FOR SEQ ID NO:110

- 55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1134 base pairs  
 (B) TYPE: nucleic acid  
 60 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 65 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 70 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1134  
 75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110



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5 GGGATAATAT CTGTTCTTTC ACATGTGGTT GACCGTCCAC AATGGGGTGC TTCTCCGGAA 60  
 GCTGCTGGCA CGCATAGTGT GTATTGCGATT CTACATCCCT COGCGGGTAT TATCCGGATC 120  
 AGGTCTATGG GTATTATCTC AGCCTGCCGT ATCGCAATTC TTGCCGGCAA GCACCCCGGT 180  
 AGCGTCTGTG CGAGGGGCAA TGTAGGTATT CTTTCTGTACA ATCCAGAAAA CACGCCCGAG 240  
 AAAAAAGAGA AACTGCAAGA AAAAAATGTT TTCTCCAAA TCCGGCTCCG TCAATCATT 300  
 AATAATTGA TACCTTCGCT CCCATTAGA ATCGATAACA CAAAAAAT CACTGAAATG 360  
 AAAAAACTA CTTTGACAGG ATCGATATGT GCTTTACTCC TGTTTTGGG TCTCTCGGCC 420  
 AATGCCCAAT CGAAGTTAAA GATCAAGAGC ATTGAGGCAG CTACCACTTT CAGTTCCGCC 480  
 10 ACGGCCGGAA ATGGTTTGG TGGCAATATC TTGGGCATGG ACATGAGCAT ACGGATGAGG 540  
 GTACACCACA GCATTCTGCC CGAAGGGTTG GATTTTTCGG TAGGAATACA TGAAGAAGA 600  
 GCACACTGGG AAGAGGCCGG AAGTCCGAAG CTCATGTATA CGAATGTCCC AAGTATCATT 660  
 GTATTGTTG AAAAGGTAAT AGTCTTCGAA GACGAGAAAG ACTTTTGA CAAAAAGCT 720  
 CTCGGCCGCT TCCTCATCAG TTTGGGGATA TCCTATACCA AGCATCTGGG AGCGTATTGG 780  
 15 GGATGGACCA ATGACGCCCA TATTCTTTTC TCACCGATAC CCAAGAGCAA GGTCCACTAT 840  
 GACACCTACA CAAGAGCTGG CAGTGACCTT GTACTTCAGT CCGAAGATGT TGCCACAGTG 900  
 AGCAATGGCT TTTACCCGGG GATCGGACTC AAAAGTTCTA TTTGGTGGAA AATGCCCATC 960  
 AAGAGCAAT ATGATTTTCG CCTCGGTTTC AGCCTGGGCT ATGAGTATCT GAACCTGCTA 1020  
 TATCCGTATC GTAATTTCAA GCTGGATGGA AATAAGCCGC TTTCAGCACT ATCTCTCGC 1080  
 20 ATGAACCACA TCGGCCATGT GGGCTTCAAC TTACCGTGG GTCTTTGGAC TAAT 1134

## (2) INFORMATION FOR SEQ ID NO:111

25 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3807 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 30 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 35 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS  
 40 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...3807  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111

45 GTAAAAATGA TGGGCAAGTA TAAAAGAGCT AAGTACCGCT AITGGCTTTT TCCTTTCTGT 60  
 TCGGATTATT ATACCTTTGA GGGAGTTACT TTTTATGCG CATCTGACGA TATGACAACC 120  
 AAGAAACCCC AAGCCATTTT AGACTTAGAG AAGGCCTATA ACATTGAAAT TCCTGATCTC 180  
 TCCTCACAA AAGGGATAAG CTGCTCGGTA AATAGATATT TCAAGCAAGA TTCTCCGGT 240  
 50 GCAGTCCGTT AGCTTTGCTT GCGAGATATG CAGATAGAAA GCATGACTTG GCTTATTGAT 300  
 TTTCTGCTC TAAAAAAGCT TGATCTATCG TATAACCAAA TCAGTAAGCT AGAGGGTCTA 360  
 GAACGTCTTA CTCTGTTAAC AAAACTTCGT CTAAGAAAGTA ACCAAATCCG TAAACTAGAG 420  
 GGCCTGGATA GTCTACCTC GCTAACAAAA CTTTCTCTCT CCGATAACCA AATCAGTAAG 480  
 CTAGAGGGTC TGGAAAGTCT CACCTCGTTA GCGGAGCTTT ATCTTTTGA TAACCAATC 540  
 55 AGTAATAGT AGGGTCTGGA ACCTCTCAGC TCCTTAGCAA CGCTTGAAGT ATCGGGTAAC 600  
 CAAATCCGTA AGCTGGAGGG TCTGGAACGT CTCACGTCCT TAGCAACGCT TGAAGTATCG 660  
 GGTAACCAAA TCCGTAAGCT AGAGGGTCTG GAACGTCTCA CTTGTTAAC AAAGCTTCGT 720  
 CTAAGAAGTA ACCAAATCAG TAAGCTAGAG GSTCTGGAAC GTCTCACGTC CTAGCAACG 780  
 CTTGAAGTAT CCGGTAACCA AATCCGTAG CTGGAGGCTC TGGAAAGTCT CAGCTCTTA 840  
 60 GCAACGCTTG AACTGTCCGG TAACCAATC AGTAAGCTAG AGGGTCTGGA ACCTCTCTCT 900  
 TCGTTAACAA AGCTTCTCTT AAGAAGTAAC CAGATCAGTA AACTAGAGGG CCTGGAACGT 960  
 CTCACCTCGC TAACAAACT TTCTCTCTCC GATAACCAAA TCAGTAAGCT AGAGGGTCTG 1020  
 GAACGTCTCA CTTGTTAGC GGAGCTTTAT CTTTGGATA ACCAAATCCG TAAGCTGGAG 1080  
 GGCCTGGAAC GTCTACCTC GTTAACAAAG CTTCTGTAA GAAGTAACCA AATCAGTAAA 1140  
 65 CTAGAGGGCC TGGATAGTCT CACCTCGCTA ACAAACCTT CTCTCTCGA TAACCAATC 1200  
 ACTAAACTAG AGGGCTGGA ACCTCTCACG TCCTTAGCGG AGCTTTATCT TTTGGATAAC 1260  
 CAAATCCGTA AGCTGGAGGG TCTTGATGGT CTTGCTTCCT TAACAGGCT TAGTCTAAGG 1320  
 CGCAACCAAA TCAATAAGCT GGAAGGACTA GACAGACTAA AGGTTTGGAG AAAACTTGAT 1380  
 GTTTCGGGCA ATGATATTCA ATCTATTGAT GATATTAAAG TAITGGCTCC GATTCTGGAG 1440  
 70 CAAACTTTAG AAAAAGTGA AATCCATGAC AATCCATTG TTGATCATC AGGCTTGATA 1500  
 CTCTCTCTCT ATGATAATCA TTTGCCGGAG ATTAAGGCTC TTCTTGAAGA AGAAAAAGAA 1560  
 AATCAGAAAA AGACTCAGT TGAATATCAC CCAATTTGCA AAGTAATGCT ATTGGGAAT 1620  
 CATTCTCGG GTAAACAAAC ATTCTTAGT CAATACGATA CAAATTATAC GTATCAGAAA 1680  
 AATACACATG TGTGTCGAT ACATCGAAGC AATAACCTTA ATGCGATCTT TTACGACTTT 1740  
 75 GGGGACAGG ACTATTATCA TGGGATTATC CAAGCCTTT TTACCAACCA ATCGTTATAC 1800

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CTCTCTTTT GGGATGCTAA GAAGGATCGA AACTTTGTGA GCGTAGATGA TAAAGAATAT 1860  
 CAGACTCTTA ATTTCAATCG CCCCTATTGG TTAGGACAGA TAGCCTATGC CTGCAATCGT 1920  
 TGTATGTCGG TTGGAGGAAA TCCTGATGGC AAGGACACAC CACAGACCAC AGACGATACA 1980  
 ATTATCATTC AGACTCATGC CGATGAACGC GCGGCTAAGC AGCAAACTT AGGCTGTGCA 2040  
 5 GCGGAGAATG GAGTATTGGA AGAAATCTAT GTATCCTTAG AGCCCAAGGC GAATAGTGCC 2100  
 GTACATGCGC TCAACTATCT GAATGAGCGG GTGCGAGAGG TTGTGCGAAG CAGGAGTAAA 2160  
 TCAATTGAGA TCACAGAAAA AGATAAGGGA TTGTACGAAG CTCTTCCAC AATCGCCGT 2220  
 GATAATAAAC ACATCCCTAT CTCTCTCGAA GCTCTTGGCG CTCATTGAA TAAGGGAAGA 2280  
 GCTGAAAAATG ATCTTTACAC CATAGAGTAT CTACAGACCG AATTGAACCA GCTTAGTCTG 2340  
 10 CAGGGGAGG TGCTTTACTA TCGTGAGTAT GAGAAGCTGA ACAATTATGT CTGGTTAGAT 2400  
 CCGGCAGCTT TTGTCCAAAT GATTCTGGA GAATCCTCC AAAAAGACAA CATCAATAGA 2460  
 GGAACAGTTC CTAAGACAT TTTGAATGC AAATGCATA ATCTAAGTTC CGGAAGTATA 2520  
 TTTGAAGAAG ATGGCCAAA TGGTAAATAT ATCTTGACG TATTATTGGA AGAGCTGATC 2580  
 GTATATGAAG ATAAGGACTG CTATGTGATA CCGGGCTATC TCCCTTTGCA TTCCGATGAC 2640  
 15 GAAGCCTATA AATGGCTAC TTTGGGATTC GAGAGGCCCA ATTTTGTCTT CAAATTCGAA 2700  
 CGTTTATGCC CTTTGGGCT GATCAACCG ATTATAGCCT ACTATGGCG GGAAGAAGGT 2760  
 GCTCTAAAGC GGTATTGGCG AGATCAGTTC ATCTTACAG CAGGCGGTGA GATGGATAGG 2820  
 CAAACGCTTG AGCAAGAAGA AGAGAAGAG GGTTTGCCCA AGACGAATGC CGAGGATTAT 2880  
 CAGATCTGGA TCAAGCTCGA CTTTACCGAC TTGGCCATAT CCATATTCTT CAAAGAGCAG 2940  
 20 AGAAGACAT CAGCTAAGGA TATGCGCGG AAAGAGGCTA CTATCCTCAG TGATATGTTG 3000  
 GATATGTATT GGAACAATAT CCTCCGAGG GAGCAATAG GAGATAAGGA TACGGAGCAA 3060  
 ACCGAGAAGCA CTATTCTGTA AACAAACAGA AAGAAGAGAC CCATCCAGGA TCTCTACCTC 3120  
 TCCTGTGCCC AAGCGGATAA AGATTGACG GAGTCTCATT ATATCCATTT GGGCAGCTG 3180  
 GACGATGANA GCAAGACTAC GGCAGGATT GCAGCCTATC CGTTGAAGAA CGGCGTTATC 3240  
 25 GATAAAGAGC GGGTGCAGAG AGTATCGACT CGTCCCTACA AACATCTTTC CGTCAATAAA 3300  
 AATCTGGCTA CTGCAAAACA GATCTTTATT TCCTATTCCA AAGAGGATCA GACTGAAGTG 3360  
 GAGACCTGTC TGCAATTTT CAAACCCCTG GAGAAGAATG GTCAGATCGA GATCTACTAT 3420  
 GATAAGTTGA CTAAGTTTGA AACACCTATT CACCTGAAA TAAGAAAGCG TATTGTGAA 3480  
 CGCGACTGTA TAATCGCTTT GATCAGCCAA CGCTATCTGG CCACGGATTA CATCTGGAT 3540  
 30 CATGAGTTGC CTGTATTTCG GGAGTATAAC AAGACCATAG TGCCGATATT GATCAAGCCT 3600  
 TGTACATTTC AAGACGATGA GTTCCCTCGG GAGAAATATT TTGCTCAGAA AGCTCAATA 3660  
 ATCAATCTTG GAAAAGAGGG AAAAACCATT AAAGCTTATG ATAGTATTAC GGCATCAGCC 3720  
 CATCGTGATG AAAATTGGG GGCAGTAGTC AGAGAGTTCA AAGAGAAGAT ATTAAGAATA 3780  
 35 ACAAACAGG AGGTAATAC AGATGAA 3807

## (2) INFORMATION FOR SEQ ID NO:112

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 693 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...693  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112

AAGTTTATGA TGA AAAAAGC ATTGTTTC GTACTACTGG TTTGCCTATT CTCCTCGTTC 60  
 AGCAGTTCCG CCCAAACAAC GACGAACAGT AGCCGGAGTT ATTITACAGG ACGAATCGAG 120  
 AAGGTGAGTT TGAACCTTAGG GGTCCCCCCC GTAAGCACAG AGGTTTGGGG AATGACCCAT 180  
 GATGCGAAGC GTCTCCCTTT CGAAATACCT ATCTCTTTCA GTCTTTTCAA CAGCAGGGA 240  
 GATATAGCTA CCACTTATTA CATAGCSAAT AGCGAGGCAA CTTTGAATGA ATGGTGGCAG 300  
 65 TATGACACCC CGGGCGGCAT CGTGAGGGTA GAAGTCTGTT TTTGGAAAAAT GACTTACAAC 360  
 ATACCAACCT ACAATGCAGT CTGCACCCGG ATTACATTGG AAAATCAAGA AATAGAAGGA 420  
 ACGATCGTCT TGATACCCAA GCCCAAAGTC TCGCTGCCTC ATGTGTGCGA ATCGGTGCCT 480  
 TGCATCCGAA CCGAAGCCGG GAGGGAAATT ATCTTTTGGG AAGAAGACGA CACCTTTGTG 540  
 TCTCACGATG GTAACGAAGT AACGATAGGC GGTAAACUTT TCTTGCTCAA TACCAACGTA 600  
 70 AAGATTGTGG GGGACGTATC TCAAAAGTAT GCGTGGGGG TAGGAGAAAT TCGATTCTCG 660  
 CAGATTGTG CCCAACAGT ATCAACAACA AAA 693

## (2) INFORMATION FOR SEQ ID NO:113

75

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77 / 490

(1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1689 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113

TCGCTAATCA	ACAATTCAAG	AGACTGGAGG	GCTCCTGTCC	GATTGAGTCT	CAAAAAAAG	60
ACAAAAACTA	TGAAGACAAA	AGTTTACGCG	AAATTCGTGG	TGGCGGCTTT	CGCCGTCGCA	120
ACCTCTGTGC	CTCTCGCCCA	AGCGCAGACG	ATGGGAGGAG	ATGATGTCAA	GGTGGTCCAG	180
TACAATCAGG	AAAAACTGGT	ACAAACGAGG	ATGAGTGTGG	CGGACAACGG	ATGGATCTAT	240
GTAAATGACC	ACAGTGGATA	CGACACCGGC	AATAGCAATG	TGAAGATCTT	CCGCTCCAAA	300
GACCAAGGTG	CCACATACCA	AAAGTTGAGG	GATTGGGATC	CATCGGATGA	TTATCAGTTT	360
CAAGACTTCG	ATATCGTGGT	AACGGGTAAG	AATGAATCCG	ACATCAAGAT	TTGGTCGGTA	420
GAGCTCATGA	ATAAGCCCGG	AGGATATAAG	AGTAGAGTTG	CGGTCTTCAG	TCGCGATGCC	480
AACGCCGAGA	ATGCGAAACT	CGTGTATAAG	GAAGACTTCT	CCAATGTGCA	GTGTGACGAT	540
GTGGATATAG	CCTCCAATA	TGTTTCGCCT	TCTTCTCTTA	ACAATGGTGG	CAACCCCTTT	600
GCTTITGGCT	TCGCTTACAC	CGGCTTCAAC	AATACGCACA	AAATAAGTTT	TGTGGACTAT	660
GTGTTCTCTC	TGAATGGAGG	GCAAAATTTT	AATAAAAACT	TACTCTTCAG	TCAAGATGGA	720
GAGAAGAAAA	TTGACAAGGT	GGATCTCTCA	TTGGGTAGCA	CCTCTGAATC	CATGGGTCAC	780
AATGCCCTGC	CGCTAATGGG	TGTGGTATTC	GAAATGAATA	AACAAGGGGG	AAAAAGCGAT	840
ATCGGTTTCT	TGTCGAACCT	TGTCGACAAAT	GATCCCGAAT	TTCAAGTGGTC	AGGCCCTATA	900
AAAGTGAGTG	AAAGCGACAT	GTCTGTCAGC	CCCAAAATCC	AAATGTTGCT	GGACGAGGAT	960
AACAATAACGA	TCAATGGGGA	GAGTTGCCAC	AACCTCATGA	TTACGTACAG	CGATTATGAT	1020
TCTGAATATT	CGGATTGGGA	CATTGCGTAT	GTATATCCCA	AGAAATCGTT	CAAGTATGAA	1080
AAAGGAAAAA	CTCCGACTAT	GGATGATCTG	GTGGAAGCTT	TCCTTACAGC	TTGTTACCAG	1140
AGTGAGACCA	ACTCGGGGCT	GGGGTATGAC	AAGAACGCCA	ATCACTACCT	GATTACATAT	1200
GCCAAAAAAG	AAGAGAACGG	TACGAAACCG	CTGAAATACC	GCTGGGCCAA	TTATGACAAAG	1260
ATTCAATAACA	AAGATTTGTG	GAGCGACACA	TTTACGTATA	CATCATCTGC	CAATGCTCTC	1320
TACACACCTC	AAGTAGACAT	CAATCCGACC	AAGGGTCTCG	TGTGCTGGTC	ATGGGTGGAA	1380
TATCTGCCGG	GCAAACGGAT	CGTTTGGTCT	GATACGCAGT	GGACCCATGC	CAACGGGTGTA	1440
GAAGACATCG	TAATGCAAGA	AGGCAGCATG	AACTCTTACC	CGAATCCGGC	TCAAGAAATAT	1500
GCTGTGATTA	GCCTGCCGAC	GGCAGCAAA	TGCAAGGCTG	TTGTTTACGA	TATGCAGGGC	1560
AGAGTAGTGC	CTGAGGCTTC	TTCTCCGGC	AACGAATACA	GGCTGAACGT	GCAGCACTTG	1620
GCTAAGGGTA	CGTACATACT	CAAGGTCGTA	TCCGATACGG	AGCGTTTCGT	AGAGAAGCTC	1680
ATCGTGGAA						1689

## (2) INFORMATION FOR SEQ ID NO:114

(1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2358 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114

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5 ATCGTTTACC TTTGTCACTG TATGAACCCAC AGACGATCAA AAACCATGCT GACGATCCGA 60  
 AACTTCCTCC TCTTTTGTG TCTGTGCTG ATAGCGTTTG CTGCCGATGC ACAAAGCTCT 120  
 GTCTCTTCGG GTAGACGACT GACAGAATAT GTCAATCCCT TTATCGGAAC GGCCAATTAC 180  
 GGTACCCAGG ATCCGGGAGC AGTATTGCC AATGGGTGA TGAGCGTTAC CCCTTTCAAT 240  
 GTCAGCGGAT CGACAGAGAA TCGCTTCGAC AAAGATTCCG GTTGGTGAG TGCGCCTTAT 300  
 TCGGCCGACA ATAGTTACTG CATCGTTTC AGCCATGTGA ATCTGAGTGG AGTAGGCTGT 360  
 CCGGAATGTA GTGGAATACT GCTGATGGCC ACTTCGGGA CATTGATCC TGATTACTGC 420  
 TGCTATGGCT CTTCGCTCAG TCGAGAATAT GCGCGCCCG GAGAATACAA GGCTGTATTG 480  
 10 GACAAATACG GTATAGATGC AGCCGTGACC GTAACCGAGC GGACTGCTT GACCGAATT 540  
 GCTTTTCCCG AAGGAGAAGG CCATATCCTG CTGAACCTGG GACAGGCCCT AAGCAATGAA 600  
 TCGGGAGCCT CTGTTCCGATT CTTAAACGAC TCACAGTCC TCGGCAGCAG GCTGATGGGG 660  
 ACCTTCTGCT ACAATCCGCA AGCAGTTTTT CGTCAGTATT TCGTACTTCA GGTGAGTCGG 720  
 CGACCGATCT CTGCGGCTA TTGGAAGAAG CAGCCTCCTA TGACAGTGA AGCCCAATGG 780  
 15 GATTGCACTG CAGGGAATA TAAGCAGTAC GACGGCTACA AGCGTGAAT GAGCGGTGAT 840  
 GACATCGGTG TCCGATTCTC GTTCAACTGC GATCAGGGGG AAAAGATCTA TGTACGATCG 900  
 GCGGTTTCCG TCGTCAGCGA AGCCAAATGCG CTCTATAATC TGGAAAGCGA GCAAGAAGAG 960  
 ATAGAGCGTT GGGAGGAAGC CCTCGGTACG GTGGAAGTGG AAGGAGGCAC ACCGGATGAA 1020  
 20 AAGACGATAT TCTATACCGC ACTCTATCAC CTGCTGATAC ATCCGAATAT CCTACAAGAT 1080  
 GCCAATGGAG AATATCCTAT GATGGGCAGT GGCAAAACGG GTAATACGGC TCACGACCGC 1140  
 TACACCGTGT TCTCTTTG GGACACGTAC CGCAATGTAC ACCCGCTGCT CTGCCTCTC 1200  
 TATCCGGAGA AGCAGTTGGA TATGGTACGG ACACTGATCG ACATGTACCG AGAGAGCGGG 1260  
 TCGCTGCCGA GATGGGAGCT GTACGGACAG GAGACCTGA CGATGGAGGG CGACCCCTCG 1320  
 25 CTATCGTCA TCAATGACAC TTGGCAAAGG GGCCTTCGTG CTTTCGATAC GGCACCGGCC 1380  
 TATGAAGCCA TGAAAAAATA TGCTTCTCG GCAGGAGCGA CCCATCCGAT CCGTCTGAC 1440  
 AACGACGACT ATCTCACCTC CGGCTTCGTA CCGCTTCGCG AACAGTACGA CAATTCCGTA 1500  
 TCGCATGCGC TGGAATACTA TCTGGCCGAC TGGAACTGTG CCCGGTTTGC CCACGCACTT 1560  
 GGGCATAAAG AAGACGAGC TCTATTGCGA AAACGCTCGT TGGGCTACAG ACATATTAT 1620  
 30 AATAAGGAGT ATGGTATGCT GTGTCCATTG CTGCCGATG GATCATTCTT CACTCTTTC 1680  
 GATCCCAAC AGGGTGAAAA CTTCGAGCCT AATCCCGTTC TCCACGAGGG CAGTGCTTAT 1740  
 AACTATGCTT TTTTCGTTCC CCACGATATA CAAGGGCTTG CCCGGCTGAT GGGAGGAGCA 1800  
 AAGGTTTTTT CGGAAGGTT GCAGAAAGTC TTGATGAAG GATATTATGA TCCGACCAAC 1860  
 GAGCCGGACA TCGCCTATCC TTACCTCTTC TCCTATTTC CCAAGGAAGC ATGGCGAAGC 1920  
 35 CAGAAATTGA CCCGGGAGTT GATAGACAAA CATTTTGCA ATGCTCTTAA CGGCTTGCCC 1980  
 GGTAATGACG ATGCCGATAC GATGAGTGTG TGGCTTGCTT ATTCATGCT GGGATTCTAC 2040  
 CCTGACTGTC CGGGCAGCCC CACCTATACA CTGACCTCGC CGGTATTCCC CCGAGTTAGG 2100  
 ATTGGCTCA ATCCGAGTA TTATCCTCAG GGGGAGTTGA TCATTACGAC CAATACAGAG 2160  
 AATCAACCGA CAGATTCCAT TTACATCCAT ACGGTTTCTC TTGGCAATAA AACACTTCCG 2220  
 40 CATGGAACAA GGCATATCAG CCATGCCGAT TTGGTGCCT GCGGTACCT CCGTTACGAA 2280  
 CTAAGCAATC GTCTCGA 2340  
 2358

(2) INFORMATION FOR SEQ ID NO:115

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2442 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 50 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 55 (iv) ANTI-SENSE: NO  
 (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 60 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2442  
 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115

CCGGTTTTC ATCCGGGAG GACACAGCT CAGCTTTGCA GAAATGGAG AAGAAACCAA 60  
 AAATCAAATC AGTCATCGTG CTTTGGCGGT GGCACAGCTC CGCGATTTT TATTATGTGC 120  
 AAAATAAGAT TCAGCCTCTT GCAGGCTCTT GTCGTCTGCT TATTGTTTCA CTCTTTTCT 180  
 70 CTCCAGCTC AAGAGGAAGG TATTGGAAT ACCCTCTTGG CTATCCACAA GACGGAAGAA 240  
 GCGGTAGAAA CGCCCAAGAA AGTCTTTGCC GTAGCCAAAG GAGTACTTTA CTCGGTGGGC 300  
 AAAGAAGCTC CCCATGAGGC AAAGATCTTC GACCGTATCA GCGGACTCAG CGATACATCG 360  
 GTAAGCAACA TAGCCTACTC CGAGCAACTA AAATCCTTGG TCATATACTA TGCAATCAGG 420  
 AATATCGACA TCTGGACGA AGCAGGCCGT GTGACCAACG TACCTGCATT GAAAGACAAT 480  
 75 ATCGATCTGA TAGACAAAC GCTCAATCGC CTTTGTATCG TAGGCAACAG GGCTTATTG 540  
 GCAGGAGGAT TCGGCCTCTC CGTCTGATG GTCCCGAAG CTCGCATACC GGCTACCTAC 600

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5 GCCAAGGGAA CTAAGGTGAC CGATGTGGCT AAGTTGGACA ATGATCGCTT GCTGATGCTG 660  
 AAAGAAGGGC AGCTCTTCAT CGGAAAGAG ACCGATAACC TGCAAGATCC GGCCGCATGG 720  
 ACAGCCTTGT CTTTGAATTT GCCGATGGGC TCGGTCACCG GTCTGGGCAT TGTCGGGGAA 780  
 GACATCTGTT TCCTGCTCGC GATGCGCGT GTATATGTGC CTGCAAAACCA ATCCCTTTGAG 840  
 CCGGAGCTAT TGCTCTCTTC CTCGCGCGAT TCACGACTGT ATGTGACGGA TCGTGGTCTG 900  
 TTCATCTGTG CCGAGAATCG AATTATTTTC ATAGAAAAAG STCGCAAAAC GACACAATTT 960  
 CCTATAGCCG ACGTCCTTGG TGTCCGTGCC ATGAACGAAA GCAATACGGC ATACATAGCA 1020  
 TTGGGAGAAG AAGGTTTGGC TTCACTTCTT CTGCGAGAGG GAAGTACGGC CGAAGCCATG 1080  
 CCTGTAGCAT TCAGCGGACC GGGGGACAAT GATTTCTACG AGATGCGGTT TAGTCACGGA 1140  
 10 CGTCTGTATG CAGCCAGCGG ACTCTGGGGA ACAAACCTGA TGGGACATGC CGGTATGGTG 1200  
 AAGCTATACG ACGGCAACCG ATGGACTAAC TTCGACAGA AGACCGTACA GGAACAGTTG 1260  
 GGCAGCGGAT TCAGTTTCAA TGATGCTATC GATATAGCTG TTTCCAAACG AGACCCGAT 1320  
 CACTTTTTTG TCGGTACATG GGGAAACGGT CTGTTGGAAT TCAAGGATGG CAAAGCGATA 1380  
 GCTCGCTATT CCGGAAACGA AACTGCTATC GCAGAAATGA ATCCCGGAGA TGCCCGTGTG 1440  
 15 AAAGCGATTG CTTTGACAA TAAGGGCAAC CTCTGGGGGA CGCTCGGTGC CGTAGGCAAG 1500  
 AACATCTTCA TGTACGATCC GCAGAGTAGC ACATGGCATT CTTTCAGCTA TCCGATGTA 1560  
 GCCAATCTGG CCTCTTCGG CAATATGATT ATCCTACCCA ACGGAGACAA ATGGGTAAT 1620  
 ATCCTTCAAC GTAGTGGCGG ATCCACGCGC AAAGGTGTCT TGATCTTCAA CGATCGGGGT 1680  
 ACACCGGAAA CGACTTOSGA CGACAGCCAT CTTTACGTGC AGCAGTTTGT CAATCGCCCTC 1740  
 20 TGGGCGAGCA TAGGACATAA GACTATCTAT GCAATGGCCG TCGATCATAA CGGCTCTGTC 1800  
 TGGATGGGAT CGGATATAGG CATTTTCGGC GTCTACAATG CAGCGGAGT ATTGTCTCTG 1860  
 ACTTCTACCC CTATCGCTGT TCGGCCGGTC GGAGGAGAAG AACCCAATTT GTACTATGTG 1920  
 CTGGACLAGG TGACGGTGAC AGACATCGTC GTGGACAAAC TCAATCACA ATGGGTTGCC 1980  
 ACCCAAGGGA CAGGACTCTA TCTCCTTCG GAAGATTGTA GTAAGATCCT CGCGCAATTT 2040  
 25 ACCGTAGAAA ACAGCCCTTT GCTTTCTAAC AACATACTAT CCCTGGCCTT AAATGACGAT 2100  
 AACGGACTGC TGTACATCGG TACGGCGGAC GGAATGATGA GGTTCCAAAC GGTACGGGG 2160  
 AGTGGATCAG CTTCCGAAGT GGACGGCGTC TATGTATACC CCAATCCGCT AAGGCGGAA 2220  
 TATCCCGATG GCGTCAACAT TGCCGGACTG CAAGCGGCT GTAGTGTCAA AATCAGCAT 2280  
 30 ACCACCGGCA GACTGCTATA CCACACTGAG AGCGTAACCA CCGAAGTCAA ATGGAATGCT 2340  
 CGAGGTGCGG ATGGCAATAG GGTAGCTTCG CGCGTATATG CCGTTGCAGT GTACGATCCG 2400  
 GTATCGAAAA AGTCCAACT AATTCGCTTC GCAGTGATTC GC 2442

## (2) INFORMATION FOR SEQ ID NO:116

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3486 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRAINEDNESS: double  
 40 (D) TOPOLOGY: circular  
  
 (ii) MOLECULE TYPE: DNA (genomic)  
  
 45 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 50 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...3486  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116

60 GCTATTTCTC AGATGAAAGC AACTCTTCCA ATAGTCGCAT TCCTTCTCT CTCTCTTGGC 60  
 CTTGCTTTGC CTGCGAAAGC GCAACGAGCT ATGGGGAAGA GGGCCGACCG TTCGCTAATG 120  
 GCTTCGGGAC ATTGGGTCAA GATACGTGTC GATGCAAGTG GAGTGTATCG CCTTACGGAC 180  
 GAACAGCTCC GTGCCAATGG CTTCTCCGAT CCGTCCAAAG TAGGTGTGTT CGGTATATGGT 240  
 GGAGGGGTGC TTCCGGAAGA TCTGAGCCGG ATCAGGACAG ACGATTTGCC TCCGGTACCG 300  
 GTACTCCGTC AGGGCAATGC GCTGTATTC TATGCCGTGG GCCCGGTGAC ATGGTTCTAC 360  
 AATCCGGCCA AAACACCAT GGAGCATACG GTGAATACAT ACAGTACGCA TGGCTACTAC 420  
 65 TTCGTGTCGG ATGCTGCCGG AGCACCTTTG CAGATGTCCG AATATACGGG TGGAGGTGCG 480  
 TCGGCCGAGG CTTTGATCGA CTACTACGAT GAGCTGATCC TCCATGAACA GGAATTGTAT 540  
 TCGCCCAAAG AATCGGACG AGATCTGTAT GCGAGTCTT TCAGTGCAGT CAATACGCGT 600  
 ACGGTCAAGT TCCCTTTGAG GGGCAACACC CGTTCGTCTG CGCAACTCGG TACCGTATTC 660  
 TCATACATAG CCAAGGCCAG ATCGGCCGGT GGGGCGCGTG AGATGTCGCT CTCGGCGAAT 720  
 70 GGCATTCTGA TCTTACGCGA TCCTTTTTC ATGACATGSA ATGAAGTCTC CAATTCCTAT 780  
 TTGGCGGCA AGAAGCGTCG TCTCTATCAC AGTACGCGCA TGAACAGCTT GGCTAATGAG 840  
 TTGGCTTGG ACGGAACTA TAGCATGACA GGAGATGCGG TCAATCTGGA TTTCATAGAG 900  
 GTGGCTACAC AGAAGCACTC CCGGTACGAT GGGCACCCTA TGCATATCAG GCGGTTTTC 960  
 AATTTCGCGG TTTTGGGGGG CGAGTCTGTC CCGTTCTGTA TCAGTAGGTT GCCGGAGTCT 1020  
 CTGGTGGTTT TGCAGGCCAA TTCTTCCCTG ACAGCATCGC TTGTTCCCGT TAAGACTGTC 1080  
 75 GGGGATAAGA CCATTGAGTT CGTGGCTCCG CCGAAGGGTC AGGATCGTAG GACTATCAAT 1140

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5 ACGTTTATG CCGTGGACTT GTCACAGGCT TCTGCTCCGG AGATCCTCGG AGCGGTACCC 1209  
 AATCAAAACC TGCATGGAGA GGAATCCCT GATCTGATCA TTGTCTCTAC TCAGGCGCTC 1260  
 CTCCTTGAGG CTGATCGACT GGGCACCTAT CGTAGAGAGA AAAACGGGCT GAAGGTTTTG 1320  
 TCCGTGTGTC AGGAACAGGT GTTCAACGAG TTTTCGGGTG GAACTCCCGA TGCTACAGCA 1380  
 TACCGCCTCT TTGCCAAAT GTTCTACGAC AGATGGGAAG CAAATGCACC TGTGGGAGAC 1440  
 ACCTTCCCGA TGCAAAATGCT TCTCTTGGT GATGGGGCTC ATGACAACAG GAAGGTCTCC 1500  
 GTAGCTTGGC AGAAACCGTA TCTCCAACAA ACGGAGTTCT TGCTGACATT CCAAGCCGTC 1560  
 AATTCGACGA ACGTAAACAG TTATGTGACG GATGATTACT TCGGCTTGCT GGATGATCAG 1620  
 CCGGCCCTCGG TCAATATCGG TTGGCGCAAT TATAATATGG CTGTAGGGCG ATTCCCGCTA 1680  
 10 CBTACTCCGG CCGAAGCTCG CATCGCAGTG GACAAGACCA TCCGATATGA GGAGGATCGA 1740  
 GAGAGTCGTG CCTGGCGTAT TCGTGCTGT TTTGCGGCAG ACAACGGGGA CAAGCAOCCA 1800  
 ACCGAGACTT CCGGTTTAT GATACCGTC AAGCGTTATG CTCCTGCCAT CATGCCGGTA 1860  
 CGCGCCTTTC AGGACGTATA TCCGCATGTC ATCGAGAACG GGTTCACAG CATTCGGGGT 1920  
 GCAAGAAAAA AGATGCTGGA AACCCCTCAG TCGGGTATTA TCCTGCTTAA TTATGCTGGT 1980  
 15 CATGCCGCTC CTGCCGGATG GTCGGACGAG CATTGTGCTA CGCTCAACGA TATACACAAA 2040  
 TTCAATTTA AGCATATGCC CATTGGATT ACTGCCACOT GCGACTTTGC CAACTATGAC 2100  
 AGTCAGACGA CCTCGGACGG GGAGGAGGT TTTCTCCATG AGAAGAGTGG CACTCCGATC 2160  
 ATGTTCTCGA CTACGCGTGT CGTTTACAA ACAGCAAGATG AGAAGATCAA TGGTTTTATG 2220  
 20 CTTCCGGCGTA TGTTCGAGAA AGCTAAGGAT GGGCGTTATC GTACGATGGG CGAGATTATC 2280  
 CGATCGGCCA AACAGGGGAT GCTCAGTACT GTTTTCCCGG ATTTCGATCAA CCAGTTGAGT 2340  
 TTCTTTCTGA TGGGTGATCC GTCCGTGCGT ATGAATCTTC CTACCCACAA AGTGCAATTG 2400  
 ACCGCAATCA ACGGGCAGGA TCCCGAAGGG CAGTATGGAA CTATTATGCT CAAGTCTTTG 2460  
 GAACGGGTAG CTCTGAAGGG TAAGGTAACC GATGAAAAGG GGACATTGSA CGAGACATTG 2520  
 25 AGTGGCAAGG TTTTCTGAC CGTCTTCGAT GGCAGAAAGA AAATGACAGC TTTGGAAGAG 2580  
 GAGGGAACCG ATCTCTCTCT TGTATATTAT GACTATCCTA ACGTGATGTA TCCCGGTATT 2640  
 GCCGAGGTGA AAGACGGACT CTTGGAAACT TCGTTTATCG TACCCAAAGGA TGTGAACAT 2700  
 TCCGAGCAGG AAGGCCGGAT CAATCTTTAT GCTTATAACG AGAGCACAAA GCGCGAAGCC 2760  
 ATGGGGGTAG ACTTCTCCAT CAGAGTCCAA CCGGGTATTC CTGATGAGGT AACGGAAGAT 2820  
 AATACACCGC CTGAAATCAT AAGCTGCTTC CTCAATGACA GTACATTCCG ATCGGGAGAT 2880  
 30 GAGGTTAATC CTACTCTCT GTTTATGGCC GAAGTATTGG ACTTGAATGG AATCAATATC 2940  
 ACGGGTAGCG GAGTAGGGCA TGATATTACG CTTTGTATCG ATGCCCTGCG CAGCTTGACC 3000  
 TACAACCTCA ATGCATATTT CACAAGTTCC GCTACGGATG CAGGTGTGGG CACTATTCTC 3060  
 TTCATGATAC CGGCTTTGGC CGAAGGAGAT CATACTGCCG GACTGACGGT TTGGGACATT 3120  
 35 TTCAATATG CCGTCCATCA TGACTTTTCA TTACAGATGG TAGATGGCAT TGTCCGGAT 3180  
 TGGGCTGATG TGATTCTATT CCGGAATCCG GTACGCGAGA GTGCTACGTT CCGAATCTTC 3240  
 CACAAATGCC CCGGAAGCGA TTTGAACGTG GCGGTGGAGA TCTATGACTT CACCGGTCTG 3300  
 CTTGTGAACA GTTTGCCAGT CAAGACCTAT TCGTCTTCT ACAGGAGACC TATAGAGATC 3360  
 AAGTGGGATC TGACCTCCAA ATACGGAGTG AAGATCGGAA ACGGATTCTA CCTCTATCGT 3420  
 40 TGTGTGCTGA ACTCTCCCGG AGGACAGACG GCCTCCATGG CCAAGAAAAA GATCGTGGTA 3480  
 GGACAA

## (2) INFORMATION FOR SEQ ID NO:117

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2919 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 50  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 55 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 60 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2919  
 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117

TTTTACACCG GAATTGACTT GCATATAGAA AGCCAAATGA AGAAACTTT CCCATTATTA 60  
 TTACTCATAT TGTGATTTT GGTCCGATGT GGAAAAAAG AAAAAACATC TGTAACTGAA 120  
 ATCGCCCGAG AGAAAAAGCG TATTACTGCA TTGCTGTACG AAAAAGAACT CCCCACTGAT 180  
 TCTGTTAAAC AGCTTTACGA GAACAGCGTA CAGAACAAGA ACCTTGTTGG ACAAATGTTA 240  
 70 TTCCGCGATG AGGTCCGGCA ACUGATGCGT AATATGTCCC AATACACAGA TGCGATGCTA 300  
 TATCACCAAA AAGGGTTGAA CGCTGCATTG AATCTAAGGG ACACCATCGT AGCCGACAAA 360  
 GCATGGAATC ATCTCGGAAC GGATAGCCGT CGTATCGGTG CTTTGGCAGA AGCTTCGGAT 420  
 TATCATTACA AGGCTCTTTC CTTGATAGAA TCTTTAGCG GAAACAGAAA TAGGCCTGCG 480  
 ATCAAGCCA GATCGGCGGC CCTGAACGGC ATCGGCAACA TCAATCTTGA GTTAGGATAC 540  
 75 CATGATGAGG CCGAAAAGAA TTTCTGAAA GCACTGCAAG GTGAGAAAGA ACTCGACAGT 600

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5	CCTCTCGGGC	AAGCTATCAA	CTATGCGAAC	CTCGGACGTA	TCTATCGACA	ACGCAAAAGAA	660
	TACGACAAGG	CTCGTACCTA	CTTCCTCTTG	TCTCTGGAGC	AGAACAATAT	GGCAGAGAAT	720
	CTGATGGGTA	TCGGACTCTG	TAGCATCAAT	CTCGGAGAAG	TAGACGAAGA	AAAAGGGGAT	780
	TATCAAAAGG	CTTTGCAAGA	GTATGCCACG	GCATACAAAC	TGATGGAACA	GTGTCCGAT	840
	CGATGGCACT	GGCTGAATTC	CTGTATCCCG	ATGGCACGTA	TCAATCTCAA	ACAAGGTAAC	900
	GAAAGGCTCT	ACCGAGCTTT	CATTTCTTTG	GCCGAAGGGA	CTGCGAAAGA	AATTAAATCG	960
	ACTTCACATC	TGATAGAAAT	ATACAATCTT	CAATACGAGA	ATCTCGAGCG	TAAAAAGAA	1020
	TACAAACAAG	CCCTCGAAGC	ATCTGTCTG	AGCAAGACGT	TGAGCGACAG	CATGTCCATT	1080
10	GCGCACAAGG	TCAGCAGCAT	ACAAGAAACG	CGATTCAACT	ACGAACGAAA	CAACTCCCAA	1140
	AAAGAGCTTG	AAGAAATACA	GCAAGTAAGC	AAGGCAAAAC	AAGAGAAATC	GAAGTTTATC	1200
	CTCTTGAGCA	CTCTTTTTCG	CCTTTTCATC	TCGATTCTTT	TGATTTCTGT	TCTGACATAT	1260
	GCATACCGTC	AGGGCAAGAA	GCATAACAAG	CTGATCAAAG	AGACGGATAA	ACTTGGCTCC	1320
	GGCTTTTTC	CCGGTATTAC	ACACGAATTT	CGTACGCCTA	TCACCGTCAT	ACAAGGTTTG	1380
15	AATGAGAAAA	TGAGTTCAAG	TCCTGATCTC	CAAGCATCGG	ACAGAACCAG	GCTGCACAAG	1440
	ATAATAGACA	GACAGAGTAG	CCATATGCTG	AATTGGGTGA	ACCAGCTGTT	GGATATTTCG	1500
	AAGATCAGAA	GCGGAGTATC	CACGCCCGAA	TGGCGCAATG	GCGACATCGT	CTCCTTCGTA	1560
	CAGATTCTCA	TCGATTCTGT	TGCACCATAC	GCACAGGCTC	AAGACATAAC	CTTGGAGCTA	1620
	CAACCCGAGA	GCAAACTTAT	TGTCGTGGAC	TTCGTCCCTT	CCTACTTGCA	AAAAATCATA	1680
20	TCCAATCTTT	TGTCCAATGC	CATCAAGTAT	TCTTTAGCCG	GAGGGAGAGT	GGTCATATCT	1740
	CTGGCAAAAA	CCAAGAATGA	AAAAAATCTG	ATCATACGCG	TTGCAGACAA	TGGCATAGGA	1800
	ATAGATAAAA	CTGATCAGGC	TCATATCTTC	GACATCTTCT	ATCGAGGACA	GTCCGCTACC	1860
	GAAAGCATG	GATCAGGCGT	CGGACTCTCG	TTTACCAATA	TACTGGTCTG	AAACCTTCGA	1920
	GGTACGATCA	AAGTGGAAAG	CCAGCCCGGG	AAAGGAAATG	CTTTCACCAT	CAGTATTCTT	1980
25	ACACAATAAC	AGTCCTCTTC	GGCAGAGATT	CTTCTTGGC	TACCTCTCTC	CGATGACATT	2040
	GTCATGCCCT	TCCACATGCG	GCCCGATGAC	TCACCGACAT	CTCCGATGGT	AGCAGCTCTG	2100
	AATCATCGCT	TCGAGGACGA	ACGTCLGACC	ATACTGCTCG	TCGAGGACAA	TAAGGATATC	2160
	AACCTGCTCG	TCAAACCTACT	CCTTTGCGAT	CGCTACAATG	TGCTATCCGC	CGCAAAACGGA	2220
	AAAGAGGGTA	TAGCCCTCGC	TACCGAGCAT	ATTCCCGACA	TTATCATTAC	GGATATTATG	2280
30	ATGCCGATAA	TGGATGGGAT	AGAAATGACA	ATCCGGATGA	AGCAATCGCC	TCTGCTCTGT	2340
	CACATTCCCA	TTGTCTGCTT	GACGCCCAAG	AGTACCGAAC	AGGACAGATT	GGAGGGAATC	2400
	AAAAGCGGTG	TAGTCTCTTA	TCTATGCAAG	CCATTCTCTC	CGGAGGAGCT	TTTGATGCGG	2460
	ATCGAGCAGC	TTCTGAAAGA	CCGTGAGTTG	CTCAAGAAGT	TCTATATGCA	AAAACCTCAT	2520
	CTGGATCGGA	AGCCGGAGGA	GGAGCCCTCAA	CCGATAGATG	ACAGCAGTAT	GCAGTTTCTC	2580
35	CTTGCTGCCA	AAGATGCAGT	GTCCGGTGGG	ATCAAAACAA	ATCCGGATT	TTCCGCTCAA	2640
	GACTTGGCCG	AAAAAATGTG	CATGAGTCCA	TCCCAACTCA	ACAGAAAGCT	CACGAGTGTC	2700
	GTAGGTTGCT	CCACCATCGG	CTACATACAG	CAGATCAAGA	TAAAATTGGC	CTGCAAGCTC	2760
	CTTGCCGATG	AGAGCAAAAA	CATCTCCGAC	ATTAGCATTG	AGGCAGGCTT	TTCGATCCG	2820
	GCTTACTTCT	CTCGCACCTT	CAACGCTAC	ATGAAGTCTG	CTCCCTCCCA	ATATCGGCAA	2880
40	AAACTCCTTG	CCATGCCGGG	GAGCGACAAG	GAGACAGTT			2919

## (2) INFORMATION FOR SEQ ID NO:118

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1689 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (D) LOCATION 1...1689
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118

65	CATCATAAAA	CATATCAAAC	AATGAAAAG	CTTTTACAGG	CTAAAGCCTT	GATTCTGGCA	60
	TTGGGACTCT	TCCAACCTGC	CGCAATCGCC	CAAACGCAAA	TGCAAGCAGA	CCGAACAAAC	120
	GGTCAATTG	CAACAGAAGA	GATGCAACGA	GCATTCCAGG	AAACGAATCC	CCCTGCAGGT	180
	CCTGTGCGTG	CTATCGCTGA	GTACGAACGC	TCTGCAGCCG	TTTGTGACG	CTACCCGTTT	240
70	GSTATCCCGA	TGGAATTGAT	CAAAGAGCTG	GCAAGAAGC	ACAAGGTGAT	TACCATTTGT	300
	GCGAGTGAAA	GCCAAAAAAA	CACCGTTATA	ACCCAGTACA	CCCAAGCGG	TGTGAATCTC	360
	TCTAATTGCG	ATTTTCATCAT	TGCGAAAAC	GACTCTTACT	GGACACGCGA	CTATACCGGT	420
	TGTTTCGCAA	TGTACGATAC	GAACAAAGTA	GGTCTCGTGG	ACTTTATTTA	TAACCGCCCT	480
	GGTCTTAACG	ATGATGAATT	CCCCAAATAC	GAAGCACAAT	ATCTGGGCAT	CGAGATGTTT	540
75	GGGATGAAGC	TCAAGCAGAC	CGGTGGCAAC	TACATGACCG	ACGGATATGG	ATCCGCTGTG	600
	CAGTCACATA	TCGCATATAC	GGAGAAGTCC	TCTCTGTCTC	AAGCTCAAGT	AAATCAAAAG	660

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5 ATGAAAGACT ATCTCGGCAT CACACATCAT GATGTGGTAC AAGATCCGAA CGGCGAATAT 720  
 ATCAACCATG TGGACTGTTG GGGCAAGTAT TTGGCACCGA ACAAATCCT CATCAGGAAA 780  
 GTGCCTGACA ATCACCCTCA GCACCAAGCC CTGGAAGATA TGGCAGCCTA CTTCGAGCA 840  
 CAGACCTGGC CATGGGGAAC GAAGTACGAG GTATATCGCG CTTTGGCCAC CAATGAACAA 900  
 CCGTACACGA ACTCTCTGAT TCTGAACAAC AGGGTATTGT TTCCTGTCAI TGGCCCCGCC 960  
 TCCGTGGACA ACGATGCTCT GAACGTCTAT AAGACGGCAA TGCCCCGTTA CGAAATTATA 1020  
 GGTGTCAAA GGGCTTCAGG AACACCTTGG TTAGGAACAG ATGCCCTGCA TTGTCGTACT 1080  
 CACGAGGTAG CGGATAAGGG CTATCTCTAT ATCAAGCACT ACCCGATACT GGGCGAACAG 1140  
 GCAGGCCCTG ATTATAAGAT CGAAGCAGAT GTCGTCTCAT GCGCCAATGC TACTATCTCG 1200  
 10 CCGGTACAAT GTTACTATCG TATCAATGGT TCCGGTAGCT TTAAGGCTGC TGATATGAG 1260  
 ATGGAATCAA CAGGTCACCTA TACTTATAGC TTTACAGGTC TTAACAGAA TGATAAGGTA 1320  
 GAATACTATA TCTCTGCCGC TGACAATAGT GGTCCGCAAG AGACTTATCC CTTTATCGGC 1380  
 GAACCTGATC CTTTCAAGTT TACGTGTATG AACGAAACCA ATACATGTAC TGTGACCGGA 1440  
 GCTGCCAAAG CTCTTCGTGC ATGGTTCAAC GCCGGTCGTT CAGAACTGGC TGTTCGGTA 1500  
 15 AGTTTGAATA TTGCCGGCAC ATATCGGATA AAGCTTTATA ACACCGCAGG AGAAGAAGTC 1560  
 ATGCAATGA CCAAGGAATT AGTAGCAGGG ACGAGTGTCT TCAGTATGGA TGTGTATTCT 1620  
 CAGGCTCCGG GCACATATGT TCTGGTTGTT GAAGGAATG GAATCCGTGA GACAATGAAA 1680  
 ATTCTCAA

20 (2) INFORMATION FOR SEQ ID NO:119  
 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1311 base pairs  
 25 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 30 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 40 (B) LOCATION 1...1311  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119

45 ACCACAAATA GAAAACCAAA TACTAATATG AAACITTCAT CTAAGAAAAT CTTAGCAATC 60  
 ATTGCATTGC TGACGATGGG ACATGCTGTG CAGGCACAGT TTGTTCCGGC TCCCACCACA 120  
 GGGATTGCGA TGTCTGTAC TACAACCAAG GCCGTAGGCG AAAAAATCGA ATTGTTGGTT 180  
 CATTCCTAG AGAAGAAAG CATCTGGATC GATCTCAATG GGGATGCCAC TTACCAACAA 240  
 GGAGAGGAAA TAACCGTATT CGATGAGGCA TACCACGAAT ACACGATCGG GACGCAAAAC 300  
 CTCATATCT ATGGTAATAC GACCCGATTG GGCTGTCTGAT CTACCCGTTG AACGGCTGTC 360  
 50 GATGTAACGA AAAACCTTAA TCTGACCTAT CTCGCATGCC CGAAAAATAA TCTGAAATCA 420  
 TTGGACTTGA CGCAAAACCC AAGCTGCTG CGAGTTTGGT GCGACTCTAA CGAAATAGAA 480  
 AGTTTGAGC TGAGTGGCAA TCCGGCTTTG ATCATCCTCG GCTGTGACAG GAATAAGCTG 540  
 ACTGAGCTGA AGACCGATAA CAACCCCAAG TTGGCCTCTC TTTGGTGTTC TGATAATAAC 600  
 CTGACGGAGT TGGAACTCAG TGCCAACTCT CGTCTCAATG ATCTTTGGTG CTTCGGTAAT 660  
 55 CGGATCACGA AACTCGATCT GAGTGCCAAT CCTCTATTGG TAACACTTTG GTGCAGTGAC 720  
 AATGAGCTTT CGACCTTGA TCTTCCAAAG AATTCCGACG TTGCTTACCT TTGGTGTTC 780  
 TCGAACAAAC TTACATCCTT GAATCTGTG GGGGTGAAGG GACTGAGTGT TTTGGTTTGT 840  
 CATTCCAATC AGATCGCAGG TGAAGAAATG ACGAAGTGG TGAATGCTTT GCCCACACTA 900  
 TCTCCGCGCG CAGGCGCTCA GAGCAAGTTC GTCGTTGTAG ACCTCAAGGA CACTGATGAG 960  
 60 AAGAATATCT GTACCGTAAA GGATGTGGAA AAAGCTPAAA GTAAGAACTG GCGAGTATTT 1020  
 GACTTCAACG GTGATTCTGA CAATATGCTT CCATACGAAG GAAGTCCGAC ATCGAACTTG 1080  
 GCAGTAGATG CTCCCACTGT CAGGATATAT CCAATCCGG TAGGAAGATA TGGCTCGTC 1140  
 GAGATCCCGG AGTCTCTTT AGGGCAGGAA GCTGCTTTAT ACGATATGAA TGGGGTAAAA 1200  
 65 STCTATAGTT TCGCGGTAGA STCTCTTCGT CAGAACATTG ACCTGACACA TCTTCCGAC 1260  
 GGCACCTATT TCTTCCGTCT CGATAACTAT ACCACTAAGC TCATCAAACA G 1311

(2) INFORMATION FOR SEQ ID NO:120  
 70 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 954 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 75 (D) TOPOLOGY: circular



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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

10 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120

15 AATCATTTGA AGACAAATAT CAAGATGAGA AAAACAATAA TTTTCTGCTT GTTGCTCGCC 60  
CTATTGGGCT GTTCTTGGGC ACAAGAAAGA GTCGATGAAA AAGTATTCTC CGCAGGAACA 120  
AGTATTTTITA GGGGCATCCT TGAAGAGGTG AAAGCACC GC TTATGTATGG AGATCGTGAG 180  
GTATGGGGTA TGGCTCGTGC GAGCGAGGAT TTCTTTTITA TACTTCCCGT TACGGATGAC 240  
20 CTCACCTCCG TGCTTTTCTA TAACCGTCTT ACRAACGAAC CCTGCTTTGT GTGAGACCAA 300  
GGAATAACTG AGTATTTCAA ATTCTGCTCA GAGGTGATT ACATTGAAGT CGAAGGAAGC 360  
TGTGTATTCA TGGCGAATCT TTGTACTAT CGTTTTTTC CGACAAGAA TACCTCCTAT 420  
AATGCTCCCA TTGAAGGTGT TGTGAGCAAG ACGGAAATC CTGCTTTTAC AATCCCGATG 480  
CTCCCGGGGG TTTCTGATTG CATAGAAATC TCAACAACCC GCAAAGTCTT TCTGACCAAT 540  
25 CAATTAGGGG TTGTAACAT CACTGACGGG ATGGAACCTC CGATTATTGC CGGAGTCTCT 600  
GCTTCCTATG GATCTTCCGT CCGGGTGAT GGTCTGTCT CACAGCGGTG GGACATCATA 660  
GGCCATTGCT ATTTGGATAT CTACCCAACC AATTGCTATC CGCTCAGCAC GAAACCCGTT 720  
GCAGGAGACG ATGAGGTTTT TGTCAAACAA CAAGGCAGGC AAATAGAGAT CGATAGCAAC 780  
AGCCCATAG TCCAAGTGGT CGTATACGAT CTTGAGGGGA AAAGTGTITT TCGCAAAGA 840  
30 ATGACCGAAA ACGCTTATAC UCTATCCTTT AGAGCACCCA TGCTCGGCTT TATGACCATC 900  
ATGATCGAAA CACAAATTC GATTATCAAT AAAAACTTA ATGTTACACA GCTA 954

(2) INFORMATION FOR SEQ ID NO:121

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1383 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

45 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

50 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1383

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121

AGACGGGCGAG TTAAATCCG ATCACCCTCC CATATCCACT CATTATTGT ACGTAAATGT 60  
CTTTTTCAG ACTTAAATA CTTATATTTA TCCGAAAAA TTACCCAGA GAGATTGGGT 120  
CGATTGTGCA TCCGTCTTAA GTCATACAA CCAATAATCA TTATTGAAAT GAAAAAACA 180  
60 ACCATTATTT CTTTGATTGT CTTGGTGCT TTCTTTGCAG CCGTGGGCCA AACCAAGGAC 240  
AATTCTTCTT ACAAACCTTT TCCGAAAGAA GATATTGCCG GAGGAGTTTA CTCTCTCCG 300  
ACTCAAAATC GTGCGCAGAA GGACAATGCC GAGTGGCTTC TTACAGCGAC CGTCTCCACA 360  
AACCAGTCTG CAGATACTCA CTTTATCTTC GATGAGAACA ACCGCTATAT CGCTCGTGAC 420  
ATAAAGCCA ATGGGGTAAG AAAATCCAG GACTCCATTT ACTACGATGC CAACGGGCGA 480  
65 ATATCGCATG TGGATCTTTA TATCTCGTTC AGTGGCGGAG AGCCTGCACT CGACACCGA 540  
TTCAAGTACA CCTATGATGA CGAGGGAAAG ATGACCGTGA GGGAGTATT CATGCTGGTA 600  
ATGGATCOGA ATACACCTAT CTCACGCTTG GAATATCATT ATGATGCACA GGGCAGACTG 660  
ACCCACTGGA TTTCTTTGCT TTTGGGGGCA GAATCCCAAA AGAATACGTA TCACTATAAT 720  
GAAAAGGTC TGTGTGTCAG CGAAGTGCTG AGCAATGCAA TGGGGACAAC CTATTGAGAC 780  
70 ACCGGCAAAA CGGAATACAG CTATGACGAT GCAGATAATA TGGTGAAGGC CGAGTACTTC 840  
GTCGTCCAGC AAGGAAGGCC ATGGCAAGTA CTCAAAAGAG AGGAATACAC CTATGAGGAC 900  
AATATCTGCA TACAATATTT GGCTATTAA GGTACCGACA CAAAGGTGTA CAAGCGAGAC 960  
ATCGAGAGCG ATAAGTCCAT CTCGCAAAAT GTCAATGACA TTCCGTCAAT CCGGACACAG 1020  
ACCTGGCCTA ATATGTACGG ATTCAACGCA AAGCGACTGA AAGAGACTTA TTCTCTCTAC 1080  
75 GAAGGAGATG TGGCTACTCC TATATTCGAC TATATCTATA CGTACAAGGC TCTTACCTCA 1140

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ATGGCAACAC CTTGCACAGA AGCTCAGGTA GCAGTCTATC TCAATCCGTC AACGGACCGG 1200  
 TTAGTGATTG TGGCCACCGG CATCACACAT CTCAGCATGT ACGACTTGCA GGGTAAGCTT 1260  
 ATCCGTGATT GTGCCTTGAG CGGCGATAAG GTGGAAATGG GTGTCGGATC TTTGACCAAA 1320  
 GGGACATACC TGCTTAAAGT GAATACGGAT CAGGGAGCCT TTGTGAGAAA AGTCGTGATT 1380  
 CGA 1383

## (2) INFORMATION FOR SEQ ID NO:122

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1353 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1353

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122

ATGGCAAAAG TTATAAAAC AAAAAAAGGC CTTGCACTTA ATCTGAAAGG AAAACCGCTG 60  
 CCCGAGATGC TGGCCGAACC GGGCCAAAGT CCTACTTACG CGCTCGTGCC CGACGATTTT 120  
 GAAGGTGTTA TCCCAAGGT GACGGCTCGT CCGGGGATA AGGTGCGTGC CGGCTCAGCA 180  
 CTGATGCACC ACAAGGCATA TCCGAGATG AAGTTTACAA GTCCGGTTAG CGCGGAAGTG 240  
 ATCGCGGTGA ATCGCGGTGC CAAGCGCAAG GTGTTGAGCA TCGAGGTGAA ACCGGACGGA 300  
 CTGAACGAAT ACGAGTCATT CCCTGTCGGG GATCCGTCG CCTCTCTGCG CGAACAGATC 360  
 AAGGAGCTTT TACTGTCGAG CGGTATGTGG GGTTTTATTA AGCAACGTCC TTACGACATA 420  
 GTGGCTACAC CGGATATAGC TCCACGCGAC ATTTATATTA CTGCCACTT TACTGCACCA 480  
 TTGGCTCCGG ACTTCGATTT CATCGTTCCA GGAGAAGAAC GCGCCCTGCA GACTGCCATC 540  
 GATGCCCTGG CCAAACTUAC GACAGGAAAG GTGTATGTGG GCTGAAGGCC GGGTTCACTC 600  
 CTGGGCTTGC ACAATGCAGA AATCGTAGAA GTACACGGAC CTCATCCGGC AGGTAACGTG 660  
 GCGGTGCTGA TCAATCATAC GAAGCCAATC AATCGGGGCG AAACGGGTG GACGCTCAAG 720  
 GCTACCGACC TGATCGTGAT CGGACGTTTC CTGCTTACGG GCAAAGCGGA TTTTACCAGA 780  
 ATGATTGCCA TGACCGGCTC AGACGCTGCA GCTCACGGAT ACGTCCGTAT TATGCCGGGT 840  
 TGCAATGTCT TTGCTTCCTT CCGCGGCCGA CTGACAATA AGGAATCTCA CGAGCGTGTG 900  
 ATCGATGGCA ATGTGCTGAC CGGTAAAGAG CTCTGCGAGA AGGAGCCTTT CCGTGCAGCC 960  
 CGGTGTGACC AGATACGGT GATCCCCGAA GCGGACGATG TGGACGAAT CTTCGGGTGG 1020  
 GCTGCACCCC GTCTCGATCA GTACAGCATG AGCAGAGCTT ATTTCTCTTG GTTGCAAGGG 1080  
 AAAAACAAG ASTACGTACT CGATGCCCG ATCAAGGGTG GCGAACGTGC TATGATCATG 1140  
 AGCAAGAGT ATGACCGCGT TTCCCGATG GACATCTATC CGGAGTATTT GCTCAAGGCT 1200  
 ATTATAGCAT TCGACATCGA CAAGATGGAG GACTTAGGCA TATATGAAGT GGTCCGGAG 1260  
 GACTTTGCCA CTTGCGAATT TGTGGATACA TCCAAGATCG AGCTGCAGCG TATCGTTCGC 1320  
 GAGGGCTTGG ATATGCTCTA TAAGGAAATG AAT 1353

## (2) INFORMATION FOR SEQ ID NO:123

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 585 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...585

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123

5	ATGGATAAAG TGAGCTATGC TCTGGGATTG AGCATCGGTA ATAATITCAA GTCTTCGGGC	60
	ATCGACAGCG TCGTTATGGA TGATTTCATG CAAGGTCTGT CTGATGTACT GGAAGAAAAA	120
	CCCCCTCAGC TCTCGTATGA CGAGGCCAAG CGCGAAATAG AGGCGTATTT CATGGATTTG	180
	CAGCAGAAGG CTGTCAAACCT GAACAAAGAG GCCGGAGAAG AATTCTCTCA	240
	CACAAGGAAG GTGTGACGAC CTACCGAGC GGCCTGCAAT ACGAAGTCAT TAAGATGGGA	300
	GAGGGCCCCGA AACCCACCTT TCCGGACACG GTAACCTGTC ATTATCACGG TACGCTCATC	360
10	AACGGTATCG TTTTCGATAG CTCTATGGAC AGGGGAGAAC GGGCCAGTTT CCTCTAAGA	420
	GGAGTTATAG CCGGCTGGAC GAGATTCTT CAATTAATGC CTGTAGGATC CAAGTGGAAG	480
	GTAACATATC CAGCGCATCT GCGTATGGA GATCGTGTG CCGGCGAACA TATCAAACCG	540
	GGTAGTACGC TCATTTTAT AATCGAATTA TTGAGTATCA ACAA	585

15

(2) INFORMATION FOR SEQ ID NO:124

(1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 819 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

20

25

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

30

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

35

(A) NAME/KEY: misc feature  
(B) LOCATION 1...819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124

40	ATGAAAAAAG CATTACTTAT TGGTCTGCT CTITTGGGAG CAGTCAGTTT TGCAAGTGCT	60
	CAGTCTTTGA GCACAATCAA AGTACAGAAC AATTCAGTAC AGCAACCTCG TGAGGAAGCC	120
	ACTATTACAGG TTTGTGGAGA ATTGGCAGAG CAAGTTGACT GCATTGGGAC AGGTAATTCT	180
	GCAATCATAG CCGCTGCAGC GAAATTTGAA AGCGATGATC TCGAAGCTA TGTTGGCTGG	240
	GAGATCATGA GTGTTGATT CTTCCTGGA TATAAGCGT GCAAGTACAC ATCTGCAGTC	300
	TGGGCTGATG ATATGACCAT TTTGGGCCAA TCAGAAAGATA GTGATCCCGA AATGCAGACT	360
45	ATCAACAATC TTGCTCTCAA GACTAGTGTC AAGATTGAAG CCGGCAAGAA TTACATAGTT	420
	GGTATATTG CTAATACCGC AGGTGGACAT CCTATCGGAT GTGATCAGGG CCCTGCCGTT	480
	GATCGTTATG GAGATTGGT TTCTATATCA GAAGATGGTG GTGCTACTTT CCCTCCGTTT	540
	GAATCTCTTC ATCAAGCAGT TCCTACCTTA AATTACAACA TCTATGTCGT TGTTCAATTG	600
	AAGAAGGGTG AAGGTGTGTA GGCTGTTCTT ACCAACGACA AGGCTAATGC TTATGTTTCA	660
50	AATGGCGTTA TCTATGTAGC CGGAGCTAAT GGTGTCAGG TATCTCTGTT CGACATGAAC	720
	GGTAAGGTTG TTTATACCGG CATTAGCGAA ACGATTGCAG CTCTCTAGAA GGGCATGTAT	780
	ATCCTCCGTG TAGGTGCTAA GAGCATCAAG CTGGCTATC	819

55

(2) INFORMATION FOR SEQ ID NO:125

(1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1662 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

60

65

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

70

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

75

(A) NAME/KEY: misc feature  
(B) LOCATION 1...1662

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## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:125

	ATGCCAAGAA	TTATGAAATT	AAAAATTGCA	CTCAGACTGC	TGCTGGCGAC	TTTTGCCATA	60
	GTTTTATTTA	GCCCTCTGGC	CAAGGCCAG	ATGGATATTG	GTGGAGACGA	TGTATTGATC	120
5	GAGACGATGT	CCACCTTATC	AGGATATTCA	GAGGATTTTT	ATTACAAGAT	GGCTGTGGCA	180
	GACAATGGAT	GGATCTATGT	GATGTTGGAT	TTCTCTCGTA	TTTTTTTGA	TGATGTCAGG	240
	CTGTATCGTT	CCAAAGACGG	TGGTGCTACT	TACCAAAAGT	TAGGGTCTTT	GGGGTCTTTG	300
	GTGCCTTATG	ACTTCGATGT	CTCGCAATTGC	GATTTTATTG	TACGGGAAA	GGATGAAGAT	360
	GATATCAATG	TTTGACAGT	CATGACAGCA	TTCCAATATG	TAGGTGGTAC	TATTGGCAAT	420
10	GGCGTTTTGC	TGATGCATCG	CCATGATGCA	GATATCAATA	ATACAGAGTG	TGTGTACAAG	480
	AAGGATTTCC	CTAATAATAG	ACTGATGGGT	GTAGCCATCG	CCTCCAATA	CGGTGCGCCC	540
	TCTCCTTAGG	GTTTGGGGGG	CGATCCTTTT	GCTCTCGCTG	TCCCGTTAG	TGGCTCGGGA	600
	AGCGATCACA	GCTTCTTGGG	CTATATTTTT	TCGTTAGATG	GTGGAGTACA	CTTTCAGCAA	660
	AAGCGTATTT	ACACAAGACC	CCAAAAACGT	ACTATCAATA	GAGTAGACCT	TTCATTAGGC	720
15	AGTACATCTC	CTTCTCTTGG	ATTTAATACT	TGGCCACTAA	TGGGAGTCGT	ATTGSAATG	780
	AATAAGAACCT	TTGATGGCTT	CGACATTGGT	TTCAATTCCA	ACTTTGTGGA	CTATGATCCC	840
	CGCTATGGAG	GGTCTGAACC	GATAATAATA	GAAGAAGACT	GTGGATGGAC	TGATTTTAAT	900
	CCTTTGGGAG	CACATAAGTAT	AGAGATCCAA	ATGATGTGGG	ATGACAAATC	GGATAATACC	960
	GTGGGTGGAG	AACGCTCCCA	TAACCTCCTG	ATCACTTACC	CGGGCCATTA	CGTATATCCG	1020
20	AAGCAATCTT	TCAATTATTC	TCCCGGACAT	ACACCGACAA	AGAAGATCT	GGTCTTTAAA	1080
	CACCTGTATG	GATTTCCGGC	TITGGCATA	GATAAGGAAG	CGCATCGTTA	TCTGACTACT	1140
	TTTCAAGATC	ACAATCTAAT	GAGATACAGA	TGGATCAAA	ACGATGACAT	TAACCTTTTT	1200
	TATGGTTGGA	GTTGGCCATA	TGTATATGCA	AAAGAAGCTA	AAGATAAAAA	GAGGCGCCGT	1260
	CCGCAAGTAG	CACCTCAATCC	TACCAATGGA	AAGGCTTGT	GGGTATGGCA	TACTCGCAAG	1320
25	AGCCCATATG	ATGAAACCAA	ACCACATCCT	ACTCCTGTAA	TTATTAACA	TTTCTATGG	1380
	TCCGATACGG	AGTGGGTACA	TGCTCTGGAC	GTGGGGGACG	TATTGCAGAA	GGAGGGTAGC	1440
	ATGAAGCTCT	ACCCCAATCC	TGCCAAGAA	TATGTTCTGA	TCAACCTACC	CAAAGAAGGG	1500
	GGGCACGAGG	CAGTCGTATA	CGACATGCAG	GGCCGAATCG	TGGAGAAAGT	TTCAATTTCA	1560
30	GGGAAAGAT	ATAAGCTGAA	TGTGCAGTAT	CTGTCCAAAG	GTACGTACAT	GCTGAAAGTT	1620
	GTAGCGGATA	CGGAGTATTT	CGTGGAAAAA	ATCATTGTAG	AG		1662

## (2) INFORMATION FOR SEQ ID NO:126

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1650 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1650

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:126

55	ATGAAATTAA	AAATTGCACT	CAGACTGCTG	CTGGCGACTT	TTGCCATAGT	TTTATTTAGC	60
	CCTCTGGCCA	AGGCCAGAT	GGATATTGGT	GGAGACGATG	TATTGATCGA	GACGATGTCC	120
	ACCCTATCAG	GATATTCAGA	GGATTTTTAT	TACAAGATGG	CTGTGGCAGA	CAATGGATGG	180
	ATCTATGTGA	TGTTGGATTT	CTCTCGTATT	TATTTTGATG	ATGTCAGGCT	GTATCGTTCC	240
60	AAAGACGGTG	GTGCTACTTA	CCAAAAGTTA	GGTCTTTTGG	GSTCTTTGGT	GCCTTATGAC	300
	TTGATGTCT	CGCATTTGCCA	TTTTATTGTA	ACGGGAAAGG	ATGAAGATGA	TATCAATGTT	360
	TGGACAGTCA	TGACAGCATT	CGAATATGTA	GGTGGTACTA	TGGCAATGG	CGTTTTGCTG	420
	ATGCATCGCC	ATGATGCAGA	TATCAATAAT	ACAGAGTGTG	TGTACAAGAA	GGATTTCCCT	480
	AATAATAGAC	TGATGGGTGT	AGCCATCGCC	TCCAACCTACC	GTGGCCCTC	TCCTTACGGT	540
65	TTGGGGGGCG	ATCCTTTTGC	TCTCGCTGTG	GCCGTTAGTG	GCTCCGGAAG	CGATCACAGC	600
	TTCTTGGACT	ATATTTTTTC	GTTAGATGGT	GGAGTACACT	TTGAGCAAAA	GCGTATTTAC	660
	ACNAGACCC	AAAACTGAC	TATCAATAGA	GTAGACCTTT	CATTAGGCAG	TACATCTCCT	720
	TCTCTTGGAT	TTTAACTTTC	GCCACTAATG	GGAGTCGTAT	TCGAATGAA	TAGAACCTT	780
	GATGGCTTCG	ACATTGGTTT	CATTTCCAAC	TTTGTGGACT	ATGATCCCCG	CTATGCGTGG	840
70	TCTGAACCGA	TAATAATAGA	AGAAGACTGT	GGATGGACTG	ATTTTAATCC	TTTGGGAGCA	900
	CTAAGTATAG	AGATCCAAAT	GATGTTGGAT	GACAATTCGG	ATATACCGT	GGGTGGAGAA	960
	CGCTCCCAT	ACTTCCTGAT	CACCTACCCG	GGCCATTACG	TATATCCGAA	GCAATCTTTC	1020
	AATTATTCTC	CCGGACATAC	ACCGACAAGG	AAAGATCTGG	TCTTTAACA	CTGTATAGGT	1080
	ATTCCGGCTT	TGGCATACGA	TAAGGAAGGC	GATCGTTATC	TGACTACTTT	TCAGATCAC	1140
75	AATCTAATGA	GATACAGATG	GATCAATAC	GATGACATTA	ACTCTTTTAA	TGTTTGGACT	1200

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5 TGGCCATATG TATATGCAAA AGAAGCTAAA GATAAAAAAG GGGCGCGTCC GCAAGTAGCA 1260  
 CTCATCTCTA CCAATGGAAA GGCTTGTTGG GTATGGCATA CTCGCAAGAG CCCATATGAT 1320  
 GAAACCAAAAC CACATCCTAC TCCTGTAATT ATTAACACAT TCCTATGGTC CGATACGGAG 1380  
 TGGGTACATG CTCTGGACGT GGGGGACGTA TTGCAGAAGG AGGGTAGCAT GAAGCTCTAC 1440  
 10 CCCAATCCTG CCAAGAATA TGTTCGTATC AACCTACCCA AAGAAGGGGG GCACGAGGCA 1500  
 GTCGTATACG ACATGCAGGG CCGAATCGTG GAGVVAAGTTT CATTTTCAGG GAAAGAAATAT 1560  
 AAGCTGAATG TGCAATATCT GTCCAAAGGT ACGTACATGC TGAAGITGT AGCGGATACG 1620  
 GAGTATTTGG TGGAAAAAT CATTGTAGAG 1650

10

## (2) INFORMATION FOR SEQ ID NO:127

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1170 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 20 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 25 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 30 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...1170  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127

35 ATGAAACGAT TACTCCCTT TCTCCTTTA GCAGGACTCG TAGCGTAGG AAACGTGTCT 60  
 GCTCAGTCAC CCCGAATCCC TCAAGTGGAT GTACACACTC GCATCGCAAG AAATGCCCGT 120  
 TATCGACTGG ACAAGATCAG TGTCCCGGAT TCTCGTCAGA TATTGATTA CTTCTATAAA 180  
 GAAGAAACGA TACCCACTAA AATACAAACG ACCACAGGAG GTGCAATTAC AAGCATCGAT 240  
 TCGCTTTTCT ATGAAGACGA CAGGTGGTGT CAGGTGCGCT ATTTTGACAA TAACCTTGAA 300  
 40 TTAACAACAG CGGAGAAGTA TGTATACGAC GGTCTTAAGC TGGTCCTTCG AGAAATTCGC 360  
 AAGTCGCCGA CAGACGAAAC GCCAATAAAG AAAGTTAGCT ATCACTATCT CTGTGGCAGC 420  
 GATATGCCCT TTGAGATTAC GACAGAGATG AGCGATGGCT ATTTTGAAAG CCATACGCTT 480  
 AACTATCTGA ATGGAAGAT TGCCCGAATA GATATCATGA CTCACAGAA CCCATCGGCC 540  
 GAATTGATCG AAACGGGTAG AATGGTATAT GAGTTTGATG CCATAATGA TGCTGTACTG 600  
 45 CTTCGTGACA GTGATTTTCT TCCTCTTCAA AACAAGTGGG TAGAAATGTT TACTCACCGT 660  
 TATACATACG ACAATAAGCA TAATTGTATT CGTTGGGAAC AAGACGAATT CGGCACCCTC 720  
 ACCCTTGCCA ACAACTTCGA ATACGACACC ACTATCCCTC TGTCGTCTGT ATTGTTCCCC 780  
 ACGCATGAGG AGTTCTTCCG TCCTCTTCTT CCCAATTTTA TGAAGCATAT GCGTACGAAG 840  
 50 CAAACGTATT TCAATAACTC CGCAGAAGGC TTGTCAGAGG TATGCGATTA CAACTACTTC 900  
 TATACCGATA TGCAGGGTAA TGCACTGACC GATGTTGCCG TGAACGAATC GATCAAGATT 960  
 TATCCTCGTC CTGCCACGGA TTTCTGCGT ATAGAAGGTT CGCAACTGCT TCGCCTTTCC 1020  
 CTATTCGACA TGAACGGGAA GCTCATCAGA GCTACCGAAT TGACAGGCGA TTTGGCCATT 1080  
 ATCGGAGTTG CATCTCTTCC GAGAGGCAC TACATCGCAG AAATAACTGC TGCAACAGC 1140  
 55 AAAACCATAC GTGCAAAAGT ATCGCTCAGA 1170

55

## (2) INFORMATION FOR SEQ ID NO:128

- 60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1233 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 65 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 70 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 75 (A) NAME/KEY: misc\_feature

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(B) LOCATION 1...1233

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:128

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5  ATGAGACAGC ATTATCTCT ATTCTCTTT ATCTTGTTT TGCTTCTTC CTTCCTTAT    60
   GTCGGTTGCA GAACAGTCCG ACAAACACCT AAGCAGTCGG AACGGTACGT CGTAGTCCTG    120
   TCTTTGGACG GCTTCCGACC GGAATATACC GATCGGGCAC GTACACCGGC GTTGGATCGG    180
   ATGGCACAGG AGGGATTGAG CGGGTCGCTC CAACCATGCT TCCCCTCGCT TACATTTCCTC    240
   AATCATTACA GCATGGCTAC GGGGCTTTAC CCCGATCATC ACGGTATCGT AGCCAATGAG    300
10  TTGTGGGATT CGCTACTGGG CATCTTTCGT ATATCCGACC GAAAGCCGT GGAGACCCOC    360
   GGATTTTGGG GGGGCGAGCC GGTTTGGAAT ACGGCCGCAC GCCAAGGCAT CCGTACCGGT    420
   GTCTACTTTT GGGTAGGATC CGAAACGGCT GTGAACGGAA ATCGGCCGTG GCGGTGGAAA    480
   AAATTCTCCT CCACCGTTCC GTTTCGTGAC CGTGCCGACT CGGTATCGC GTGGCTCGGA    540
   CTGCCCGAAA AGGAGCGACC GCGCTTGCTC ATGTGGTACA TCGAGGAGCC GGATATGATC    600
15  GGACACAGCC AAACGCCCGA AAGCCCGCTG ACACTGGCAA TGGTAGAGCG GTTGGACAGT    660
   GTGGTCGGCT ATTTCCGCAA GCGGTTGGAC TCTCTGCCA TAGCCGCACA GACCGACTTC    720
   ATCATAGTAT CCGATCACGG TATGGCCACG TACGAAATG AGAAATGTGT CAACTGTGCG    780
   CATTATCTGC CTGCGGACAG TTCTCTCTAC ATGGCCACCG GGGCCTTCAC CCACTTGTAC    840
   CCGAAGCCCT CCTATACCGA GCGAGCCTAT GAGATCCTGC GGGCCATTC ACATATATCG    900
20  GTTTACCGCA AGGGGGAGGT GCCCAAGCGT TTGCGCTGTG GCACCAATCC TCGTTTGGGC    960
   GAACTGGTCC TGATTCCGGA CATAGGCTCC ACCGCTCTTT TCGCAATAAA TGAAGACGTT    1020
   CGTCCGGGAG CGGCACATGG CTATGACAA CAAACACCGG AAATGCCGGC TTTACTCCGG    1080
   GCTGTCCGAC CCGATTTCGG TCCGGGCAGT AGGGTGGAAA ACCTGCCGAA TATCACCATC    1140
   TATCCGCTCA TATGCAGGCT GTTGGGTATA GAGCCTGCAC CCAACGATGC GGACGAAACG    1200
25  TTGCTGAACG GCCTGATCCG AGACAAACGA CCA                                     1233

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(2) INFORMATION FOR SEQ ID NO:129

```

30  (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 738 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: double
     (D) TOPOLOGY: circular

35  (ii) MOLECULE TYPE: DNA (genomic)

     (iii) HYPOTHETICAL: NO

40  (iv) ANTI-SENSE: NO

     (vi) ORIGINAL SOURCE:
     (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

45  (ix) FEATURE:
     (A) NAME/KEY: misc feature
     (B) LOCATION: 1...738

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(x1) SEQUENCE DESCRIPTION: SEQ ID NO:129

```

50  ATGAAAGTAG GTTGTTCAT CCCCTGTTAT GTCAATGCAG TGTATCCGGA AGTGGGTATC    60
   GCCACGTACA AACTGCTGAA GAGTTTGGAC ATAGATGTG ACTACCGAT GGATCAGACA    120
   TGTTCGGGCC AGCCTATGGC CAATGCCGGA TTGCAACAGA AAGCTCAAAA GCTGGCTTTG    180
   CGATTCAAGS AGCTGTTCSA GTCCATATGAT GTAGTCGTAG GGCATCCGGC CAGTTGCGTT    240
55  GCTTTCGTGA AAGAAACTA TGATCATATC CTCAGACCGA CAGGACATGT CTGCAAGTCS    300
   GCAGCCAAGG TTCGGGATAT ATGCGAGTTC TTGCAAGATG ACCTGAAGAT CACCAGCCTC    360
   CCCTCCCGAT TCGCCCATAA GGTGAGCCTG CACAACAGTT GCCAGGTTGT GCGCGAAGTC    420
   CATCTGTCCA CCCCAAGTGA AGTGCAACGA CCGTACCACA ACAAGGTGCG CCGGCTATTG    480
   GAGATGGTGC AGGGCATAGA GGTATTCGAG CCGAAGCGAA TAGACGAATG CTGCGGTTTC    540
60  GCGGATATGT ACTCGGTGGA GGAGCCGGAG GTATCCACCT GTATCGGCA TGACAAGGTG    600
   CTGGATCACA TATCCACAGG TGCGGAGTAC ATCAGAGGCG CGGACAGCTC GTCCCTCATG    660
   CATATGCAGG GAGTGATAGA CAGAGAGAAA TTGCCGATCA AGACAATTCA TGCAAGTAGAA    720
   ATTTTAGCAG CAAACTTA                                     738

```

(2) INFORMATION FOR SEQ ID NO:130

```

70  (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 738 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: double
     (D) TOPOLOGY: circular

     (ii) MOLECULE TYPE: DNA (genomic)

75

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(111) HYPOTHETICAL: NO

(1v) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
10 (B) LOCATION 1...738

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:130

15	ATGGATATTG TAAGTATGGC CGATAAAGCT CTTGTAGTGG AGATGAGAGA TGTGACGCTC	60
	TGTCAGGAGG AAAACGTCAT TTTTCAAAAT TTGAATCTGA CCCTTTCCGC CGGAGACTTC	120
	GTCTATCTGA TAGGCTCAGT GGGATCGGGG AAGAGCACTT TGCTGAAGGC TTTGTATGCT	180
	GAGGTGCCTA TCTCTGCCGG TTATGCCCGC GTGATAGATT ATGATCTGGC AAAGTTGAAA	240
	CGGAAGCAGT TGCCCTATCT GCGCAGGAAT TTGGGCATTG TGTTCAGGA TTTCCAGTTG	300
20	CTGAACGGAC GTACTGTTGC GGAGAATTG GATTTCGTTT TGGGAGCTAC GGACTGAAA	360
	AACCGAGCG ATCGCGAGCA GCGTATCGAG GAGGTTTGA CCCGTGTGGG AATGTCTCGG	420
	AAGGCTTATA AGAGACCGCA CGAAGTGTCC GGAGGGGAGC AACCAACGTGT GGGTATAGCC	480
	ACAGCTTTGC TGGCGAAGCC TCGTGTGATC CTGGCCGACG AACCCACAGG CAACCTCGAT	540
	TCCGTGACCG GATTGCAGAT CGCTTCTCTG CTCTACGAAA TCAGTAAGCA GGGCACTGCA	600
25	GTACTTATGA GCACGCACAA CAGCAGCCTG CTGTCCGATC TGCCGGCAGG GACATTGGCC	660
	GTTCGTAAGA ATGGCGATGC CTCCTCTTTG GTCGAGCTGA GTGCAGATGC TGTTCACAGA	720
	AAAAATACGG AATAGAT	738

(2) INFORMATION FOR SEQ ID NO:131

(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 723 base pairs  
(B) TYPE: nucleic acid  
35 (C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(1v) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
45 (B) LOCATION 1...723

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:131

50	ATGGCCGATA AAGCTCTTGT AGTGGAGATG AGAGATGTGA CGCTCTGTCA GGAGGAAAAC	60
	GTCAATTTTC AAAATTGAA TCTGACCCCT TCCGCCGAG ACCTCGTCTA TCTGATAGGC	120
55	TCAGTGGGAT CGGGGAAGAG CACTTTGCTG AAGGCTTTGT ATGCTGAGGT GCGTATCTCT	180
	GCCGTTATG CCCGCGTGAT AGATTATGAT CTGGCAAAGT TGAAACGGAA GCAGTTGCCC	240
	TATCTGCCGA GGAATTTGGG CATTTGTGTT CAGGATTTC AGTTGCTGAA CGGACGTACT	300
	GTTCGCCGAGA ATTTGSAATT CGTTTTCGGA GCTACGGACT GGAAGAACCG AGCCGATCGC	360
	GAGCAGCGTA TCGAGGAGGT TTTGACCCGT GTGGGAATGT CTCGGAAGGC TTATAAGAGA	420
60	CCGCACGAAC TGTCCGGAGG GGAGCAACAA CGTGTGGGTA TAGCCAGAGT TTTGCTGGCG	480
	AAGCCTGCGT TGATCCTGGC CGACGAACCC ACAGGCAACC TCGATTCCGT GACCGGATTG	540
	CAGATCGCTT CTCTGCTCTA CGAAATCAGT AAGCAGGGCA CTGCAGTACT TATGAGCAGG	600
	CACAACAGCA GCCTGCTGTC GCATCTGCCG GCACGGACAT TGGCCGTTCC TAAGAAATGGC	660
65	GATGCCCTCT CTTTGGTCTG GCTGAGTGCA GATGCTGTTT CAAGAAAAAA TACGGAATA	720
	GAT	723

(2) INFORMATION FOR SEQ ID NO:132

(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 696 base pairs  
70 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

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- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...696
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132
- |    |  |     |
|----|--|-----|
| 15 | ATGAGAGATG TGACGCTCTG TCAGGAGGAA AACGTCATT TTCAAAATTT GAATCTGACC   | 60  |
|    | CTTTCCGCCG GAGACTTCGT CTATCTGATA GGCTCAGTGG GATCGGGGAA GAGCACTTTG  | 120 |
|    | CTGAAGGGCTT TGTATGCTGA GGTGCCTATC TCTGCCGGTT ATGCCCGCGT GATAGATTAT | 180 |
|    | GATCTGGCAA AGTTGAAACG GAAGCAGTTG CCTATCTGC GCAGGAATTT GGGCATTGTG   | 240 |
|    | TTTCAGGATT TCCAGTTGCT GAACGGACGT ACTGTTGCCG AGAATTGGGA TTTCGTTTGT  | 300 |
| 20 | CGAGCTACGG ACTGGAAAAA CCGAGCCGAT CGCGAGCAGC GTATCGAGGA GGTTTTGACC  | 360 |
|    | CGTGTGGGAA TGTCTCGGAA GGCTTATAAG AGACCGCAGC AACTGTCCGG AGGGGAGCAA  | 420 |
|    | CAACGTGTGG GTATAGCCAG AGCTTTGCTG GCGAAGCCTG CGTTGATCCT GCCCGACGAA  | 480 |
|    | CCACAGGCA ACCTCGATTG GGTGACCGGA TTSCAGATCG CTCTCTGCT CTACGAAATC    | 540 |
|    | AGTAAGCAGG GCACTGCGT ACTTATGAGC ACGCACAACA GCAGCCTGCT GTCGCATCTG   | 600 |
| 25 | CCGGCACGGA CATGGCCGT TCGTAAGAAT GGCGATGCCT CCTTTTGT CGAGCTGAGT     | 660 |
|    | GCAGATGCTG TTTCAGAAA AAATACGGAA ATAGAT                             | 696 |
- (2) INFORMATION FOR SEQ ID NO:133
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 657 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...657
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133
- |    |   |     |
|----|---|-----|
| 55 | ATGATTGAAA TCAGCAACCT CACCAAGGTT TTCAGAACAG AAGAAATAGA GACGGTAGCC | 60  |
|    | CTCGATGGCG TATCGCTCAA AGTGGACAAA GGCGAATTTA TCGCCATAAT GGGGCTTGG  | 120 |
|    | GGATGCGGTA AGTCCACTCT GCTCAATATC CTCGGCCTTC TCGACAATCC CACTTCCGGT | 180 |
|    | ATCTACAAGC TCGATGGGGC AGAAGTGGGC AACCTCCGGG AAAAAGACAG GACTGCCGTC | 240 |
|    | CGTAAGGGCA ATATCGGCTT CGTATTCCAG AGCTTCAACC TCATCGAAGA GATGACGGTA | 300 |
|    | AGCGAGAACG TGGAGTTGCC GCTCGTCTAT CTGGGTGTGA AGGCCTCCGA GCGGAAAGAG | 360 |
|    | CGAGTGGAGG AGGCACTGCG CAAGATGAGC ATCAGCCACC GGGCCGGCCA CTTCCTCAAT | 420 |
|    | CAGCTCTCG GAGGACAACA CGAGCGCGTG GCTATCGCCC GTGCCGTGGT GGCCAATCCG  | 480 |
| 60 | AAGCTCATCC TCGCCGATGA ACCCAGGGT AACCTCGACT CCAAAAACGG AGCCGATGTC  | 540 |
|    | ATGGAACTGC TCAGAGTCT CAATCGCGAA GGTGCAACCA TCGTCATGGT GAGCACTCC   | 600 |
|    | GAGCACGATG CACGTAGTGC CGGCCGATC ATCAATCTGT TCGACGGTAA GATTGCG     | 657 |
- (2) INFORMATION FOR SEQ ID NO:134
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1785 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO



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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

5 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1785

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134

ATGAAAGAAT TTTTCAAAAT GTTTTTCGCC TCGATCCTCG GGGTTATAAC GGCAGGAATC 60  
 ATCTTGTCT GTATCTTCT ATTTATCTTT TTCGGCATCG TAGCCGGTAT TGCTCCAAG 120  
 15 GCAACGGGAG GAACCATTC GAAGATCGAA GCAAACTCCA TCCTACATAT ANACAATTCT 180  
 TCTTTCCTG AGATCGTATC GGCCAATCCC TGGAGCATGC TCACAGGCAA AGACGAGTCC 240  
 GTATCGGTCT CACAGGCAGT CGAAGCCATC GGCCAACCCA AAAATAATCC CAACATAACC 300  
 GGTATCTTCC TCGATCTGGA CAACCTTTCC GTCCGTATGG CATCGGCAGA GGAATTGUGT 360  
 CGCCGCTTGC AGGATTTCAA CATGTCGGGC AAGTTCGTG TATCCTATGC CGACAGATAC 420  
 20 ACCUAAAAGG GTTACTACCT CTCAGTATT GCAGACAAAC TCTACCTCAA TCCGAAAGGA 480  
 ATGTTGGGCG TTATCGGGAT TGGACCCCAA ACAATGTTCT ACAAGATGC CCTCGACAAA 540  
 TTCGGCGTGA AGATGGAGAT CTTCAGGTA GGCACCTACA AGGCAGCCGT AGAGCCATTC 600  
 ATGCTCAACA GGATGAGCGA TGCCAATCGC GAACAAATCA CCACATACAT AAACGGGCTT 660  
 TGGGACAAGA TCACATCCGA TATTGCAGAG TCGCGCAAGA CGGCAATGGA TTCCGTGAAA 720  
 25 ATGTTTCCCG ACAAAAGGCGA AATGTTCCGT CTTCGCCAGA AAGCGGTGGA GATGAAGCTC 780  
 GTGGATGAGC TGGCTTACCG TACCGATGTG GAGAAAGAAC TCAAAAGAT GTCCCAACGC 840  
 GGAGAGAAAG ATGAACCTCG GTTCGTATCG CTTCCTCAGG TTCTGGCCAA TGGCCCGATG 900  
 AACAAACGA AAGGCAGTCG GATCGCCGTT CTCTTGCCTG AAGGTGAAT AACGGAAGAA 960  
 ATAATAAGA AGCCGTTCGA CACTGACGGT AGCTCCATCA CACRAGACT CGCCAAAGAA 1020  
 30 ATCAAGGCAG CAGCCGATGA CGATGATATC AAAGCCGTAG TACTTCGTGT CAATTCCTCG 1080  
 GGAGGTAGTG CTTTCACTTC CGAACAGATA TGGAAAGCAGG TAGCCGATCT CAAAGGCCAAA 1140  
 AAGCTATTCG TGGTCTCCAT GGGCGACGTA GCAGCCTCGG GCGGATACTA CATAGCCTGC 1200  
 GCAGCCAAAC GTATCGTGGC AGAGCATACG ACTCTGACCG GCTCCATCGG CATATTCCGGC 1260  
 ATGTTCCCGA ACTCGCGGGG CGTAGCCAAG AAGATAGGAG TGAATATGGA CGTCGTACAG 1320  
 35 ACATCCAAGT ATGCAGACTT GGGCAACACC TTCGCTCCGA TGACGGTCCA AGATCGTGCC 1380  
 CTATCCAAC GCTACATAGA GCAGGGCTAC GACCTCTTCC TCACTCGCGT ATCGGAAGGC 1440  
 CGCAACCGCA CCAAGGCACA GATCGACAGC ATCGCTCAAG GCCGTGTATG GCTCGGCGAG 1500  
 AAAGCTCTTG CACTCGGTTT GGTGGATGAG CTTGGAGGTT TGGACACAGC TATCAAAACGG 1560  
 GCCCGAAGC TGGCTCAGCT CGGTGGCAAC TACAGCATAG AGTATGGCAA GACCAAGCGC 1620  
 40 AACTTCTTCG AAGAGTTGCT CTCCTCATCA GCAGCGGATA TGAAGTCTGC CATCTGAGT 1680  
 ACCATTCTCT CCGATCCGGA AATAGAAGTT CTGCGCGAAC TCCGTCCAT GCCGCCCGT 1740  
 CCTTCGGGCA TACAGGCAGG TCTCCCCTAT TACTTCATGC CGTAC 1785

45 (2) INFORMATION FOR SEQ ID NO:135

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1767 base pairs

(B) TYPE: nucleic acid

50

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

55

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

60 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1767

65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135

ATGTTTTTCG CCTCGATCCT CGGGGTTATA ACGGCAGGAA TCATCTTGTT CTGTATCTTT 60  
 CTAATTTATCT TTTTCGGCAT CGTAGCCGGT ATTGCCCTCCA AGGCAACGGG AGGAACCAAT 120  
 70 CCGAAGATCG AAGCAAATC CATCCTACAT ATATACAAAT CTCTTTCCC TGAGATCGTA 180  
 TCGGCCAATC CTTGGAGCAT GCTCACAGGC AAAGACGACT CCGTATCGCT CTCACAGGCA 240  
 GTCCGAAGCCA TCGGCCAAGC CAAAAATAAT CCAACATRA CCGGTATCTT CCTCGATCTG 300  
 GACAACTTTT CGTCCGGTAT GGCATCGGCA GAGGAATTGC GTCGCGCGTT GCAGGATTTT 360  
 AAGATGTCGG GCAAGTTTGT CGTATCTAT GCCGACAGAT ACACCCRAAA GGGTTACTAC 420  
 75 CTCTCCAGTA TTGCAGACAA ACTTACCTC AATCCGAAG GAATGTTGGG GCTTATCGG 480

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ATTGCGACCC AACAATGTT CTACAAAGAT GCCCTCGACA AATTCGGCGT GAAGATGGAG 540
ATCTTCAAGG TAGGCACCTA CAAGSCAGCC GTAGAGCCAT TCATGCTCAA CAGGATGAGC 600
GATGCCAATC GCSAACAAAT CACCACATAC ATAAACGGGC TTTGGGACAA GATCAGATCC 660
GATATTGCAG AGTCGGCGCA GACGGCAATG GATTCCGTGA AAATGTTTGC CGACAAAGGC 720
5 GAAATGTTGC GTCTTGCCGA GAAAGCGGTG GAGATGAAGC TCGTGGATGA GCTGGCTTAC 780
CGTACCGATG TGGAGAAAGA ACTCAAAAAG ATGTCCCAAC GCGGAGAGAA AGATGAACCT 840
CGGTTCTGAT CGCTTTCTCA GGTTCCTGCC AATGGCCCGA TGAACAAAAC GAAAGGCGAT 900
CGGATCGCGG TTCTCTTTGC CGAAGGTGAA ATAACGGAAG AAATAATAAA GAAGCCGTTT 960
GACACTGACG GTAGTCCCAT CACACAAGAA CTGCGCAAAG AAATCAAGGC AGCAGCCGAT 1020
10 CACTATGATA TCRAAGCCGT AGTACTTCGT GTCAATTCTC CGGGAGGTAG TGCTTTCAT 1080
TCCGAACAGA TATGGAAGCA GGTAGCCGAT CTCAAGGCCA AAAAGCCCTAT CGTGGTCTCC 1140
ATGGGCGACG TAGCAGCCTC GGGCGGATAC TACATAGCCT GCGCAGCCAA CAGTATCGTG 1200
GCAGAGCATA CGACTCTGAC CGGCTCCATC GGCATATTCT GCATGTTCCG GAACTTCGCG 1260
GGCGTAGCCA AGAAGATAGG AGTGAATATG GACGTCTGAC AGACATCCAA GTATGCAGAC 1320
15 TTGGGCAACA CTTCTGCTCC GATGACGCTC GAAGATCGTG CCTCATCCA ACGCTACATA 1380
GAGCAGGGCT ACGACCTCTT CCTCACTCGC GTATCGGAAG GCCGCAACCG CACCAAGGCA 1440
CAGATCGACA GCATCGCTCA AGGCCGTGTA TGGCTCGGCG ACAAAGCTCT TGCATCTCGT 1500
TTGGTGGATG AGCTTGGAGG TTTGGACACA GCTATCAAAC GGGCCGCGAA GCTGGCTCAG 1560
CTCGGTGGCA ACTACAGCAT AGAGTATGCG AAGACCAAGC GCAACTTCTT CGAAGAGTTG 1620
20 CTCTCTCAT CAGCAGCGGA TATGAAGTCT GCCATCTCTA GTACCATCTT CTCCGATCCG 1680
GAATAGAAG TTCTGCGGGA ACTCGCTCC ATGCCGCCCG GTCTTCGGG CATACAGGCA 1740
CGTCTCCCTT ATTACTTCAT GCCGTAC 1767

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## 25 (2) INFORMATION FOR SEQ ID NO:136

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(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 939 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: double
  (D) TOPOLOGY: circular

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30

(ii) MOLECULE TYPE: DNA (genomic)

35

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

40

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

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  (A) NAME/KEY: misc feature
  (D) LOCATION 1...939

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45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136

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ATGAGAGCAA ACATTGGCA GATACTTCC GTTCGGTTC TCTTTTCTT CCGGACAGCG 60
ATCGGACAGG CTCAGAGTCG AAACCGTACA TAGGAGGCTT ATGTGAAACA GTACGCCGAC 120
50 GAAGCTATCC GACAGATGAG CCGCTACAAT ATACCGGCAA GCATCACCAT AGCAGAGGCT 180
TTGGTGGAGA CAGGAGCCGG AGCCAGTACA CTGGCCAGCG TACACAAACA TCACTTCGGG 240
ATCAAAATGCC ACAAATCGTG GACGGGCAAG CGCACCTATC GTACCGACGA TGGCCGGAAC 300
GAATGCTTCC GCAGCTATTC GGGCGCTCGC GAATCGTAGG AAGATCATTG CCGATTCTG 360
CTCCAACCCG GCTATCGTCC CTTGTTCAA CTGAGAGAG AAGACTATCG GGGCTGGGCT 420
55 ACGGGGTTGC AACGCTGTGG CTATGCCACC AATCGGGGCT ATGCCAATCT GCTGATCAAG 480
ATGGTGGAGC TGTATGAGT ATATGCTTTG GATCGGAGAG AGTACCCTC ATGGTTCCAG 540
AAGCTTTACC CCGGTCCAA CAAAAATCC CATCAACGA CCAAGCAGAA GCAGAGCGGA 600
CTCAAGCAGC AAGCTTACTT CAGCTACGGA CTGCTCTACA TCATAGCCAA GCAAGCGAT 660
ACCTTCGATT CTTTGGCCGA AGAGTTCGAC ATGAGAGCCT CCAAACTGGC CAAATACAC 720
60 GATGCTCCCG TGGATTCCC GATCGAAAAG GCGATGTGA TCTATCTGGA GAAAAGCAC 780
GCATGCTCCA TCTCAAACA CACACAGCAC GTAGTGCCTG TGGGCGATTC GATGCACAGT 840
ATCTCCCAAC GCTATGGCAT CCGGATGAAG AACCTCTACA AGCTCAACGA CAAGGATGGC 900
GAATATATAC CCCAAGAGGG CGATATACTG CGCTTGC3C 939

```

65

## (2) INFORMATION FOR SEQ ID NO:137

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(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 1569 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: double
  (D) TOPOLOGY: circular

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70

(ii) MOLECULE TYPE: DNA (genomic)

75

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
10 (A) NAME/KEY: misc feature  
(B) LOCATION 1...1569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137

15	ATGGACGGAC	GTGATATTC	GGATGGCCTC	CATCAGGCTA	TGGAAGCCAA	AGAGCATGTG	60
	AAAGTAGAGG	CTGCGACACA	GACATTTGCA	ACTATCACTT	TGCAGAACTA	TTTCCGCATG	120
	TATCATAAAC	TGGCAGGGAT	GACCGGTACT	GCTGAAACTG	AAGCGGGAGA	GCTTTGGGAC	180
	ATCTACAAAC	TGGACGTTGT	AGTTATTCGG	ACAAACAAGC	CTATCGCCCG	TAAGGATATG	240
	AATGATCGTA	TCTATAAGAC	GGCACGTGAA	AAATATGCAG	CAGTTATCGA	AGAGATTGTA	300
20	CGTCTTGTCG	AAGAGGGCAG	ACCTGTACTT	GTCCGTAATA	CTTCGGTGGG	AATATCCGAA	360
	TTGTTGAGCC	GTATGTTACG	CTGCGTGCCG	ATCCAAACACA	ATGTACTCAA	TGCCAAATTG	420
	CATCAGAAGG	AGGCCGAGAT	TGTAGCTCAG	GCCGGTCAGA	AAGGAACTGT	TACCATCGCA	480
	ACGAACATGG	CCGGTCGTGG	TACCGACATC	AAGCTCTCTG	CCGAGGTTAA	GAAAGCCGGG	540
	GGTTTGGGTA	TCATTGGTAC	GGAAAGGCAC	GAATCCAGAC	GAGTGGACAG	ACAGCTTCGT	600
	GGTCGTTCCG	GCCGTCAGGG	TGATCCCGGT	TCGTCCATAT	TCTATGTTTC	CCTTGAAGAT	660
25	CATCTGATGC	GCCTCTTTGC	CACAGAAAAG	ATTGCATCAT	TGATGGATCG	TTTAGGTTTC	720
	AAGGAAGGAG	AAGTGCTCGA	AAACAACATG	CTGAGTAAGT	CCGTGGAGCG	TGCTCAAAAG	780
	AAGGTGGAAG	AGAACAACCT	CGGTATCCGT	AAACATCTGC	TGAGTACGTA	TGATGTAATG	840
	AATTGCGAGC	GTGAAGTCAT	TTATACCCGT	CGCCGTCATG	CTTTGATGGG	AGAGCGTATC	900
	GGTATGGATG	TACTCAATAC	CATATACGAC	GTATGTAAGG	CTCTGATTGA	CAATTATGCA	960
30	GAAGCCCAATG	ATTTGSAAGG	CTTCAAGGAA	GATCTGATGC	GTGCATCTGC	GATAGAATCT	1020
	CCTATCACGC	AAGAAATATT	CAGAGGTAAG	AAAGCAGAAG	AGCTGACCGA	TATGCTTTTC	1080
	GATGAAGCTT	ACAAGTCTTT	CCAACGTAAG	ATGGATCTGA	TGCGAGAAGT	GGCCCAACCT	1140
	GTGGTTTCATC	AGGTATTGTA	GACCAAGGCC	GCCGTGTACG	AGCGCATTTCT	AATCCCCATT	1200
	ACGGATGGTA	AACGTGTCTA	TAACATAGGA	TGCAATTTCG	GTGAAGCGGA	TGAAACTCAA	1260
35	GGGAAAGCA	TCATCAAAGA	ATTGAGAAA	GCTATCGTAC	TGCATACAT	CGATGAGTCT	1320
	TGGAAGAAAC	ATCTGCGTGA	GATGGACGAG	CTTCGTAATT	CCGTTTCAGAA	TGCCAGCTAC	1380
	GAACCAAAAG	ATCCACTACT	TATCTATAAA	CTCGAATCTT	ACGAACTGTT	CCGCAAGATG	1440
	GTAGAAGCCA	TGAACGTA	GACCGTAGCG	ATCCTAATGC	GTGCTCGGAT	ACCGGTACCG	1500
40	GAGGCTCCTT	CCCAGAAGA	GCTGGAACAC	AGGCGGCAAA	TAGAAATCCG	ACATGCAACC	1560
	CAACAACGT						1569

(2) INFORMATION FOR SEQ ID NO:138

45 (1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1125 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

50 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

55 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

60 (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...1125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138

65	ATGAATTTCT	TAAAAAAGA	ACCGTTTAA	ATATTCTCTA	TGATTTATCT	GCTGTTAGAT	60
	ACAATAACAA	ACCGTGCCGG	TACAGAAGCC	GCCGTGATCA	ACTTGGCTAA	CAACCTGCAT	120
	GCCAAATGTC	ATCGCGTATC	ATTAGTCAGC	GTTTGTACAA	AAGAAGGAGA	GCCTTCCTTC	180
	CAAGTAGAAA	AAGGAATAGA	AGTACACCAT	CTCGGAATTA	GGCTTTATGG	CAATGCATTA	240
70	GCCCGCAAAA	CAGTATATTT	CAAGGCTTAT	CGAAGGATAA	AAGCCCTATA	CAAGAAGCGT	300
	GAACCGGTTT	TATTGATAGG	GACTAATATT	TTTATCAATA	CAATTTTGTC	TCAGATCAGT	360
	AACAGAGGCA	GAATATTTAC	GATCGGATGC	GAACATATCT	CTTATGATA	TGCCCGCCCT	420
	ATTACAAAAC	GCATAAGGGG	GTTTCTGTAT	TCAGGGCTTG	ATGCCGTTGT	AGCACTGACA	480
75	AAAAGAGATC	AGCAATCGTT	CGAGGCAATC	TTACGTGGAC	GCTCTAAAG	ATATGTCTAT	540
	CCCAATCAAG	TTCATTATAC	TACAGTCCAA	AGAGATGCTA	CTACTCACA	ACAAATGTTG	600

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5 GCGATTGGCA GGCTTACCTA CCAGAAGGGT TTTGAATTCA TGATAGAAGA TGCATCAGCA 660  
 GTGCTGCGAG AAAGGCCCTGA TTGGAAGCTT ATCATAGTCG GAGATGGCGA AAATGAATCG 720  
 ATGCTACGTA AAGAATATGC ATCTCGCAAT ATGGAGTCGC AATAGAAAT ACATCCATCT 780  
 ACACCGGAAA TTGCAATA CTACGAATCA TCTGCTATTT ATCTAATGAC GTCCCGTTTC 840  
 10 GAAGGACTAC CAATGGTACT TCTCGAAGCA GAAGCATATG CACTACCTAT AATCTCATAC 900  
 GATTGTCCGA CCGGCCCGAG GGAAGTATC GAAACGGTC GCAATGGTTT CCTTGTGCCA 960  
 ATGGAAGCAC ATGAAGACTT CGCGGATAAG TTACGCTTAT TGATGGATGA TGAAACTCTT 1020  
 CGTAAGAAAA TGGGACAAGA ATCAGAGTTG ATGGTCAAAT CCTACTCTCC GGCAAAATATC 1080  
 TATGAATGTT GGAAGAAACT ATTCGTGCAA ATCGGCTACA TGAAT 1125

(2) INFORMATION FOR SEQ ID NO:139

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1086 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

20 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

25 (iv) ANTI-SENSE: NO

(v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

30 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139

35 ATGATTATC TGCTGTAGA TACAATAACA AACCGTGCG GTACAGAAGC CGCGGTGATC 60  
 AACTTGGCTA ACAACCTGCA TGCCAATGGT CATCGCGTAT CATTAGTCAG CGTTTGTACA 120  
 AAAGAAGGAG AGCCTTCCTT CCAAGTAGAA AAAGGAATAG AAGTACACCA TCTCGGAATT 180  
 AGGCTTTATG GCAATGCATT AGCCCGCAAA ACAGTATATT TCAAGGCTTA TCGAAGGATA 240  
 AAAGCCCTAT ACAAGAAGCG TGAACCGGTT TTATTGATAG GGAATAATAT TTTTATCAAT 300  
 40 ACAATTTGT CTCAGATCAG TAACAGAGGC AGAATATTTA CGATCGGATG CGAACATATC 360  
 TCTTATGATA TTGCCCGCCC TATTACAAA CGCATAAGGG GGTTCGTGTA TTCAGGGCTT 420  
 GATGCCGTTG TAGCACTGAC AAAAGAGAGT CAGCAATCGT TCGAGGCAAT CTTACGTGGA 480  
 CGCTCTAAG CATATGTGAT ACCCAATCAA GTTTCATTTA CTACAGTCCA AAGAGATGCT 540  
 ACTACTCACA AACAAATGTT GGCGATTGGC AGGCTTACCT ACCAGAAGGG TTTTGAATTC 600  
 45 ATGATAGAAG ATGCATCACG AGTGCTGCGA GAAAGGCCTG ATTGGAAGCT TATCATAGTC 660  
 GGAGTGGCG AAAATGAATC GATGCTACGT AAAGAAATTG CATCTCGCAA TATGGAGTCG 720  
 CAAATAGAAA TACATCCATC TACACCGGAA ATTGCAAAAT ACTACGAATC ATCTGCTATT 780  
 TATCTAATGA CGTCCCGTTT CGAAGGACTA CCATTTGGTAC TTCTCSAAGC AGAAGCATAT 840  
 GCACTACCTA TAATCTCATA CGATTGTCCG ACCGGCCCGA GGGAACTGAT CGAAAACGGT 900  
 50 GCCAATGTTT TCCTTGTGCC AATGGAAGCA CATGAAGACT TCGCGGATAA GTTACGCTTA 960  
 TTGATGGATG ATGAAGTCT TCGTAAGAAA ATGGGACAAG AATCAGAGTT GATGGTCAAA 1020  
 TCCTACTCTC CGGCAAAATAT CTATGAATGT TGGAGAAAC TATTCGTGCA AATCGGCTAC 1080  
 ATGAAT 1086

55 (2) INFORMATION FOR SEQ ID NO:140

60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1920 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

65 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

70 (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1920

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## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:140

5	ATGGGAAAAA	TCATTGGAAT	TGACTTAGGC	ACAACGAACT	CTTGTGCTC	TGTATTGGAA	60
	GGTAACGAAC	CTATCGTTAT	TACAAACAGT	GAGGGCAAGC	GCACAAACGCC	CTCGGTAGTG	120
	GCTTTTGTGG	ATGGTGGCGA	GCCTAAGGTG	GGCGATCCGG	CCAAGCGTCA	GGCCATCAAC	180
	AATCOGACCA	AGACGATATA	CTCTATCAA	CGCTTCATGG	GGGAAACTTA	GSATCAGGTT	240
	TCCAGAGAAG	TGGAGAGAGT	GCCATTCAAG	GTAGTACGTG	GGGACAATAA	TACTCCGCGC	300
	GTAGATATAG	ACGGTCGTCT	CTATACGCCG	CAGGAAATTT	CGGCCATGAT	CCTTCAGAAG	360
10	ATGAAGAGA	CGGCCGAAGA	CTACCTCGGT	CAGGAAGTAA	CGGAGGCCGT	GATCACTGTG	420
	CCCGCATACT	TCAACGACGC	TCAACGTCAG	GCAACGAAAG	AAGCAGGAGA	GATCGCCGGC	480
	CTGAAAGTTC	GCCGTATTGT	GAACGAGCCT	ACGGCAGCTT	CTCTGGCCTA	CGGTCTGGAC	540
	AAGTCCAATA	AGGATATGAA	GATCGCTGTC	TTGACCTTGG	GTGGCGGTAC	CTTCGATATC	600
	TCTATCTTGG	AATTGGGCGA	CGGCGTTTTC	GAAGTGAAAT	CGACCAACGG	TGATACGGAC	660
15	CTCGAGGAG	ACGACTTCSA	CCACGTGATC	ATTGACTGSC	TGGCAGAAGA	GTTCAAGTCT	720
	CAGGAAGGTG	TGGATCTTCG	CCAGGATCCT	ATGGCTATGC	AGCGTCTGAA	AGAAGCTGCC	780
	GAAAAAGCCA	AGATAGAGCT	CTCCAGCACT	TCATCTACGG	AGATCAACCT	CCCTATATC	840
	ATCGCGGTGA	ACGGCATCCC	CAAGCACTTG	GTGATGACCC	TTACAGGGGC	TAAGTTCGAG	900
	CAGTTGGCCG	ATCGCTGTAT	TCAGGCATGT	GTGGCACCCT	GGGAAACGGC	CTTGAAGAT	960
20	GCCGGTATGT	CACGTGGCGA	TATCGATGAA	GTGATTCTCG	TAGGTGGTTC	CACACGTATT	1020
	CTTCTATTTC	AGGAGATTGT	GGAGAAGATC	TTGGTAAAGG	CTCCGTCCAA	GGGTGTGAAT	1080
	CCCGACGAAG	TGCTAGCTGT	GGGTGCCGCT	ATTCAGGCGG	GTGTTCTGAC	CGGTGAGGTA	1140
	AAGGATGTCT	TGCTGTTGGA	CGTTACCCCC	TTGTGGCTCG	GTATCGAGAC	TATGGGAGGC	1200
	GTGATGACTC	GCTTGATCGA	TGCCAATACC	ACTATCCCGA	CGAAGAAGAG	CGAAATCTTT	1260
25	ACCACACCGA	TGGACAATCA	ACCTTCGGTA	GAGATTCTAT	TACTTCAGGG	TGAGCGTTCT	1320
	TTGGCTAAGG	ACAATAAGAG	CATCGGCCGT	TTCATCTTGG	ACGGTATTCG	TCCGGCGCCC	1380
	CGTCAGACAC	CGCAGATCGA	AGTAACGTTT	GACATCGATG	CCAACGGTAT	CCTGAATGTA	1440
	ACGGCTCATG	ACAAAGCTAC	CGGCAGAAGG	CAGATATCC	GCATCGAAGC	CTCCAGCGGT	1500
	TTGTCCGATG	ATGAGATCAA	GCGCATGAAG	GAAGAGGCGC	AGGCCAATGC	CGAAGCAGAT	1560
30	AAGAAAGAGA	AAGAACGTAT	CGACAAGATC	AATCAGGCCG	ACAGCATGAT	CTTCCAGACG	1620
	GAAAGACAGT	TGAAGGAGTT	GGGAGACAAA	TTCCCGGCCG	ACAAGAAGGC	TCCGATCGAT	1680
	ACCGCTCTCG	ACAAACTGAA	AGAAGCACAC	AAAGCACAGG	ATGTAGCTCG	TATCGATACA	1740
	GCCATGGCCG	AACTGCAAAAC	CGCTCTTTCC	GCAGCGGGCG	AAGAGCTTTA	CAAGAATGCC	1800
	GGAGCAGCCC	AAGGTGGCGC	ACAACCCGGT	CCGGACTTCG	CGGCTGCTCA	AGGTCCCTCT	1860
35	GCCGGTGATC	AGCCCTCTCA	CGACAAGAAC	GTACAGACG	TAGACTTCGA	GGAGTGAAG	1920

## (2) INFORMATION FOR SEQ ID NO:141

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1347 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

45 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

50 (iv) ANTI-SENSE: NO

(v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

55 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1347

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:141

60	ATGCGCTACG	ACTTAGCTAT	CATCGGTGGA	GGGCGGGCGG	GTATACGGC	TGCCGAACGT	60
	GCTGCCAAAG	GTGGCCTGAA	AACCTCTCTA	ATTGAGAAGA	ATGCTCTCGG	TGGTGTATGC	120
	CTCAACGAAG	GATGTATACC	GACCAAGACG	CTACTCTACT	CGGCCAAAGT	GCTACATCAA	180
	ATTGCTACCG	CATCTAAATA	TGCAGTAAGT	GGAAACGGCG	ATGGACTTGA	CCTCGGCAAG	240
65	GTGATTGCCA	GAAAGGTAA	AATCATTCGC	AAGCTGACTG	CAGGCATCCG	TTCACGCGTG	300
	ACAGAGGCGG	GAGTAGAGAT	GGTGACGGCA	GAAGCTACCG	TAAACGGATG	CGATGCAGAC	360
	GSCATCATCG	GCATTACTGC	GGGCGAAGCA	CAGTACAAAG	CTGCCAACCT	GCTACTATGT	420
	ACCGGTTCCG	AGACGTTTAT	TCCACCCATC	CCCGAGTGGG	AGCAGACAGA	GTATTGGACA	480
	AACCGTGAAG	CTCTACAGAA	CAAAGAGATT	CCGACCTCTC	TCTTCATCAT	CGGTGGTGGG	540
70	GTGATCGGAA	TGGAGTTCCG	TTCTTTCTTC	AACGSTATCG	GTACGCAAGT	GCACGTGGTG	600
	GAGATGCTGC	CGGAAATACT	CAACGGTATC	GATCCCGAAC	ATGCAGCTAT	GCTACGCGCT	660
	CACATGAAAA	AAGAAGGAAT	CAATTTCTAC	CTCGGCGACA	AAGTAAACATC	GGTTCGCAAC	720
	GGAGCTGTTA	CGGTAGAATA	CGAAGGAGAA	AGCAAGAGAA	TGGAAGGAGA	ACGTATCCGT	780
	ATGAGTGTGG	GACGTGCGCC	CGTCTGCAA	GGATTGAGT	CGCTCGGATT	GGTGTCTGCC	840
75	GGCAAGGTTG	TAAAGACTAA	TGAGAGGATG	CAAACTTCCC	TGCCCAATGT	CTATGCTGCA	900

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	GGTGATATTA	CAGGCTTCTC	GCTTTTGGCA	CATACGGCTG	TACGGGAAGC	AGAGGTAGCA	960
	GTAGATCAGA	TTTTGGGCAA	AACAGACGAA	ACGATGAGCT	ACCGTGCCGT	ACCAGGTGTG	1020
	GTGTACACCA	ATCCCGAGGT	CGCCGGTGTG	GGAGAGACGG	AAGATCGCT	TCGCAAGCA	1080
	GGACGTGCT	ACACTGTTCG	TCGCTTCT	ATGGCTTCT	CCGGTCGATT	TGTAGCAGAA	1140
5	AACGAACAAG	GCAATGGAGA	GTGCAAACTA	CTACTTGATG	AAGAGAACC	CTTGATCGGA	1200
	GCACACCTCA	TTGGCAATCC	GGCCGGCGAA	CTCATCGTAA	CCGCTGCCAT	GGCCATCGAG	1260
	ACCGGCATGA	CGGATCGACA	AATCGAACGA	ATCATATTCC	CTCATCCGAC	TGTAGGCGAA	1320
	ATCCTAAVAG	AAACTCTCCG	CGGAGGT				1347
10	(2) INFORMATION FOR SEQ ID NO:142						
	(i) SEQUENCE CHARACTERISTICS:						
	(A) LENGTH: 2823 base pairs						
15	(B) TYPE: nucleic acid						
	(C) STRANDEDNESS: double						
	(D) TOPOLOGY: circular						
20	(iii) MOLECULE TYPE: DNA (genomic)						
	(iiii) HYPOTHETICAL: NO						
	(iv) ANTI-SENSE: NO						
25	(vi) ORIGINAL SOURCE:						
	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS						
	(ix) FEATURE:						
30	(A) NAME/KEY: misc_feature						
	(B) LOCATION 1...2823						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142						
35	ATGGAATTGA	AAAGATTTT	ATCACTGGT	CTTCTGCTG	TGGGATTCAT	TCCGATGAAG	60
	CTTCTGCCCC	AACAGGCTCA	GCCACTCCCT	ACAGATCCCG	CTGTTCCGTG	CGGTAAGTTG	120
	GACAACGGAT	TGACTTATTT	CATCCGTCAC	AACGAGAAC	CGAAAGATCG	TGCGGATTTT	180
	TTTATCCGAC	AAAGAGTAGG	TTCTATTCTT	GAAGAAGATA	GCCAGTCCGG	TTTGGCTCAC	240
	TTCTTGGAAC	ACATGGCTTT	CAACGGTACG	AAGAACTTCC	CCGGTAAGAA	CTTGATCAAC	300
	TATCTCGAAA	CGATCGGTGT	ACGTTTCCGT	CAGAACCTGA	ACGCTTCTAC	CGGATTCGAC	360
40	AAAGCGGAAT	ATACGATAAT	GGATGTGCGG	ACTACACGTC	AGGGAATCAT	CGACTCCTGC	420
	TTGCTTATCC	TGCATGATTG	GAGTAACAAT	ATTACCTCCG	ACGGGCATGA	GATCGACGAG	480
	GAGCGCGGTG	TGATCCAGGA	AGACTGGCGT	GCTCGTCGCG	ATGCCAACCT	TCGTATGTTT	540
	GAGGCTATAC	TTGCCAAGGC	TATGCCGGGT	AATAAATATG	CAGAACGCAT	GCCCATCCGT	600
	CTGATGGACG	TCGTGCTCAA	CTTCAAGCAT	GATGAGCTGC	GCAACTATTA	TAAGAAATGG	660
45	TATCGTCCCG	ACCTGCAAGG	TCTGGTGAIC	GTGGGAGATA	TCGATGTGGA	CTATGTGGAG	720
	AACAAGATCA	AAGAATCTT	CAAGGACGTT	CCTGCTCCCG	TGAATCCAGC	AGAGCGTATC	780
	TATACGCCGG	TAGAGGACAA	CGATGAGCCT	ATCGTAGCCA	TTGCTACCGA	TGCTGAGGCT	840
	ACTACACGCG	AGCTCTCCAT	CAGCTTCAAG	AGCGAGCCCA	CTCCTCAAGA	AGTGGGAGGA	900
	TCGATATTCG	GACTTGTGGA	AGACTATATG	AAACAGGTGA	TCATACAGCG	CGTGAATGAG	960
50	CGTCTGTCCG	AGATTACTCA	CAAGCCTAAC	GCTCCTTTCC	TCAGTGCAGG	AGCTTTCITC	1020
	TCIAACTTCA	TGTACATCAC	CCAGACTAAG	GAGGCATTCA	ATTTTGTTCG	CACGGTTCGT	1080
	GAGGGTGAAG	CGGAGAAAGC	GATGAACGCA	TTGGTGGCAG	AGATAGAAAG	CCTCCGTGAG	1140
	TTCCGTATCA	CCAAAGGCGA	ATACGATCGT	GCACGACGTA	ATGTGCTCAA	GCGATACGAG	1200
	AATCAATACA	ACGAAAGAGA	CAAGCGTAAG	AACAATGCTT	ATGCCAATGA	ATACTCCACC	1260
55	TACTTCCACG	ATGGCGGCTA	TATCCCGGCT	ATTGAGGTGG	AATATCAGAC	GGTGAATGCT	1320
	TTTGCTCCTC	AGGTTCTCTT	GGAAGCATTC	AATCAGGCTA	TTGCCCAAT	GATCGATCCG	1380
	GTGAAGAATG	CTGTCTTAC	CCTCACCGGT	CCTTCAAAGG	CTGAAGCCAA	GATTCGAGC	1440
	GAAGCAGACT	TCCTCGCTGC	TTTCAAAGCT	GCTCGTCAGC	AGAAAGTAGA	AGCCAAGAAA	1500
	GAGGAAGTCT	CCGACCAAAA	ATTGATGGAG	AAAGCTCCTA	AGGCGGAAAA	GATCGTTTCC	1560
60	GAGAAGAAAG	ATCAGAAGTT	CGGTACCCAG	GAACCTACCC	TTAGCAATGG	CATCAAAGTA	1620
	TACCTCAAGA	AGACCGATTT	CAAAATCAAAC	GAAATCCTGA	TGATGTCTCT	CAGCCCGCGT	1680
	GGTATCCTCT	CCGGAAAGCA	TGCTCCCAAC	CAATCTGTGA	TGAATTCGTT	CATGAACGTG	1740
	GGTGGCTTGG	GCAACTTCGA	TGCTATCCAG	CTGGATAAGG	TGCTGACAGG	TCGCTCTGCT	1800
65	TCCGTATCTC	CCTCTTTGTC	TCTGCTCAGT	GAAGTCTTT	CGGGCAAAAC	GACTGTAGAA	1860
	GATATGAAAA	CTTCTTCCCA	GTGATCTAT	CTCCAATGA	CTGCTAACCG	CAAGGATCCC	1920
	GAAGCGTTCA	AGGCCACACA	GGAAAAGTTG	TACAATAACT	TGAAAAATCA	GGAGGCCAAC	1980
	CCGATGGCTG	CGTTTATGGA	CTCTATCCGT	CATACCATGT	ACGGCGATAA	TCCGATGATG	2040
	AAACCCATGA	AACTGCTGA	CGTGGAGAAA	GTAATTTACG	ATCAGGTAAT	GGCTTTCTAC	2100
	AATGAGCGAT	TCGCTGATGC	CGGCCACTTT	ATGTTCTTCT	TTATCGGTAA	TCGGATGAA	2160
70	GCCCAAGATGA	AGCCATTGAT	CGAACTTAT	CTTGCTTCAT	TGCCCAACCT	CAAGCGTGGC	2220
	GATAAGATGA	ATAAGGCTCA	GCTACGGGCT	GCCGTTCCG	GAAAGATCGA	TTGCCAAGTT	2280
	GAGAAGGAAA	TGGATACTCC	TTGACTACT	ATATTGATG	TCGTGTCGGG	AAATGTGGAA	2340
	TATACGCTCA	AGAAGCTCT	CCTGCTGGAA	GTCTTCTCAG	CCGTAATGGA	TCAGGTGTAC	2400
	ACCGCTACCG	TTCCGAGAAA	GGAAGGCGGT	GCATACAGTG	TGGCTGCATT	CGGCGTCTC	2460
75	GAGCAATATC	CTACGCCCAA	GGCTCTGATG	CAGATCTATT	TCCCAACGGA	TGCTGCTGCT	2520

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GCCGAGGAAA TGAATGCTAT CGTTTTGCT GAGTTGGAGA AGCTTGCCAA GGAGGGCCCC 2580  
 AATGTGGAAT ACTTTAAGAA GACTATCGAA AACCTGAATA AGCAGCACAA AGAAAAGTCTG 2640  
 CGTGAGAAAT GTTTCCTGGCT CGAAGCCATG AAGGCGTCTT TCTTCGAAGG AATGACTTC 2700  
 ATCACAGACT ACGAATCCGT ACTGAACGGT CTTACTCCTG CTGAATTGCA AAAGTTTGGC 2760  
 5 GCACACCTCT TGAAGCAGCA GAATCGGGT GTTGTCATCA TGGCTCCTGT TGCAAAGGCT 2820  
 CAA 2823

## (2) INFORMATION FOR SEQ ID NO:143

10

## (i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 2052 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

20

## (iv) ANTI-SENSE: NO

## (v) ORIGINAL SOURCE:

25

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2052

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143

ATGAGTAAGA AAGGAACAA CCGGGTAACG AGGACRATA TATCCCGCT CATCAAAAA 60  
 TTCTGTACA GCGACCATGA GATATTCCTG CGTGAGATCG TCTCCAATGC CGTGGATGCT 120  
 ACGCAGAACG TGAAGACGCT TACATCCGTC GGCGAATCA AAGGCGAGAC GGTGACCTC 180  
 35 CGCGTAACGG TCAGCGTGG TGAAGTGGCA CGCACGATCA CGGTCAGCGA CCGCGCGSTA 240  
 GGGATGACCG AAGAGGAGGT GGAGAAGTAC ATCAATCAGA TTGCTTCTC CACTCGGAA 300  
 GAGTTTCTTG AAAAGTACAA AGACGACAAG GCCGCCATTA TCGGCCACTT CGGACTCGGA 360  
 TTTTACTCGG CTTTCATGGT GTCCGAGGGA GTGGACCTGA TCACGCGCTC TTTCCGAGAA 420  
 GATGCTACGG CGGTGAAATG GAGCTGCGAC GGATCGCCCG AATACACGCT CGAACCTGCG 480  
 40 GACAAGGCTG ACCGTGGCAC CGACATCGTG ATGCACATCG ATGAGGAGAA TAGCGAGTTC 540  
 CTCAAAAAG AAAAGATAGA GGGGCTCCTC GGCAAACTACT GTAAGTTCTT TACCGTGCCG 600  
 ATCATTTTCG GCAAGAAGCA GGAATGGAAA GACGGCAAGA TGCAAGATAC GGACGAGGAC 660  
 AATCAGATCA ACGACACACA TCCTGCTCGG ACCA/AAAGC CTGCCGACCT CAAGGACGAA 720  
 GACTATAAGS AATTTTACCG TTGCTCTAT CCCATGTCCG AAGAGGCTCT CTTCTGGATC 780  
 45 CACCTCAATG TGGACTATCC GTTCAATCTG ACAGGTATCC TCTATTTCG GAAGATCAAA 840  
 AACAACTTGG ATCTGCAGCG CAACAAGATT CAGCTCTACT GCAATCAGGT TTACGTCAAC 900  
 GATGAAGTCA AGGATATCGT CCGGACTTC CTCACCTCC TCGACGGGGT CATCGATTTC 960  
 CCGGATATTC CCGTCAACGT ATCGGCTCC TATCTGCAGA GCGATGCCAA TGTGAAGAAG 1020  
 ATCTCGTCTC ATATCACCAA GAAGGTGGCA GACCGTCTGG AAGAAATTTT CAAAACGAC 1080  
 50 CGCCCCCAT TCGAGGAGAA ATGGGATAGT CTGAAGCTCT TCGTCAATA CGGTATGCTG 1140  
 ACGGATGAGA AGTTCTATGA GCGTGCAGCC AAATTCCTCC TTTTACCGA TATGGACGGA 1200  
 CACAAGTACA CGTTCGACGA ATACCGAAGC CTCGTGGAAG GTGTACAGAC GGATAAGGAC 1260  
 GGACAGGTAG TGTATCTCTA TGCTACGGAC AAGCATGGAC AGTACAGCCA CGTGAAACGT 1320  
 GCATCCGACA AAGGCTACAG CGTGATGCTG TTGGATGCTC AGTTGATCC GCATATCGTG 1380  
 55 AGCCTGCTGG AGCAAAAGT' GGAGAAGACA CACTTGTCC GTGTCGATAG CGATACGATC 1440  
 AACAACTGTA TCCGCAAGGA GGAAAGAGCC GAAGTGAAC TGTCCGATAC GGAGCGCGCC 1500  
 ACTCTCGTGA AGCTGTTGGA AGCAGCCTG CCACGGGACG AGAAGAAGCA CTTCAATGTA 1560  
 GCTTCTGAAT CGCTCGAGC CGAAGGTGAA GCCATCCTTA TCACACAAGC CGAATTCATG 1620  
 CGCCGTATGC GCGATATGGC ACAGCTGCAG CCGGAAATGA GCTTCTACGG CGAACTCCCC 1680  
 60 GATTGCTACA ATCTGGTACT TAATACGGAT CATCCGCTCA TCGACAGGGT ACTCTCCGGT 1740  
 GAGAAAGAAAT CGGTAGAGCC TTCGCTCACA GAGCTTAGAG CGAAATCGC CGAGCTGAAA 1800  
 GCGGAAGAGG CCAAGCTGCT CGATGAGGAA AAAGGGAAGA AACCGGAGGA AATCCCTGTT 1860  
 GCCACGAAGG AAGCCAAGGA GAACAAGGCC GTCGAACAGG CCAAAACCGA AGGCAGTATC 1920  
 AACGATCAAC TGACCAATA TGCTCAGGAC AACGAGCTGA TAGGTGAGCT CATCGACTTG 1980  
 65 GCTCTGCTCG GAAGCGGATT GCTGACGGGA GAGGCTTTGG CCGAATTCAT TCGTCCGAGC 2040  
 CAGGCTCTTC TC 2052

## (2) INFORMATION FOR SEQ ID NO:144

70

## (i) SEQUENCE CHARACTERISTICS:

75

- (A) LENGTH: 1392 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...1392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144

ATGGA	AAAAAC	TGATCGATAT	TTTGGTCGTA	GACGATGATG	TGGCAGTCTG	TGCCGCACTG	60
CGTCT	GGTGC	TCAAGCGAGC	GGGCTATAAT	CCCGTATAG	CCAACAGTCC	CGACGAAGCT	120
TTGTCC	ATAA	TGCGGAATCC	TGATGGCGGC	TGTAAGCCGG	CTGTGATTCT	GATGGATATG	180
AATTTC	TCCC	TTTCGACCTC	CGGCAGGGAA	GGATTGGAAC	TACTGGAGAA	GATGCAGATA	240
TTCACTT	CCT	GCCCTGTCT	ACTGATGACG	GCTTGGGCTT	CGATTCCACT	GGCACTGGAG	300
GGAA	TGAGGC	TTGGAGCTTT	CGACTTCATA	GGCAAGCCAT	GGGACAACGA	TGGGCTCCTT	360
CGTACCA	TAG	ATACGGCCTT	GCATCTGGCT	GCTCCCTCAG	CTGTGGCGAA	TCCATCGGAA	420
CACTCTG	ACA	GAGATACAGC	CGCTCAGCCG	AAAGCTACAG	TCCAAGAGAA	TGACCCCTGT	480
GCCCA	TATCA	TAGGCGCGAG	CGATGCCATC	TGTAAGATCA	AGGAACGGAT	ACGCCGCATA	540
GCTCC	ACCC	ATGCCTCTGT	GCTGATCAG	GGCGAGAGCG	GTACGGGCNA	AGAGTTGATA	600
GCGGA	AGCTC	TGCACCGTGG	GAGCAACGA	GCCTCAGCCC	CATTCTGCAA	GGTCAATTG	660
GGTGG	GATT	CCGAAAGTTT	GTTCGAAAGT	GAGCTGTTCC	GACATAAGAA	AGGAGCTTTT	720
ACCAAT	GTCT	TTTCCGACAG	GAAAGGACGG	TTCCAGCTGG	CTGATGGCGG	CACGATCTTT	780
CTGG	ACGAA	TAGGCGAACT	ACCGGTCCGC	AACCAAGTAA	AACCTGCTCG	AGTGCTACAG	840
GAAC	AGACAT	TGAGCCGCTT	GGCGGAGAGC	GTCTCCCAAC	GAGTGGACAT	CCGTGTGGTA	900
TCGG	CTACGA	ATGCTTCCTT	GGAGCGAATG	GTAGCCGAAG	GACGTTTCAG	AGAGGACCTC	960
TACT	ATCGAA	TCAACCTGAT	ACATCTGCAT	CTGCCTCCGC	TGCGTGAGCG	TCAGGAGGAT	1020
ATAC	AGCTGC	TGCTGGAAGC	CTTCAGTGAA	GCCTTTGCC	AATCGAACGG	ATTGCCCCAT	1080
GCCG	TTTGA	GTGCGGAAGC	TATGCGACGT	ATCTGTGCCA	TGCCCTACC	GGGCAATGTA	1140
CUG	AACTGA	AAAAAGTAGT	GGAGCGTAGC	CTATTGTCT	CGGGATCGAG	AGAAATCAGT	1200
GCCCG	GATG	TGGCTGACTT	CGGTTCCGAG	GTGACGGCAG	CAGACCACTC	CGACGAACGG	1260
GCTTT	GACCG	ACATGGAGGA	AGCTGCTATC	CGAGAGACGC	TGACTAAATA	CAACGGCAAC	1320
GTTAG	TCGTG	CTGCACGAGC	CTTGGGATTG	AGCGGGGCAG	CTCTTTACCG	GCGAATGGAG	1380
AAAT	ACGGAC	TG					1392

(2) INFORMATION FOR SEQ ID NO:145

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 750 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145

ATGCT	TAAAG	TAAAGAACCT	CCACGCCACA	GTACAGGGCA	AAGAGATATT	GAAAGGAATC	60
AATCT	GGAGA	TCAATGCCGG	AGAGATTCT	GCTATCATCC	GGCCGAACGG	ATCGGGGAAA	120
AGTAC	GTCT	CTTCGGTTTT	GGTGGGACAT	CCCTCCTTTG	AAGTCACGGA	AGGAGAGGTG	180
ACATT	CAATG	GAATCGACCT	GCTCGAATC	GAACCGGAAG	AACGTGCACA	CCTCGACTGC	240
TTTCT	CAGTT	TCCAATATCC	GGTCGAGATC	CGGGCGTCA	GCATGGTGAA	TTTCATGAGG	300
GCACT	GTGCA	ATGAACATAG	GAAAGCGATC	GGAGCAGAAC	CCGTATCGGC	AAGCGACTTC	360
CTCA	AGATGA	TGCGAGAGAA	GCGTGCCATT	GTGGAGCTGG	ACAACAAATT	GGCCAGCCGT	420
TCTGT	GAACG	AAGGCTTCTC	CGGTGGAGAA	AAAAGAGGCA	ACGAAATCTT	CCAAATGGCT	480
ATGCT	CGAAC	CCAAGCTGGC	TATTTTGGAC	GAAACCGATA	GCGGGCTCGA	TATCGACGCT	540
CTCCG	CATCG	TAGCAGGGCG	GTAACCGGA	CTCCGCTCTC	CGGAGATGTC	TGCTATTGTG	600



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ATCACACACT ATCAGCGTTT GCTCGAGTAC ATCAAGCCGG ACTTCGTACA CGTCCTTTAC 660  
 AAGGGGCGCA TCGTCAAGTC GGGAGGAGCC GAGCTGGCTC TCACGCTCGA AGAAAAAGGC 720  
 TACGACTGGA TCAAGGAAGA GATAGGAGAA 750

5

(2) INFORMATION FOR SEQ ID NO:146

(1) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 1383 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

15

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

25

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146

30 ATGGCTAAGG AGAAACGAT CTACGTCTGC CGTTCGTGCG GAACCAAATA CGCCAAATGG 60  
 CAAGGCAACT GCAATGCCTG TGGAGAGTGG AACTGCATTG ATGAGGAGAA GGTGCCGGCA 120  
 CCGGCATCGG GCAAGCATGC AGCCAAGAGT TTTATGCCTC GGGAGCAGGA CAACCGGCCA 180  
 AGACTCTTAC AGGATGTGGA GTCCGGCGAT GAAGAGCGTA TTCGCCTCGG CGATGAAGAG 240  
 TTGGACCGCG TACTGGGTGG AGGAATTGTC AAAGGAGCAT TTGTCTGCT TGGCGGCGAG 300  
 CCGGGAATCG GTAAGTCCAC GCTTATCCTC CAGACGGTGC TGGCTCTGCC GCAGTTGCCG 360  
 35 ACGCTCTATG TGTCCGGCGA AGAAAGTGCC CGACAACTGA AGATGCGCGC CGAACGACTG 420  
 GGGCAAGCCA TGAATGGGTG CTACGTATAC TGGGAAACGA ATATAGAGAG GATACTCTCC 480  
 CGTGCAGAAG AACTCACACC CGATCTCCTC GTGATAGACT CTATACAGAC GGTCTATACC 540  
 GAGGAAATGG AAAGCTCGGC CGGCAGCGTG GGGCAGATCC GCGAATGTGC CGCCTTACTG 600  
 CTCAAACTAC GCAAGACTAC GGGTATCCCC GTCATCGTCA TCGGACACAT CACCAAAGAA 660  
 40 GGTAGCATAG CCGGACCGAA GGTGCTGGAG CATATAGTGG ATACGGTGCT TCTCTTCGAC 720  
 GGGGATAAGC ATCATCTCTA CCGGATACCT CGAGGACAGA AGAACCGCTA TGGCAGTACT 780  
 TCCGAGCTGG GGATATACGA GATGCGGCAG GACGGTCTGC GTGGCGTGA GAATCCGAGC 840  
 GAACATCTCA TCACACGCA TAGGGAAGAC CTCAGTGGCA TAGCCATAGC CGTAGCGATG 900  
 GAGGGCATTC GCCCGATACT CATCGAAGCG CAGGCTTTGG TCAGCTCGGC CATTTATGCC 960  
 45 AATCCGACGC GTTCGGCCAC GGGCTTOGAT ATTGGGCGGA TGAACATGCT CTTAGCCGTA 1020  
 CTGGAGAAAC GTGCCGCTT CAAGCTCATA CAGAAGGATG TGTTCCTGAA CATTGCGGA 1080  
 GGTATCAAAA TAGCCGATCC GGCTACGGAT CTGGCCGTTA TCTCGGCAGT GCTGCGCTCG 1140  
 AGTCTGGACA TCGTTATCCC GCCGGCCGTA TGCAATGACG GCGAGGTGCG ACTCTCCGGA 1200  
 GAGATACGTC CCGTGAGCCG CATCGAGCAG CGCATAACGG AAGCGGCTCG CATAGGGTTC 1260  
 50 AAAGAGATAT TGGTACCGGC CGATAATTTC CGCCAGGAGG ATGCCGGCCG CTTCGGTATT 1320  
 CGGCTCGTGC CGGTGAGAAA GGTGGAGGAA GCCTTCCCCC ATCTGTTCTC GAAAGGAAGA 1380  
 GAA 1383

55

(2) INFORMATION FOR SEQ ID NO:147

(1) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 813 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

65

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

70

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

75

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...813

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## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:147

```

5  ATGAATAGCA GACATCTGAC AATCACAATC ATTGCCGGCC TCTCCTCTT TGTACTGACA 60
   TTGGGCGGCT GCTCCGTAGC CCAACAAGAT ACGCAGTGGG CTCTCGGCGG AAAGCTCTTT 120
   ACTTCGGCGT GGATACAACG TTCGGCGGAA TATCAAGCGC TTTCGATTCA GGCATACAC 180
   ATCGCTACGG AAAGAGTGGG CGCTCTACCG GCAGAACGTA AACAAAGAGA TAGGCCTTAT 240
   GCCATCGTAA CGGACATAGA CGAAACCATT TTGGACAATA CGCCTAACTC CGTGATCAG 300
   GCTCTCAGCG GCAAGGATTA TGATGAAGAG ACTTGGGGGA AATGGTGTGC ACAGGCGGAT 360
   GCCGACACAC TGGCAGGAGC TTTGTCTTTC TTCTCCATG CAGCGAACAA GGGGATCGAG 420
   GTCITTTTACG TCACCAACCG CAGAGACAAT CTGGCGGAAG CAATCTTTCA GAACCTTCAG 480
   CGTTACGGAT TCCCTTTTGC CGATGAAGAA CATTTGCTTA CGACCCATGG GCCATCCGAC 540
   AAAGAAGCCCC GTCCGCTCAA AATACAAGAA CAGTATGAAA TAGTATTGCT CATAGGAGAC 600
   AACTTGGGCG ACTTCCACCA CTCTTCAAT ACGAAAGAA AGTCCGGACG CAAACAGGCT 660
   CTGGGCGCTGA CAGCCGGGGA GTTTGGCCGG CACTTCATCA TGCTGCCCAA TCCCAACTAC 720
15 GCATCTTGGG AACCGCATG GTACGCGGG AAGTATCCGC CACTGCCCGA AAGAGACAAA 780
   GCACCTTAAC AACTGCACCT ACAGAACAGC AGA 813

```

## (2) INFORMATION FOR SEQ ID NO:148

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20 (1) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1251 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
25 (D) TOPOLOGY: circular

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

30 (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

35 (ix) FEATURE:
    (A) NAME/KEY: misc feature
    (B) LOCATION 1...1251

```

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:148

```

40 ATGAGCACCA ATATAGATGT ACAACAGATC AACAGCGTT TCGGCATCAT CGGTAGCAGT 60
   CCGCTGATGG AACATGCCAT ACGAGTGGCA GCACAGGTGG CTCTACCGA CATGTCCGTC 120
   CTCGTGACGG GGGAGAGCGG TTCGGGAAA GAGTTCCTCC CACAGATAAT CCACTACTAC 180
45 AGCGCCCGGA AACATCATAG CTACATTGCA GTCAATTGCG GAGCCATCCC CGAAGSAACC 240
   ATCGATTCCG AGCTGTTCCG ACACCGCAA GGTTCCTTTA CCGGAGCCGT ATCGGATCGC 300
   AAGGGGTACT TCGAAGAAGC ATCCGGCGGC ACGATCTTTC TGGACGAAGT GGGCGAAGTG 360
   CCTTTGCCCA CGCAGGCGAG GCTGCTGAGG GTGCTGGAGA CGGGCGAGTT CATCCCCGTA 420
   GGAGCCAGCG AGTCCGAGAA GACGGATGTC CGTATCGTAG CGGCGACGAA TGTGAACCTC 480
50 AAGGAGGCGG TAGCGAAGCG GAAGTTCCGG GAAGACCTCT TCTTCCGGCT CAATACGGTA 540
   CUXATCGAGG TGCTGCGCT GCGTATGCGA CCGGACGAG TGCCCTTGCT TTTTCGCGGA 600
   TTGCGCCCGC ACAGCGCCGA GAAGTATCGG ATGCTCCGC TCGCCTATC GGACGAAGCC 660
   CGTACCATAT TAATGCGTTA CCGCTGGCCC GGCAATGTGC GAGAGCTGCG CAATATAACC 720
   GACAGGCTGA GCATCTTGA GGAGGAGCGG ACGGTATCGG CAGAGACCAT CACTCGCTAC 780
55 CTGACGCTG AGGGGATGCA AGACCTCCAC CCGTCTGTA TCCGACGGA CGAAGCGACC 840
   GAAGCGGACA AACAAATCCC CCATTACGAG CGCGAAATCA TCTACCGGT GCTATACGAT 900
   ATGAAGAAAG AGATAGCCGA TTTGAAGGGG ATGATGAACC GCCTGGCGCA CCACGAACAG 960
   CCCTCATGGC CTGTAGGGTC GGAAGTCTGG GGCACGACG ACAAGCGCAC CGCAGATCCG 1020
60 AAGTGGGGCG TCAGACGCA CAAGGCCCCC ATCGCGAAGC CGGCAGAAC CGTGGAGCCG 1080
   ATACAGGAAG CCAGCGAATA CACCGAGGAT CCGGTTTCGC TGGAGGAGGT AGAGAAGAAA 1140
   ATGATTTCCT TTGATTGGA ACGCCACGGC GGAAGGCGCA AGCAGACAGC CGAGGAAGTG 1200
   AAGATTTCGG AGCGGACACT ATACCGTAAA ATCAAGGAGT ATGGACTGGA A 1251

```

## (2) INFORMATION FOR SEQ ID NO:149

```

65 (1) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1806 base pairs
    (B) TYPE: nucleic acid
70 (C) STRANDEDNESS: double
    (D) TOPOLOGY: circular

    (ii) MOLECULE TYPE: DNA (genomic)

75 (iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149

ATGATCCTAC	TCTTCGGCGG	TACTACGGAA	GGCCGTGCCG	CAGCTCGCGT	GCTGGATGAA	60
GCGGGAAGTC	CGTITTTTCTA	CTCCACCAAA	GGCAATCTGC	AAGAGATCCA	GAGTAGCCAC	120
GGCCATCGTC	TGACAGGAGC	CATGACGGTT	GCGACATGG	TTTCGTTTGG	TCGGAAGAGAA	180
GAGATCCGAC	TGATCGTGGA	CGCCGTCAT	CCTTCGCGG	AAGAATTGCA	CGCTTCAGTG	240
GCAGAAGCCT	CTGAACAAAC	AGGTATCCCC	GTAGTAAGAT	ACGAGAGACA	ATACCCCTCCA	300
CGCGAAGAAG	GTATCGTCTG	GTGTGCAAAAC	TACGATACGG	CTGCCGAGCG	GATGCTTGSC	360
GATGGCGTGC	AGCGTCTGCT	GATGCTCACA	GGAGTGAATA	CGATCCCCAA	GCTGGCTGCT	420
TTCTGGAAAG	AGCGCACCAC	CTTITGCCGC	ATATTGAAGC	GAGACGAATC	GGTTGCTTTG	480
CCAGAGAAGA	ACGGCTTTCC	TGCGGAGCGC	ATCGTTTCT	TCGAACCGCA	TGCGGACGAG	540
GAGCTGATGC	AAGCGGTTCC	CCCCGATGCC	ATTATCACA	AAGAAAGCGG	AGAGAGCGGT	600
TACTTCCGAG	AAAAGATAGA	AGCTGCCCGA	CGGATGGGCA	TCCGTATATA	TGCCGTCGTA	660
CGTCCCCCTT	TGCCTCCTTC	ATTCAATCCC	GTAGGCGGGC	CTGTGGTTT	GAGACGGGCG	720
GTAGAACGCC	TGCTGCCGGG	ATTCTTTTCA	CTCGGAAGCG	GATTCAGTAC	CGGCACCAAC	780
GCTACCGCTG	CAGTAGTAGC	AGCCATGTAC	CGATTGATGG	GGCTTGGCTC	TCTCGCCGAA	840
GCTCCCGTAG	AATTGCCTTC	GGCGAAATA	GTCACTCTGC	CCATAGCGGA	AATTGAGAG	900
GAAGAAGATG	CTGTCTATC	CGCAGTCTCG	AAAGATCGAG	GTGATGATCC	GGATGTGACC	960
AATGGCATGG	CGGTATGCCG	TACGATCAGG	CTCAATCCCG	AACATGAGGA	AGTCCGCTTC	1020
CTGCAGGGTG	AAGGGGTGGG	GGTAGTGACG	CTCCCCGCTC	TGCGTCTGGA	GGTCGGAGGT	1080
CCGGCTATCA	ACCTCGTACC	TCGACGAATG	ATGACAGCAG	AGGTACGCGG	ACTCTATGCG	1140
CAGGGAAGTC	TGGATATTAC	GATTAGCGTA	CCCGAAGGCC	GAGAGGCTGC	TACCCAGACA	1200
TTCAATCCCC	GACTCGGCAT	ACGGGACGGC	ATCTCTATTA	TCGGAACATC	GGGAGTCGTG	1260
AAACCTTTTT	CGGCCGAAGC	GTTCGTTGGT	GCCATCGGTA	AGCAAGTGGG	TATTGCCACC	1320
GCCTTGGGAG	CCAATCATAT	CGTCCTCAAT	TCGGGAGCCA	AGAGTGAGCG	TTATGTAAAA	1380
GGAGCCTATC	CGGCACCTAT	TCCACAGGCC	TTTGTGCACT	ATGGCAATTT	CGTCGGCGAA	1440
TCACTCAGTT	GTGTAGCTTC	CTTCCCTTCT	GTCCGTTCGG	TAACGGTAGG	AATCATGCTC	1500
GGCAAGCAG	TGAAACTCGC	CGAAGGCTAT	CTGGATACGC	ACAGTAAAAA	GGTAGTGATG	1560
AATCGGGATT	TCTGCACGGA	ACTGGCTCGT	CAGGCAGGTT	GTTCGGAAGA	CATCCATGCC	1620
ATAATAGACA	GCCTGAATTT	GGCTCGTGAG	CTATGGACTA	TGCCGAGTGC	GGAGGACAGC	1680
GATCGACTGC	TACGAAAGAT	TGCCGAACGA	TCTTGGGAAA	CTTGCCGCCC	ATCGGTACCA	1740
TCGGCCGAAT	TAGAACTCCT	GCTGATCGAT	GAGTCCGGAG	CGATTCTGTT	TCGTATCGGT	1800
GGAGAA						1806

(2) INFORMATION FOR SEQ ID NO:150

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1329 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150

ATGTTGAGGA	CTTCCGAAT	CGGTGGTATT	CACCCCCCG	AAAACAAGTT	GTCCGCAGGC	60
AAGCCCGTAG	AGGTGTTGCC	TATCCCCCTCA	CAGGTAGTCA	TCCCTCTTGG	TCAGCACATC	120
GGTGACCCGG	CAACTGCCAG	GGTCAAGAAA	GGGGATGAAG	TTAAGGTGGG	GACTATCATT	180
GCTCAGGCCG	GAGGATTCGT	ATCAGCTAAT	ATCCACTCAT	CTGTGTGGGG	TAAGGTGCTG	240
AAGATCGATA	ACGTATACGA	CTCAAGCGCC	TATCCCAAGC	CGGCAGTCTT	CATTAGCGTA	300
GAAGGTGACG	AATGGGAAGA	GGGCATCGAT	CGCTCACCAG	CCATCGTCAA	AGAATGCAAT	360
CTGGATGCAA	AAGAAATCGT	AGCCAAAATT	TCTGCAGCCG	GTATTGTGGG	TCTTGGCGGT	420

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5 GCTACCTTCC CTACCCATGT GAAGCTGTCC CCTCCTCCGG GCAACAAACC TGAGATCTTG 480  
 ATCATCAACG CCGTAGAGTG CGAGCCTTAT CTGACGAGCG ACCATGTCCT TATGCTGGAG 540  
 CACGGCGAAG AGATCATGAT CGGCGTGAGT ATCCTGATGA AAGCCATTCA GGTAAACAAG 600  
 GCCGTCATCG GAGTTGAGAA TAATAAGAAA GATGCTATTG CTCACCTCAC CAAACTGGCC 660  
 10 ACTGCATATC CCGGCATAGA GGTAAATGCCG TTGAAGGTGC AATATCTTCA AGGCGGTGAG 720  
 AAGCAGCTGA TCGATGCAGT GATCCGCAAG CAGGTAAAAA GCGGTGCCTT GCCTATCAGC 780  
 ACAGGTGCCG TAGTACAAAA CGTGGGTACG GTATTGCGTG TGTACGAAGC AGTACAGAAG 840  
 AACAGCCCTC TGGTCCGACG CATCGTGACG GTTACAGGAA AAAAAGTCTC TCGTCCGTCT 900  
 AACCTCCTCG TTCGTATAGG TACTCCTATT GCGGCTTTGA TCGAAGCAGC AGGTGGCTTG 960  
 15 CCGGAGAATA CCGGCAAGAT CATCGGCGGA GGTCCGATGA TGGAGCGCGC TCTGCTGTCA 1020  
 CCGGATGTGC CTGTGACCAA AGGCAGCTCC GAGTATTGA TTCTCGATAG AGAAGAGGCA 1080  
 GTTCGCAAGC CTATGCGCGA CTGTATCCGA TCGGCCAAGT GCGTCGGAGT GTGTCCGATG 1140  
 GGACTCAATC CGGCTTTTCT TATGCGCGAC ACCTTATATA AGAGCTGGGA AACAGCGGAA 1200  
 AAAGGCAACG TGGTTGACTG TATCGAATGC GGTTCGTGCA GCTTCACCTG TCCGCGCAAC 1260  
 20 CGTCTCTGCG TGGATTATAT CCGCCAAGCC AAGAAGACTG TGATGGGTAT CCAAGAGACA 1320  
 CGTAAGCAA 1329

## (2) INFORMATION FOR SEQ ID NO:151

20

## (i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 1437 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

25

## (ii) MOLECULE TYPE: DNA (genomic)

30

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

35

## (A) ORGANISM: PORPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1437

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151

45 ATGAAAAGAA TACAACAAAC TCCTATCGCT CTCTTCGCGG CTGTTGCCGG TTTGGTGGCT 60  
 CAAAATGCTT ACGAGGGAGT AATTTTCATAT AAAATTTTCGT TGGACAAAAC CGGAACAAG 120  
 GTTGTAAGCA ATGGTGGCGG AGATATGAGT AATTTAAAGC TCAAGAGCAC TCAGATGATC 180  
 ATTGTTACGC CTATTCTTCG TTCAGAAGAT GGTACCAAGC GGGTGAATT TCCTTCGGTA 240  
 GTCATTACAG GCCGCAATAG AACAAAAGCT CTCAGCGGTG AAATCGCATT TAGTTCGGCT 300  
 TTGCCCAAG CAAAACATGC AGCTCAATAC ATTCGCGGTC ATAATGGGAA GAGCGAGCAG 360  
 TTTGCTTTTA CAGGAGAACA TGCTTATGCA TCATGGATGA TGGATGCCAA GTTTGTGGTT 420  
 50 CGTGAGGAGG TACGAGGTTG TGCTAAATGC CCTGTAGGTC TCTCGAGTAA TATTGTTCTT 480  
 TTTGATCCAC TCTTCAATCC GGCAGAGGCT CGTTATTGTT TGGCACACAT TACTCCGGCA 540  
 GAAGAAGTGG AAAACAGCG AGAGTCCAGC TTCGATGCTT ATATCAACTT CAAAGTCAAT 600  
 AAGGCAGATG TCCTTCTCGA GTATCGCAAC AATAAGGCGG AGTTAGAGAA AATCAAAGAA 660  
 TTTGTAAGCA CCGTTAAGGC TAATCCAAC TATTCCGTCA ATAAATGAT CATCGAAGGG 720  
 TTTGCTTCTC CCGAGGCTTC AATAGCCAC AATAAGGCTT TGTGGAGCG CCGTGCTAAA 780  
 55 AGACTCGCGG AAGAATTGGT GCGTAAGTAT GGCAAAACAT TGCCGAATAT AACCACTGAA 840  
 TTCGCGGTG AAGATTGGAA GGGGCTGAAA CTGGCTATCG AAAAGAGTGA TATAGCCGAT 900  
 CGTGACCGCG TATTGGAGAT AATCAACTCC GATAAATATG CCGATGATGA TGCACGTGAA 960  
 CAGGCTCTGA AGCAACTTTC GTCTTATCGT TATATCTTGG ATCAGATCTA TCCGAATTTG 1020  
 60 CGTCGCAATA CGATAACCAT GGGGTATATC GTTCGTGATT ATACCTCGA AGAAGCTCGT 1080  
 GAAATCATTA AGACTGCTCC GAAAGAACTT AGTGAGGCCG AAATGTACCG TGTGGCAATG 1140  
 TCTTATCTCG AGGGGCAACA AGAGCGTTTG TTTGCTCTGA ATACGACCCT TAAGTATTTT 1200  
 CCTGAAGAGT TAACGGGCCG AATCAATTTG GCTGTAGCCG CTTTAAATGG TGGAGACGTT 1260  
 CAAACAGGCA TTGCTCTGTT GAGTCCGATT CAGACAGAAA AGGGTGTAAG CAATATCCTT 1320  
 65 GGAGCTGCTT ATGCTCGTAC GGGAGATTTT GCTCGTGCCG AAACCTTCTT CGTAAGGCC 1380  
 GTTCGAGAAG GAGATGCAAA TGCAGAGCGC AACCTCGATA TGCTGCTTGG CAAAAG 1437

## (2) INFORMATION FOR SEQ ID NO:152

70

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1149 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

75

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(ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 5 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 10 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1149  
 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:152

ATGGCAGAAA	AAAGAGACTA	TTACGAAGTC	CTCGGTGTAT	CGAAGAATGC	CACCGACGAT	60
GAACTGAAAA	AAGCATATCG	CAAGAAGGCT	ATCCAATACC	ATCCTGATAA	GAACCCCGGT	120
GACAAGGAGG	CGAAGAGCA	CTTCAAAGAG	GTAGCTGAAG	CCTACGACGT	ATTGAGCGAT	180
CCGCAGAAAG	GCAGTCAATA	TGACCAAGTTC	GGCCATGCCG	GATTGGGCGG	AGCTGCCGGT	240
GGAGGTTTCA	GCGGAGGCGG	TATGTCCATG	GAGGATATTT	TCAGTCCGCT	CGGTGATCTA	300
TTCGGTGGGT	TCGGCGGTTT	CGGCGGATTC	TCCGATATGG	GCGGTGGCAG	TCGCAGACGT	360
GTTCGCAGAG	GGTCTGACCT	GCGAGTACGA	GTGAAGCTTT	CTTTGGCCGA	TATAAGTAAA	420
GGTGTGGAGA	AGAAAGTGAA	GGTAAAAAAG	CAGGTAGTGT	GCAGCAAATG	TCGTGGCGAT	480
GGCACGGAAG	AAGCCAATGG	CAAGACTACC	TGCCAGACCT	GCCATGGAAC	CGGCGTGGTT	540
ACACGTGTGA	GCAACACTTT	CCTTGGGGCC	ATGCAGACCC	AGAGCACTTG	TCCCACTTGC	600
CACGGAGAGG	GTGAGATCAT	CACGAAGCCA	TGCTCCAGT	GTAAGGGCGA	AGGTGTGGAG	660
ATCGGCGAAG	AGGTGATCTC	ATTCCACATC	CCTGCCGCTG	TAGCCGAAGG	AATGCAAATG	720
TCCGTGAACG	SCAAGGGAAA	TGCCGCGCCC	CGAGGAGGCG	TGAATGGCGA	CTTGATAGTC	780
GTGATCGCGG	AGGAACCGGA	TCCGAATCTG	ATCCGCAATG	GCAACGATCT	GATATACAAT	840
CTGCTTATAT	CCGTTCCGTT	GGCTATAAAA	GGAGGTAGTG	TGGAAGTGCC	GACGATAGAC	900
GGAGGAGCCA	AGATCCGCAT	CGAGGCGGGG	ACACAACCCG	GCAAGATGCT	GCGTTTGCGC	960
AATAAGGGGT	TGCCCAGCGT	AAACGGCTAT	GGCATGGGAG	ACCAACTGGT	GAATGTCAAT	1020
GTCTATATCC	CCGAATCGAT	CGATGCCAAA	GATGAGCAGG	CTATCGCAGC	GATGGAAAC	1080
TCGGACAGCT	TCAAACCTAC	CGATGCTGCT	CGTAAGGATA	TAGACAAGAA	ATACAGAGAG	1140
ATGCTGGAT						1149

(2) INFORMATION FOR SEQ ID NO:153  
 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 879 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 50 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 55 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...879  
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:153

ATGAAAAAAC	TGATTTTAGC	GACTTTGGGA	CTTATGGCCA	TTGCCATGCT	CTCATGTTCA	60
AGCAACAACA	AGGATTTGGA	GAACAAAGGG	GAGGCTACTC	TTTGGTAAC	GTITGGTAGC	120
TCCTATAAAG	CTCCACGCGA	AACCTATGCG	AAGATTGAGA	AGACTTTTGC	CGCAGCTTAT	180
CCCGATCAAA	GGATAAGCTG	GACATACACG	TCTTCTATTA	TCCGAAAGAA	ACTGGCTCAG	240
CAGGGTATTT	ATATCGATGC	TCCGGATGAG	GCTTTGGAGA	AATTGGCTCG	TCTGGGTTAT	300
AAGAAGATCA	ATGTACAGAG	TCTTCATGTG	ATTCCCGGCC	GAGAATATGA	TGAGATGATC	360
GACTTTGTCA	ATAAGTTTAA	GGCAGCACAT	AGTGATATTA	CTGTGAAGGT	AGGGGCTCCG	420
CTTTTCGATA	CCGATGAAGA	TATGCGCGAC	GTGGCAGAGA	TCTTGACAAA	GCGTTTTCAG	480
CAATCGATAG	AGAAAGGTGA	AGCTATTGTA	TTTATGGGAC	ACGGCACCGA	GCATGCTGCC	540
AATGACAGGT	ATGCCCGTAT	CAATAAGATC	ATGAAGAACT	ATAGCAAGTT	CATGATCGTC	600
GGAACCCGTC	AGTCCGATCC	CTCTATCAAT	GATGTTATTG	CCGAACTGAA	AGAAACCGGT	660
GCCACGGCGG	TAACAATGAT	GCCGCTGATG	AGTGTGGCAG	GCGACCATGC	TACGAATGAT	720
ATGGCCGGAG	ATGAGGACGA	TAGCTGGAAG	ACGTTGCTGA	CCAATGCCGG	CTACACAGTT	780
TCTATAGACA	AGCTGGACAA	TGGCAATTTT	TCAGCTCTTG	GAGATATAGA	AGAGATCCGG	840
AATATCTGGC	TCAAGCATAT	GAAAGCCACC	TCTGCTCGC			879

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## (2) INFORMATION FOR SEQ ID NO:154

5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1060 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

10 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

15 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

20 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154

25 ATGACATCCG TCAGCCACTT ACGTACAATT TCTGTGCGAG GTATCCTGGC TCGCTGGGA 60  
 GGGCTGTAC TCATTCTCTT CCGGGTTAAT CTCTTCCTCG GCTCGGTGGC TATCCGATG 120  
 AGCGAGATCT TCCGACATCT TTTTTCAGAT CGTCCCGAAG GAGGAGAAGC ACTCGTGAC 180  
 TACAATATCC TATGGAATC CCGCCTGCCC GAAGCCCTCA CGGCTGCTTT TGCCGGGCGA 240  
 30 GGTATTATCC TTAGTGGCTT GCAGATGCAG ACCGTCTTTC GCAATCCTTT GGCCGGTCCG 300  
 TCCGTTCCTG GCATCAGCTC CGGTGCCAGT TTGGGTGTG CTTTGGTGGT TCTGCTGAGC 360  
 GGCTCGCTGG GAGGAGTGGC ATTGAGTAGC CTGGGTATA TGGGCGAGGT GGCCATGAAT 420  
 ATAGCCGCTG CCGTAGGCTC GCTGGCAGTA ATGGGGCTGA TCGTTTGTGT CAGCACCAAG 480  
 GTCCGCAGCC ACGTTACGCT GCTCATTATC GCGGTTATGA TCGGATATGT AGCCACTGCC 540  
 35 GTCATCGGGG TATTCAAGTT TTTCAGTATC GAAGAAGATA TTCGGGCATA CGTAATTGG 600  
 GGGTTGGGCA GCTTTTCCCG TGCCACGGAT TCGCAACTGA GTTCTTTGC CATTCTGATG 660  
 TTGATCTTTA TCCCGCCCGG TATGCTCCTT GTCAGCAGT TGAATCTCT ATTGCTGGGA 720  
 GAAAGCTAGC CACGTAATCT GGGACTGAAT ACTCGTCGGG CACGGCTGCT CGTGATCTCT 780  
 TCCGCGGTTT TGCTCATCGC TACCGTCACG GCCTATTGCG STCCCATCGG CTTTGTGGG 840  
 40 ATGGCTGTGC CACACTTGGC ACGGGTTATC TTTCACAGAT CGGATCATCG GATCCTGATG 900  
 CCTGCTACCT GTTTGATTGG AAGTGTCTG GCTCTTTCT GCAATATCAT TGCTCGTATG 960  
 CCGGGGTTTG AGGGGGCTTT GCCCGTCAAT TCCGTAACGG CTTTGGTGGG AGCACCTATT 1020  
 ATCGTCACCG TTTTGTCCG GCGCAGACGC TCAAGGAAG AAACCGAC 1060

## (2) INFORMATION FOR SEQ ID NO:155

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2271 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

55 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

60 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2271

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:155

70 ATGCGGACAA AAATATCTT TTTTGGGATT ATCTCTTTTA TTGCTCTATT GTCTCTTCT 60  
 CTGTCCGGCTC AGAGCAATGC CGTTTAAACC GGTAGTGTGT CGGATGCCGA AACCGGAGAG 120  
 CTTCTTGGCG GTGCTCGAAT CGAAGTCAA CACACCAACA TAGTAGCCGG TGCCGATGCC 180  
 GCGGGACATT TCGAGATCAA GAACCTGCCG GCAGGGCAGC ATACTATTAT ATGTTCTGTTG 240  
 GGGGGGTATG GACAGAAAGA GGAGGTGTT GCCATCGAAG CCGGACAGAC CAAAACGATC 300  
 TCTTTTGCAT TGCGACTGCG AACGAACAAC TTGGAGGAAG TCGTCGTTAC CGGTACCGGT 360  
 75 ACACGTTACC GCTTGGTCGA TGCTCTGTG GCAACGGAAG TCCTTACCGC TAAGGACATA 420

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 10  
 15  
 20  
 25  
 30

GCCTCTTCT CGGCTCCTAC TTCCGAGGCC TTATTGCAGS GGCTGAGTCC GTCTTTTGAC 480  
 TTCGGCCCCA ATCTGATGGG CTCTTTTCATG CAGCTGAACG GCCTTAGCAG TAAGTATATC 540  
 CTCATCCTTA TCGATGGTAA GCGTGTGTAC GCGGTCAGCG CGATTGAGT 600  
 CGTATTCTCT CTGATCAGAT CGAACGGATC GAAGTGGTGA AAGGTGCTTC GAGTTCGCTC 660  
 TACGGATCCG ATGCCATCGC CGGGTAATC AATGTGATCA CAAAAAGAA TACGAATCGA 720  
 CTGAGTGCAT ATACGTCACA TCGCATATCG AAGTACAACG ATCGGCAAC CAATACTTCG 780  
 CTCGATATAA ACATCGGTAA GTTCAGTAGC AATACCAACT ATTTCTTCTA CCATACGGAT 840  
 GGCCTGGCAGA ATAGTCCGTT CGAAATAAAA AAGAAAAAAG GATCCGGCGA ACCGGTCTTG 900  
 GAGGAAACGT ATAAGAAAAC TTTTCGTGCA CAGGAAAATC AGGGTGTAAG CCAATCGCTT 960  
 TCCTATTATG CAACTAACAA TCTTAGCTTC AGCGSAAATG TGCAGTACAA TAAACGTCAG 1020  
 ATCTTCACTC CGACTTTTTC CGAAAAGAAG GCCTATGACA TGGATTATCG TGCTTTGACG 1080  
 GCTTCACTCG GTACGAACATA TCTTTTCCCC AATGGTCTGC ATAGGCTTTC TTTGATGCC 1140  
 GTCTACGATC GCTTCGTTT CGGATATTG TATCATGACA AGGACAGCAG TGAGAGCCTG 1200  
 ATCAACAACC AAGGTCAGAC CGAGCAACCC ACATTCTTTC CGGGTCAGCT ACACAATAAA 1260  
 AACCTACAGA TCCGATACAC GGCAGAGGCT CGCGGTGTAT TTACTCTGCC TTATGCGCAG 1320  
 AACTGACTCG GCGGTTTGGG GTATTTCGCT GAGGAATTGA TCTCTCCCTA TAATTGATT 1380  
 ACCGACAGG CAGATGCTTC CACGCTCTCT GCTTATGTAC AAGATGAATG GAAACCGCTC 1440  
 GATTGGTTCA ATATGACAGC CGGTTTCGCT CTGGTACACC ATCAGGAGTT CGGTACACGA 1500  
 ATGAOAGCTA AGGTATCCAT ACTCGCCAA GATGGGCGCG TGAACCTCCG CGCTACGTAT 1560  
 GCTAACGGCT ATAAGACTCC CACGCTGAAA GAGCTTTTTC CACGGAACGA ACTCACCACT 1620  
 ATGGGTTCCG ACAATCTCTA TCTCGGCAAT GCGGATCTTA AGCCACAGAT GTCGGATTAT 1680  
 TATGCTTTGG GCTTGGAGTA CAATCAAGGC CCTATCTCGT TCAGTGCAAC GTTTTATGAC 1740  
 AATCAACTTC GCAATCTGAT CTCTTTTATG GATATACGA UCTCACCCGA GCACGAAGCT 1800  
 CAGGGAATCA AGAAAACCA GCAGTATGCC AACATAGGAA AAGCTCGCAG CCGCGGCTT 1860  
 GATGTCTCAT GTGATGCCTC TATCGGTTGG GGTATCAAGT TAGGAGCGGG ATACAGCCTC 1920  
 GTGGAAGCTA AGAATCTCCA GACGATGAG TGGCTGGAAG GAGCTGCACG TCATCGTGCC 1980  
 AATGTGCACG CCGATTGGGT TCACTACTGG GTTCAGTATA GACTTGCGCT GAGCCTTTTC 2040  
 GGCCTATTTC AGAGCGAGCG TTAATAACAA GACGGCAATG CTCGGGACTA TACCTTGTGG 2100  
 GACTCGCCA CATCGCATCG TTTGCTCAT TTCCGCCACA TCATCTGGA TGAACGCTC 2160  
 30 GGTATAGACA ACCTGTTTGA CTAGTGGAT GATCGTCTA TGGGTGTCAA TTATGCTACC 2220  
 GTAACGCCGG GACGTACTTT CTTTGCTCAA ATAGCGATTC GATTCAACAA C 2271

## (2) INFORMATION FOR SEQ ID NO:156

35  
 40  
 45  
 50  
 55

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 993 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
  
 (ii) MOLECULE TYPE: DNA (genomic)  
  
 (iii) HYPOTHETICAL: NO  
  
 (iv) ANTI-SENSE: NO  
  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...993  
  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156

60  
 65  
 70

ATGACGGACA ACAACAACG TAATATCGTA TTCCCGCGT TTCTCCTCT GCTGGGAGTC 60  
 ATCGCAGTGG TGACGATCGT TGGTTTTTTC ATGCTCAGAC CGGCCGAGGA GATTATCCAA 120  
 GGACAGATAG AAGTGACCGA ATACGAGTG TCCAGCAAAG TGCCCGGGCG CATCAAGGAA 180  
 CTTAGGGTAT CCGAGGGACA GCAGGTGCAG GCGGCGGATA CCTCGCTGT CATCGAAGCC 240  
 CCCGACGTAG CCGCTAAGAT GGAGCAGGCA AAGGCTGCCG AAGCAGCTGC ACAGGCTCAG 300  
 AACGCCAAGG CTCTCAAAGG AGCAGCAGC GAACAGATAC AGGCAGCCTA TGAGATGTGG 360  
 CAGAAAGCTC AGGCCGGCGT AGCCATAGCG ACCAAGACAC ACCAGCGCGT GCAGAACCTC 420  
 TATGACCAGG GAGTGGTACC GGCTCAGAA TGGAGCAAG CCACTGCCCA GCGGATGCG 480  
 65 GCCATCGCTA CGCAAAAGC GGCCGAAGCT CAGTACATA TGGCTCGCAA CGGTGCCGAA 540  
 CGGAAAGACA AGCTGGCAGC TTCTGCCCTC GTCGATAGAC CGAGAGGAGC CGTCGCGAG 600  
 GTGGAGTCTG ACATCAACGA AACCTACCTC ATCGCCGAC GGGCAGGCGA AGTGTGCGAG 660  
 ATATTCCCCA AAGCCGCGCA ACTCGTAGGT ACCGGGACAC CTATCATGAA TATCGCCGAG 720  
 ATGGGCGATA TGTGGGCGAG CTTTGCCGTT CGTGAGGATT TCCTCAGCAG CATGACCATG 780  
 70 GGAGCCGTTT TGGAGACTGT GGTGCGGCT CTGAATGAAG AAAAAGTACG CTTCAAGATC 840  
 ACATTATCA AGAACATGGG TACCTATGCT GCCTGGAAG CGACCAAGAC AACAGGGCAG 900  
 TACGACCTGA AGACCTTCCA GGTAAAGGCC ACCCTTGCGG ATAAAGACAA GGCACAAAAG 960  
 CTACGCCCGG GTATGTCGT GATCATAGC AAG 993

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## (2) INFORMATION FOR SEQ ID NO:157

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 801 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...801

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157

25 ATGCGTATTG TCAGTAATTT TTTGTTTCGTC TCTTTTTCGG TTTTGCTTTT TGCATCATGC 60  
CGTTCGCCAGC GAGAAAAGGT CGTTTACCTG CAAGATATCC AAACCTTTTAA TCGGGAGATT 120  
ATCGCTAAAC CATATGACGT AAAAATTGAG AAGGACGATG TGCTGAACAT CCTTGTGAGC 180  
AGTAGAGACC CGGAGCTTTT AACGCCCTAC AACCAAGTGT TGACCACTCG TGGACTGGCC 240  
CGCAACGGCT ATGGAACGAA CTCGAACGAA GGCTTCCTGG TCGATTGAA AGGGTACATC 300  
AATTATCCTA TTTTAGGCCA GATCTATGTA GAGGGCCTTA CTCGTACCGA ACTGGAGAAG 360  
30 GAGATACAGA AGAGGATTAT TTCCAGTGGA TTTATCAAGG ATCCTAGGGT AACGGTGCAG 420  
CTTCAAAATT TCAAGGTGTC GGTTTTGGGA GAGGTGAATC ATCGGGGTTT GATGTGCGTA 480  
AAAGGAGAGC GAATAACTCT TTTGGAAGCG ATCGGAATGG CCGGAGACCT GACAATCTAT 540  
GGTCGCCCGC ATCGGGTTT TGTGATTAGA GAAACCGATG GGCATCGCGA GGTTTTCCAG 600  
ACGGATCTCA GAAAGGCCGA CTGCTCGCA AGCCCGTGT ACTATCTGCA TCAGAACGAC 660  
35 GTCATCTATG TGGAGCCGAA CGACAAGAAA ACACAGATGA GCGAGATCAA CCAGAATAAT 720  
AACGTAAACG TATGGCTGAG TGTACCTCC ACTTTGGTAT CCATTTCAC GGTGACGATT 780  
ACGATAATAG ATAAGACCAA A 801

## 40 (2) INFORMATION FOR SEQ ID NO:158

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1707 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1707

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158

65 ATGAAAAAGA CCAATCTGTT TTTATCTCTG CTGGTGATCT TTATCACCAG TAGTTTTATG 60  
ACTGCCTGTG CACAGAAGTC CAAGACGAAC AAACCTACCG AAGAAGATCG GAGCCGCAAT 120  
GAGTATGTAC AGTCGATGGA TGTGCTTAGC AATATTATCG GTAACGTCAG GCTGTATTTT 180  
GTCGATACCA TAAGTATCAA ACATATGACT CGGCGTGGTA TAGATGCGAT GTTGGGCGGG 240  
CTTGACCCCT ATACCGAATA CATTCTTAC GAGGAAATGG ATGAAGTAA ATTGATGACT 300  
ACGGGAGAGT ATGCCGAGT CGGAGCTATC ATATCGCAGC GCCCGGATAG TGCTGTGATT 360  
70 ATCCGAGAGC CTATGGAAGG TATGCCCGCA GACGAAGCAG GATTGATAGC AGGCGACCGC 420  
ATCCTGACTA TCGATGGGAA AGACTTCCGC AAATCCACCA CACCGAAAGT AAGCCAGCA 480  
CTGAAAGGGA TAGCCGGTAC TGTTCGAAAG GTGACAGTAA TGGCTATGG CGAAACCAAA 540  
CCTCGTACTT TTTCCGTGAA ACGTCAAAA GTGATTATGA ATTCCGTGAC TTACAGCGGA 600  
ATGCTCGATG GCTCGATAGG ATATATCCGC TTGAACAAC TTACGGACAA AAGTGCAGAA 660  
75 GAGGTGCGCA CGGCCTTGTG GGATCTCGT GACAAACAAG GAGCGAAAGG TCTCATTTTG 720  
GATTTAAGAG GCAATGGTGG CGGACTGATG CAGGCTGCTA TCGAGATAGT CAATCTGTTT 780

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5 GTCCCTAAGG GCAAAGAGGT GGTAAACGACC AAAGGTGCGA TTGCAGAGTC GGCCTCCGTA 840  
 TTTCGCACAT TGAAGTGAAC GATGACACGC AAAGTCCCGA TAGTAGTCCT GATCGATGGA 900  
 CAATCGGCAT CTTCCTCGGA GATTGTAGCC GGAGCACTGC AGGATATGGA CAGGGCTGTA 960  
 CTGATGGGAC AAAAGAGCTA TGGCAAAGGG CTGTACAAA CGACTCGTCA GCTACCATAC 1020  
 AACCGCGTGA TCAAATTGAC TACGGCCAAG TACTACATCC CAAGCGGACG TTGTATTGAG 1080  
 CGTTTGGACT ACAGCGGCAC CAATCGGACA GGTATGGCAA CGGCCATTCC TGACAGTCTG 1140  
 CACAAAATCT TTTACACTGC TGCCGGAAGA CGTGTAGAAG ATGCAGGAGG AATCCTGCCT 1200  
 GACATCGAGG TCAACACAGA TACAGTGCCT ACATTACTTT ATTATATGGC CATCAATAT 1260  
 GACGTTTTCC ATTTGCTCAC AGGTTATGTC CTCAAGCATA AACGATTCG CAAGCCGGAG 1320  
 10 GATTTTTCCA TAAGCAACGA GGACTATGCA GCTTTCTGCA AGATGATGGA AGAAAAGAAA 1380  
 TTTGACTATG ATGCCAGAGG TGGCAAGATG CTTGACAAAC TGGAGGAACT GGCTAAGATA 1440  
 GAAGGCTACC TGCCGGAGGC CAAGTGGAGG CTTAAGACAC TACGCGAAAA GCTAAACCCC 1500  
 AACCTGCTGC GTGATCTGCT ACGATTCAAA AAGGAGATAA CAAACTATCT CAACATGAG 1560  
 ATTGCTACTC GCTATTATTA TGAGCGAGGC AGTATCCGCG AGAGTTTGCC GGAAGATAAG 1620  
 15 GTAGTCAAGG AAGCTATTAA GCTGCTGAAG GACCATCCGG AACAAATTCG ACAGATCCTT 1680  
 GCAGCTCCGA AAGCAGAGAA TAAAGGG 1707

## (2) INFORMATION FOR SEQ ID NO:159

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2943 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(14) ANTI-SENSE: NO

(16) ORIGINAL SOURCE:

(A) ORGANISM: PORPHYROMONAS GINGIVALIS

## (18) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2943

(21) SEQUENCE DESCRIPTION: SEQ ID NO:159

ATGCAAAACA AAGGATTGT GATTGTTATC ACATGGGCTC TGGCCATCAT CTGTGGTTT 60  
 TACTCTGCAT TCTCTTTCGT TACGAACCGT TACGAAAAGA AGGCTAAGGC GATGGGCCAT 120  
 GTTCCCGGAA TGGCCTATCT TGATTCCATG TCGAATGAGA AGGTCTGGTT CGGCTACACG 180  
 45 CTGAAGAAG CTCAAGCCCA GCAAAATGGT CTGGCCCTTG ACTTAAAGGG GGGTATGAAC 240  
 GTTATCTTGA AACTTAACGC AAGCGATCTG CTTCGTAACC TCTCTAACAA AAGTTTGAT 300  
 CCCAATCTCA ACAAGGCTCT GGAGATGCTT GCCAAGACA CGGAGCAATC CGACTTCATC 360  
 GATATTTTCG TGAAGGAATA TCGCAAGCTC GATCCCAAG GTGCTTGGC GGTATCTTTC 420  
 GGTTCGGGTG ACCTTCGCGA CCAGATTACC GCAAGTCTA CGGATGCAGA CGTAGTGGT 480  
 50 CTGCTCAAG AAAAATATAA TAGTGTGTA GAAGCTTCT TCAATGTGT CCGTGTCTGT 540  
 ATGATGCTT TCGGTGTGGT TGACCTAAT TTGCAGCAT TGGAGGGCA AGGGGCTATC 600  
 CTGTGCGAAC TCCCGGAGT GAAGACCGT GAGCCTGTTT GTACCTTTT GCAACCGAGT 660  
 GCCAACCTAC AGTTCTGGCG TACATACAAA TTGTAAGAGG TCAGCCGAGA CTTGATCGCT 720  
 55 GCCAATGATC GTCTGAGCGA ATTGGCTATG AACACACGG ATGCTACCCC GGAACAGAG 780  
 CCTGCAACTA CTGACTCTGT AGCTGCATCA GCGGATTCTG CTGCTGTACA AGCTGTAGCT 840  
 GATTCTGCTA CTGTAGCACA AAAAGAGGCC AAGGATGCTA CTGTAAAGA CGCACTCTTC 900  
 TCTCTGCTTA CTCCCGTGAA TCGTGGCGGT GCAAGTAGTG GTGTGGCTCG TCGTGTAAAT 960  
 ATGGCTCAGA TATCTGAAAT GCTCCAGCAA GCTCAGACT TGAAGGTTAC ACGTGAAGAT 1020  
 60 GTGCTTTTC TCTGGGTGC TAAAGCAATC GAAGACCCG AAACCAAAA GGAGACCGAC 1080  
 CTCTACGAAC TCTATGCTAT TCGTACCAAT CGTACGGAG ATCCTGATT GGGAGGTGAT 1140  
 GTAGTGACTT CCGCAAGAG TGATATCCAA AATGACTTCG GTGCTTCCA ACCGATCGTT 1200  
 TCGATGACGA TGAATGAGA AGGTGCTGT AAATGGGCG GTATCAAAA GGATAACGTG 1260  
 GGACGGGCAA TCGTATCGT TTTGGATGGT GTGGTTTATT CTGCTCGMA COTGAATGAT 1320  
 GAGATCAGGG GCGGTGCTG TCAGATCTCC GGGCACTTCA CCGTGGAGGA GCGCGGTGAC 1380  
 65 CTTGCCAAG TACTCACTC CGGTAAATG GATGCTACG TAAGCATCGA ACAGGAAGAC 1440  
 GTGATTGGTC CTACGCTGGG TSCGAGTCC ATTAAGCAG GATTCTGTC GTTCTGCTC 1500  
 GCTTTGGTIA TCTGATGTG TTACATGTGT CTGGCTTAAG GTTCTTGGC GGTCTTATC 1560  
 GCAACGGCGG CATTGATTGT AACAGCTTC TTCACATTGG CGGTATTGGC TTCTTTCCAT 1620  
 70 GCGGTGCTGA CCTCTCGGG TATCGAGGT TTGGTCTGA CGCTGGGTAT GGCTGTGGAT 1680  
 GCCAACGTAC TTATCTTGA GGTATCAAA GAAGAGCTTC GTGCGGTAA GACTCOGATT 1740  
 CGTGCCGTTA CGGATGTTA TGGCAACGCT TTCTCTGCGA TCTTCGACT GAACTTACG 1800  
 ACTATTATTA CCGGTATCAT CCTATTCTC TACGGGACGG GGCCGATTCC CGGTTTGGC 1860  
 ACTAGTTGA TTATCGGTCT TATGCTTCT TTCATTACGG CTGCTTCTT GACTCGTATC 1920  
 75 GTCTTCGASA AACTGGCGAA AAAAGGTCGT TTGGATAAGA TTACATTAC TACGAGCAT 1980  
 ACTCGCAATC TCCTTGTCAA TCCTCATAC ATCATCTTG GTAAGCGCAA GACCGGCTT 2040

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5	ATCATTCCGG	TGATTATCAT	CGTTTGGGA	CTTATAGCTT	CATTTACAAT	CGGTCTCAAT	2100
	AGGGGTATTG	AATTCCTCGG	AGGACGTAAC	TACGTAGTTA	AATTCGACCA	GCCTGTATCT	2160
	TCCGAAGCCG	TTCTGTCGGC	CTTGTCTTCT	CCCCTGCAGG	AAAAGGTATT	GGTTACCTCC	2220
	ATCGTACTG	AAGGGACAGA	GGTGCCTATA	TCTACGAACT	ATAAGATCCA	GGAGGAAAGC	2280
	GAAGAACTG	AAGCAGAGAT	TACTGACAAA	TTGTATCAGA	GCCTGAAAGG	TTTCTACACC	2340
	CAGCAGCCTA	CTGCTGATCA	GTTCCTGGAC	AATATCATT	GCTCTCAGAA	AGTAAGTCCC	2400
	AGTATGTGCA	GTGACATCAC	GAGAGGTGCT	ATTGGGGCTG	TGCTGTTATC	GATGATCTTC	2460
	ATGGCCATTT	ATATTCTGAT	TGCTTCCGT	GACATTTCTT	TCTCTGCCGG	GGTATTCTGA	2520
10	TCTGTGGCCG	CTACTACATT	CTGCATTATT	GCTCTGTATG	CGTTGCTGTG	GAAGATTCTG	2580
	CCCTTCACCA	TGGAGATCGA	TCAGAACTTC	ATCGCTGCTA	TTCTGGCTAT	CATCGGTTAC	2640
	TCGCTCAATG	ACACCGTGGT	TGTATTGTAC	CGTATCCGAG	AGACGATGAA	ATTGTACCCC	2700
	AACAGAGATC	GCTATCAGGT	GATCAACGAT	GCCCTTAATT	CAACATTGGG	TGGAACATTA	2760
	AATACGTCTT	TGACTACGTT	TATCGTTATG	TTGGTAATCT	TCATCTTTGG	AGGTGCTACG	2820
15	ATGCGTAGTT	TCACGTTCTC	GATCTGCTC	GGTATCGTTA	TCGGTACATA	CTCTACGCTC	2880
	TTTGTGCTA	CACCCCTTGC	CTACGAGATC	CAAAAGCGCA	AGCTCAACAA	AGCAGCTAAG	2940
	AAA						2943
20	(2) INFORMATION FOR SEQ ID NO:160						
	(i) SEQUENCE CHARACTERISTICS:						
	(A) LENGTH: 3051 base pairs						
	(B) TYPE: nucleic acid						
25	(C) STRANDEDNESS: double						
	(D) TOPOLOGY: circular						
	(ii) MOLECULE TYPE: DNA (genomic)						
	(iii) HYPOTHETICAL: NO						
30	(iv) ANTI-SENSE: NO						
	(vi) ORIGINAL SOURCE:						
35	(A) ORGANISM: FORYPHYROMONAS GINGIVALIS						
	(ix) FEATURE:						
	(A) NAME/KEY: misc_feature						
	(B) LOCATION 1...3051						
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160						
	ATGAAAAGAA	TGACGCTATT	CTTCCTTTGC	TTGCTGACGA	GCATTGGGTG	GGCTATGGCC	60
	CAGAATAGAA	CCGTGAAGGG	TACAGTTATC	TCCTCCGAGG	ATAATGAGCC	CCTGATCGGC	120
45	GCGAATGTCG	TGGTTGTCCG	AAACACCACT	ATCGGTGCTG	CAACCGACTT	GGATGGCAAC	180
	TTCAACGCTTA	GCGTGCCATG	CAATGCCAAA	ATGTTGAGAG	TGTCCTATTC	CGGTATGACT	240
	ACCAAGAGAG	TCGCCATCGC	TAATGTGATG	AAGATCGTAC	TGGATCCGGA	CTCTAAGGTT	300
	CTGGAGCAGG	TAGTTGTATT	GGGTTACGGT	ACGGGACAGA	AATCAGACAC	TGTTTCCGGT	360
	TCTGTGGCCA	AAGTGTCCAG	CGAAAAAGCTC	CGCGAAAAGC	CCGTTGCCAA	TATCATGGAT	420
50	GCCCTCCAAG	GTCCAGGTAGC	CGGTATGCAG	GTTATGACTA	CATCCGGTGA	CCCTACTGCC	480
	GTGCTTCTG	TGGAGATCCA	TGGTACAGGG	TCGTTGGGGG	CAAGCTCTGC	ACCAITGTAT	540
	ATCGTGGATG	GTATGCAAAAC	TTCTTTGGAT	GTTGTGGCTA	CGATGAATCC	GAATGATTTT	600
	GAATCTATGT	CCGTTTGTAA	AGATGCTTCT	GCAACATCTA	TTTATGGAGC	TCGTGCTGCA	660
	AACGGAGTCG	TTTTATTCCA	AACGAAGAAA	GGTAAATGA	GCGAGAGAGG	TCGTATTACC	720
55	TTAATGCCA	GTTACGGGAT	TTCTCAAAATC	CTGAATACTA	AGCCCTTGA	TAATATGATG	780
	ACTGGAGATG	AATTGCTGGA	TTTTCAAGTG	AAGGCAGGTT	TTTGGGGGAA	CAATCAAAAC	840
	GTTCAGAAAG	TTAAAGATAT	GATCCTTGCC	GGAGCTGAAG	ATTTGTATGG	CAATTATGAT	900
	TCTTTGAAAG	ATGAGTATGG	TAAGACATTG	TTCCCACTGG	ATTTTAATCA	TGATGCAGAC	960
	TGGCTCAAGG	CTTTGTTTAA	AACAGCACCC	ACCAGTCAAG	GTGATATTTC	TTTCTCCGGA	1020
60	GGGTCTCAGG	GAACTTCATA	TTATGCCTCT	ATAGGCTACT	TCGATCAGGA	AGGTATGGCT	1080
	CGTGAACCCG	CAAATTTTAA	GCGCTATAGT	GGCCGGCTCA	ACTTCGAAAG	TCGTATCAAT	1140
	GAATGGCTGA	AAGTTGGTGC	AAATTGTCT	GGTGCATAG	CGAATAGACG	ATCTGCCGAC	1200
	TATTTTGGAA	AGTATTATAT	GGGGTCAGGT	ACTTCCGCTG	TGTTAACGAT	GCCTCGTTAT	1260
	TATAACCCCT	TTGATGTGAA	TGGGGATTTA	GCAGATGTCT	ATTACATGTA	TGGAGCTACC	1320
65	AGACCTTCTA	TGACAGAACC	GTACTTCCGA	AAAATGAGAC	CGTTCAGTTC	CGAATCACAT	1380
	CAGGCCAATG	TAAATGGTTT	CGCCAGATT	ACTCCGATCA	AAGGCCTTAC	TTTAAAGGCA	1440
	CAGGCTGGTG	TTGATATTAC	TAATACTGCG	ACTTCTTCTA	AGAGAATGCC	CAATAATCCG	1500
	TATGATTCTA	CTCCTCTTGG	GGAAAGAAGA	GAAAGAGCTT	ATCGAGATGT	TAGCAAGTCT	1560
	TTTACAAATA	CGGCTGAATA	TAAGTTTCTA	ATTGATGAAA	AACATGATCT	TACAGCATTG	1620
70	ATGGGGCATG	AATATATTGA	ATATGAAGGG	GATGTTATTG	GGGCATCTTC	TAAAGGATTT	1680
	GAAAGTGATA	AGTTGATGTT	ACTGAGCCAG	GGAAAAACCG	GAAATAGTTT	GTCTTTGCCCT	1740
	GAACACAGAG	TCGCTGAATA	TGCCTATTTG	TCCTTCTTTA	TCGCTTTTAA	TTACGGTTTT	1800
	GACAAATGGA	TGTATATAGA	TTTCTCTGTT	CGTAATGACC	AATCCTCTCG	ATTCCGGATCC	1860
	AATAATAGAA	GCGCGTGGTT	CTATTCTGTC	GGTGAATGT	TTGACATATA	TAATAAATTC	1920
75	ATTCAAGAAA	STAATTGGCT	CAGTGATCTT	CGACTGAAAA	TGAGTTATGG	TACAACGGGT	1980
	AATCCGGAGA	TTGGTAATTA	CAACCACCAA	GCACTCGTTA	CTGTGAACAA	TTTACTGAA	2040

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5 GATGCTATGG GGCTTAGCAT TTCTACAGCA GGCAATCCCG ACCTCTCGTG GGAAAAGCAG 2100  
 TCTCAGTTCA ACTTCGGTTT GGCTGCAGGG GCTTTCATA ATCGCTTATC TGCAGAGGTA 2160  
 GATTTCATAT TCCGCACTAC GAATGATATG TTGATTGATG TCCCGATGCC TTATATCAGT 2220  
 GGTTTCTTCT CACAGTATCA GAATGTAGGC TCTATGAAAA ATACGGGTGT AGACCTTTCT 2280  
 CTTAAGGGGA CGATCTACCA AAATAAGGAC TCGAATGTAT ATGCTTCTGC GAATTTCAAC 2340  
 TACAATAGAC AGGAAATAAC AAAGCTTTTC TTCGGTCTCA ATAAGTACAT GTTGCTTAAT 2400  
 ACCGCTACTA TATGGGAAAT TGGGTACCCC AATTCTGTTCT ATATGGCTGA ATATGCTGGA 2460  
 ATCGACAAAA AAACCGGTAA GCAGTTGTGG TATGTTCTCG GTCAAGTCA TCGGGATGGT 2520  
 AATAAAGTTA CAACAAGCCA GTACTCAGCT GACTTGGAGA CAAGAATTGA TAAGTCTGTT 2580  
 10 ACTCTCTCTA TTACAGGTGG TTTCTCCTTA GGTGCTTCTT GGAAAGGACT TTCTTTAGAT 2640  
 GCTGATTTTG CCTACATCGT TGGTAAATGG ATGATCAATA ATGACCGTTA CTTTACAGAG 2700  
 AATGCAGGTG GATTGATGCA ATTAATAAAA GATAAAATGC TATTGAATGC CTGGACAGAG 2760  
 GATAATAAAG AAACAGATGT TCCAAATTTG GGACAGTCTC CTCAGTTTGA TACGCATTGG 2820  
 TTGGAGAAATG CTTCTTTCTT GCGTTTGAAG AATCTCAAAC TCACCTATGT ACTCCCAAT 2880  
 15 AGTCTTTTGG CTGGGCAGAA TGTGATTGGT GGAGCTCGTG TCTATTGAT GGC CGCAAT 2940  
 CTGTTAAGTG TTACGAAGTA TAAAGGCTTT GACCTGAAG CAGGGGGGAA TGTGGGAAAA 3000  
 AATCAATATC CTAATTCTAA GCAGTACGTT GCGGGTATTC AGTTGTCTTT C 3051

20 (2) INFORMATION FOR SEQ ID NO:161

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3042 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

30 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature  
 (B) LOCATION 1...3042

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:161

ATGACGCTAT TCTTCCTTGG CTTGCTGACG AGCATTGCGT GGGCTATGGC CCAGAATAGA 60  
 ACCGTGAAGG GTACAGTTAT CTCTCCGAG GATAATGAGC CCCTGATCGG CGCGAATGTC 120  
 45 GTGGTTGTTCG GAACACCCAC TATCGGTGCT GCAACCGACT TGGATGGCAA CTTACGCTT 180  
 AGCGTGCCTG CCAATGCCAA AATGTTGAGA GTGTCCTATT CCGGTATGAC TACCAAAGAG 240  
 GTCCCATCG CTAAATGTAT GAAGATCGTA CTGGATCCGG ACTCTAAGGT TCTGGAGCAG 300  
 GTAGTTGTAT TGGGTTACGG TACGGGACAG AAACCTCAGCA CTGTTCCGG TTCTGTGGCC 360  
 AAAGTGTCCA CGCAAAAAGCT CGCGGAAAAG CCCGTGCGCA ATATCATGGA TGCCCTCCAA 420  
 50 GGTCAAGTAG CCGGTATGCA GGTATGACT ACATCCGGTG ACCCTACTGC CGTCTGTTCT 480  
 GTGGAGATCC ATGGTACAGG GTCGTTGGGG GCAAGCTCTG CACCATTGTA TATCGTGGAT 540  
 GGTATGCAAA CTCTTTTGGG TGTGTGGCT ACGATGAATC CGAATGATT TGAATCTATG 600  
 TCCGTTTGA AAGATGCTTC TGCAACATCT ATTTATGGAG CTCGTGCTGC AAACGGAGTC 660  
 GTTTCATTTC AAACGAAGAA AGGTAAATG AGCGAGAGAG GTCGTATTAC CTTTATGCC 720  
 55 AGTTACGGGA TTTCTCAAAT CCTGAATACT AAGCCCCTTG ATAATATGAT GACTGGAGAT 780  
 GAATTGCTGG ATTTTCAGGT GAAGGCAGGT TTTTGGGGGA ACAATCAAAC CGTTCAGAAG 840  
 GTTAAGATA TGATCCTTGC CGGAGCTGAA GATTTGTATG GCAATTATGA TTCTTTGAAA 900  
 GATGAGTATG GTAAGACATT GTTCCAGTG GATTTTAATC ATGATGCAGA CTGGCTCAAG 960  
 GCTTTGTTTA AAACAGCACC CACCAGTCAA GGTGATATTT CTCTCTCCGG AGGGTCTCAG 1020  
 60 GGAACCTCAT ATTATGCCCT TATAGGCTAC TTAGATCAGG AAGGTATGGC TCGTGAACCG 1080  
 GCAAAATTTA AGCGCTATAG TGGCGGCTC AACTTCGAAA GTCGTATCAA TGAATGGCTG 1140  
 AAAGTTGGTG CAAATTTGTC TGGTCCGATA GCGAATAGAC GATCTGCCGA CTATTTTGGG 1200  
 AAGTATTATA TGGGGTCAGG TACTTTCCGT GTGTTAACGA TGCTCTGTTA TTATAACCTT 1260  
 TTTGATGTGA ATGGGGATTT AGCAGATGTC TATTACATGT ATGGAGCTAC CAGACCTTCT 1320  
 65 ATGACAGAAC CGTACTTCGC AAAAAAGAGA CCGTTCAAGT CCGAATCACA TCAGGCCAAT 1380  
 GTAAATGGTT TCGCCAGAT TACTCCGATC AAAGGCCTTA CTTTAAAGGC ACAGGCTGGT 1440  
 GTTGATATTA CTAATACTCG CACTTCTTCT AAGAGAATGC CCAATAATCC GTATGATTCT 1500  
 ACTCCTCTTG GGGAAAGAAG AGAAAGAGCT TATCGAGATG TTAGCAAGTC TTTTACAAAT 1560  
 70 ACGGCTGAAT ATAAGTTTTC AATTGATGAA AAACATGATC TTACAGCATT GATGGGGCAT 1620  
 GAATATATTG AATATGAAGG GGATGTTATT GGGGCATCTT CTAAGGATTT TGAAGTGAT 1680  
 AAGTTGATGT TACTGAGCCA GGGAAAAACC GGAATAGATT TGTCTTTGCC TGAACACAGA 1740  
 GTCGCTGAAT ATGCCTATTT GTCTTTCTTT AGTCGTTTTA ATTACGGTTT TGACAAATGG 1800  
 ATGTATATAG ATTTCTCTGT TCGTAATGAC CAATCCTCTC GATTCGGATC CAATAATAGA 1860  
 AGCGCGTGGT TCTATTCTGT CCGTGGAAAT TTTGACATAT ATAATAAATT CATTCAAGAA 1920  
 75 AGTAAATTGGC TCAGTGATCT TCGACTGAAA ATCAGTTATG GTACACCGGG TAACTCGGAG 1980

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5 ATTGGTAATT ACAACCACCA AGCACTCGTT ACTGTGAACA ATTATACTGA AGATGCTATG 2040  
 GGGCTTAGCA TTTCTACAGC AGGCAATCCC GACCTCTCGT GGGAAAAGCA GTCTCAGTTC 2100  
 AACTTCGGTT TGGCTGCAGG GGCTTTCAAT AATCGCTTAT CTGCAGAGGT AGATTCTTAT 2160  
 GTCCGCACTA CGAATGATAT GTTGATTGAT GTCCCGATGC CTTATATCAG TGGTTTCTTC 2220  
 TCACAGTATC AGAATGTAGG CTCTATGAAA AATACGGGTG TAGACCTTTC TCTTAAGGGG 2280  
 ACGATCTACC AAAATAAGGA CTGGAATGTA TATGCTTCTG CGAATTTCAA CTACAATAGA 2340  
 CAGGAAATAA CAAAGCTTTT CTTCGGTCTC AATAAGTACA TGTTCCTTAA TACCGGTACT 2400  
 ATATGGGAAA TTGGGTACCC CAATTCGTTT TATATGGCTG AATATGCTGG AATCGACAAA 2460  
 10 AAAACCGGTA AGCAGTTGTG GTATGTTCTT GGTCAAGTCG ATGCGGATGG TAATAAAGTT 2520  
 ACAACAAGCC AGTACTCAGC TGACTTGGAG ACACGAATIG ATAAGTCTGT TACTCCTCCT 2580  
 ATTACAGGTG GTTTCTCCTT AGGTGCTTCT TGGAAVGGAC TTTCTTTAGA TGCTGATTTT 2640  
 GCCTACATCG TTGTAATG GATGATCAAT AATGACCGTT ACTTTACAGA GAATGCAGGT 2700  
 GGATTGATGC AATTAAATAA AGATAAAATG CTATTGAATG CCTGGACAGA GGATAATAAA 2760  
 15 GAAACAGATG TTCCAAAATT GGGACAGTCT CCTCAGTTTG ATACGCATTI GTTGGAAT 2820  
 GCTTCTTTCC TGGCTTTGAA GAATCTCAAA CTCACCTATG TACTCCCCAA TAGTCITTTT 2880  
 GCTGGGCGAGA ATGTGATTGG TGGAGCTCGT GTCTATTGTA TGGCGCGCAA TCTGTAACT 2940  
 GTTACGAAGT ATAAAGGCTT TGACCCCTGA GCAGGGGGGA ATGTGGGAAA AAATCAATAT 3000  
 CCTAATTCTA AGCASTACGT TGGGGGTATT CAGTTGTCTT TC 3042

## (2) INFORMATION FOR SEQ ID NO:162

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2463 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2463

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:162

45 ATGAAGAAAA AGAATTTTTT GCTTCTTGCG ATTTTCGTTG CTTTGCTGAC TTTCATCGGC 60  
 AGCATGCAGG CACAACAGGC CAAAGATTAT TTCAACTTTG ACGAACGGGG CGAGGCCCTAC 120  
 TTCTCAITTA AAGTGCCTGA TAGGGCCGTT CTACAAGAGC TGGCTCTGAT CATGTCCATC 180  
 GACGAGTTTG ACCCCGTAA CAAATGAAGC ATTGCCTATG CCAGCGAAGA GGAGTTCGAG 240  
 GCATTCTCTG GCTATGGGCT CAAGCCTACA TTCTTGACTC CTCCATCCAT GCAGCGCGCT 300  
 50 GTCGAGATGT TCGACTACCG CTCAGGAGAA AAATACGAAT GGAATGCTTA CCCCACCTAT 360  
 GAAGCCTATA TCAGCATGAT GGAAGAGTTC CAAACAAAGT ATCCATCACT TTGTACTACT 420  
 TCCGTCATTG GCAAGTCCGT AAAGGATCGT AAATCTGATG TTTGCAAGCT GACGTCCTCT 480  
 GCCAATACAG GGAAAAAGCC TCGCGTGCTC TATACTTCTA CGATGCACGG AGACGAAACG 540  
 ACCGGATATG TGGTACTGCT CCGACTCATA GACCATCTGC TGTGCAACTA CGAATCCGAT 600  
 CCGAGGATTA AGAATCTTCT GGATAAAACG GAAGTATGGA TCTGCCCTTT GACCAATCCG 660  
 55 GACGAGCATC ACAGAGCCGG AAACACACCC GTACAAGGAG CTACTCGCTA CAATGCCAAC 720  
 AATGTCGATT TGAACCGTAA CTTCAAGGAT GATGTAGCCG GTGATCACCC CGATGGAAAA 780  
 CCTTGGCAGC CGGAGGCCAAC TGCATTCATG GATTGGGAAG GAAACACCTC TTTCTGTCTC 840  
 GGTGCCAATA TACATGGAGG AACAGAGGTG GTGAACATC CATGGGATAA TAAAAAAGAA 900  
 AGACATGCAG ACGATGAGTG GTACAACTG ATCAGTCGCA ACTACGCAGC CGCTTGTCAG 960  
 60 AGTATTTCCG CCGCTACAT GACCTCGGAA ACCAATTCGG GAATCATCAA CGGTTGAGAC 1020  
 TGGTATGTAA TTGCGGGAAG TCGTCAGGAC AATGCAAAAT ATTTCCATCG TCTGCGAGAA 1080  
 ATTACCTTTG AAATCAGCAA CAGGAAGTTG GTGCGGCGCT CTCAACTTCC AAAGTATTGG 1140  
 AATCTGAACA AAGAATCTCT GCTTGCTCTG ATCGAAGAAT CCTTATACGG CATCCATGGT 1200  
 65 ACAGTGACTT CCGCTGCGAA CGGACAGCCT CTCAAATGCC AGATCTTGAT AGAAAACCAT 1260  
 GACAAGCGCA ACTCCGATGT TTAATCCGAT GCTACACAG GCTACTACGT ACGTCTTATC 1320  
 AAAGCCGGCA CTTATACGGT GAAATACAAA GCGGAGGTT ATCCTGAGGC AACTCGTACC 1380  
 ATTACGATCA AGGACAAAGA AACCGTCATC ATGGACATTG CATTTGGGCA CTCGGTTCTT 1440  
 CTGCGGTGAC CCGATTTCAC AGCTTCTCCT ATGACCATCT CAGTAGGCGA AAGCGTCCAA 1500  
 70 TTCCAAGATC AAACGACAAA TAACCCACAG AATTGGGAGT GGACGTTTGA AGGCGGACAG 1560  
 CCGTCCATGA GTACAGAGCA GAATCCGCTC GTATCCTATA GTCATCCCGG TCAGTACGAC 1620  
 GTTACGCTCA AAGTGTGGAA TGCAAGTGGT TCCAACACGA TTACGAAAGA AAAATTCATC 1680  
 ACTGTCAATG CCGTTATGCC TGTAGCTGAA TTGTCGGTA CCCCAGCGGA AATAGAAAGAG 1740  
 GGCAGACGGT TATCTTTCCA AAACCAATCC ACCAATGCCA CCAACTACGT ATGGATATTC 1800  
 75 GATGSCGGCA CTCGCCCTAC CAGTGAAGAC GAAAAACCGA CTGTGCTTTA CAGCAAGGCC 1860  
 GGCCAATACG ATGTCACGCT CAAGGCGATC AGTGTTCCTG GTGAAACGGT GAAGACGAAA 1920

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5 GAAAAATACA TCACTGTCAA GAAAGCTCCG GTCCCTGCTC CGGTAGCCGA CTTCGAAGGA 1980  
 ACACCTCGAA AAGTAAAGAA AGGCGAGACA GTTACTTTCA AAGACTTGTC TACGAACAAAT 2040  
 CCGACTTCAT GGCTTTGGGT GTTCGAAGGC GGCTCTCCTG CCACCAGCAC GGAGCAAAAC 2100  
 CCGGTGGTCA CCTACAATGA AACAGGCAAG TACGATGTCC AGCTGACTGC CACCAACGAG 2160  
 GGCGGAAGCA ATGTGAAGAA AGCAGAAGAC TACATTGAGG TTATCCTCGA TGACAGTGTC 2220  
 GAGGACATAG TGGCACAGAC GGGTATCGTC ATTGCTCCGC AAAACGGAAAC GAAGCAGATC 2280  
 CTCATAGAA CCAACGCTGC TATCAAAAGC ATCGTTCTCT ATGACATCAA TGGACGGGTC 2340  
 GTACTCAAAA CTACTCCGAA TCAGCTCCGC TCGACCGTAG ATCTTTCCAT CCTGCCCGAA 2400  
 10 GGAATCTACA CCATCAATAT CAAAACGGAA AATCCGCTC GCACGGGAAA GATCCATATC 2460  
 GGG 2463

## (2) INFORMATION FOR SEQ ID NO:163

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 228 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 20 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 25 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 30 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...228
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163

ATGCGACTGA TCAAGGCTTT TCTCGTGCAA CTCTTACTGC TCCCCATTTT CTCTACAAG 60  
 CGGTTTATAT CGCCGCTTAC ACCGCCTTCA TGCCGGTTTA CCCCCTCATG TTCGTCCTAT 120  
 GCCATCGAAG CCTTACGTAA ATATGGCCCG GGCAAAGGAC TATTGCTGAG CATCAAGCGT 180  
 40 ATTCTCCGCT GTCACCCCTG GGGTGGAGT GGCTATGACC CCGTTCCG 228

## (2) INFORMATION FOR SEQ ID NO:164

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2577 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 50 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 55 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 60 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2577
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164

65 ATGGCATACG ACTTTACACA AACATTCCGC AACAGCCTGG AGTACAGCTA TCAGGAAGCA 60  
 ACCCGTCTCG GCGTCGTAGC CGTGACGCAA GATATGCTCG TACTCGGTAT CATTCGCGAC 120  
 GGAGACAATG GCGCATCGA CATCATGGG CACTATGGGA TCAACTTGT CAACTCAA 180  
 CGGTTGATCG AGTTGGAAGC CATCGCCGAG AGTTTGCCTG CTTCGCTGA GGGATCGCCC 240  
 ATCTTCAACC CTTCGGCTCG GGAGGCTATC GATGATGCCA CAGACATCTG TGCCGACATG 300  
 70 GAGGACGAG CCGTCAGCCC GGTCCATCTG TTGCTGAGTA TCCTCAACTC GACACAGGAG 360  
 AGCTTAGTAC AAAAGATATT TATGAAACAA GGTATAAAAT ACGACACCAT CCTGTCGGAT 420  
 TACTTCGGAC AGCGCAACCC CTCGGAAGGG AAGTCTCCT CCGAAATGA GATCCTCGAC 480  
 GGGTACCAAG ACAACGACTT CGACGACGAA GAGGACGAAT CCTCTCCGCC TTCGGGAAT 540  
 AGCGGGACAG GCGGAGGCTC CGGCGACGCC CCCGAACAGA ATACCGGCGG AGGCGATATC 600  
 75 ACCACCACGA CACGGAGTGG AGGCGACACG CCGCACTGG ACACCTTCGG CACCGACATC 660

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ACTGCCATGG CGGCAGCAGG CAAGCTCGAC CCGGTAGTGG GTCCGGAGCA GGAGATCGAA 720  
 AGGGTGATAC AGATACTCAG CCGGCGCAAA AAGAACAATC CGGTGCTCAT CGGCGAACC 780  
 GGTGTAGGCA AGAGTGCCAT CGTGGAAGGA CTGGCCGAAC GCATCGTGAA CAGGAAGGTG 840  
 AGCCGTATTC TTTTCGACAA CGCGATCATC AGCCTCGATT TGGCTCAGAT GGTAGCCGGC 900  
 5 ACCAATATATC GCGACAGTT CGAAGAGCGG TTGAAAGCCG TGCTCGATGA GCTGAAGAAG 960  
 AATCCGCAGA TCATCCTCTT CATCGACGAG ATACATACCA TCGTGGGAGC AGGCTCTGCA 1020  
 GCCGGATCGA TGGATACGGC CAATATGCTC AAACCCGCTC TTGCCCGTGG ACAGGTACAG 1080  
 TGCATCGGAG CCACATACCT GGATGAGTAT CGTAAGAACA TAGAAAAGGA CGGAGCACTC 1140  
 10 GAACGCGCTC TCCAGAAGGT GCCGATAGCC CCTCGACTG CAGAAGAAAC GCTGACCATC 1200  
 CTGCAAAACA TCAAGAGAA ATACGAGGAC TATCACGGTG TACGCTATAC GGACGAAGCG 1260  
 ATCAAGCGG CAGTGGAACT GACCGATCGC TATGTATCCG ATCGTTTCTT CCCAGATAAG 1320  
 GCGATAGATG CCATGGACGA GGCCGGCGCG AGCGTCCATA TCACCAATGT GGTGGCTCCG 1380  
 AAAGAAATCG AGATACTGGA GGCCGAATTG GCATCGGTGC GAGAGAACAA GCTCTCGGCC 1440  
 15 GTAAAGGCTC AGAATCTAGA ACTGGCTGCC TCCTTCGCG ATCAGGAGCG GCGCACTCAG 1500  
 CAGCAGATAG CGGAAGAGAA GAAAAAATGG GAAGAGCAGA TGTCCAAGCA CCGCGAGACG 1560  
 GTGGACGAGA ATGTAGTGGC GCATGTAGTG GCGTTGATGA CAGGCGTTCC GGCTGAGCGG 1620  
 CTGAGCAGCG GCGAAGGCGA ACGTCTGCGC ACGATGGCAG ATGATCTCAA GACCAAAGTA 1680  
 TTAGGTGAGG ACACAGCCAT CGAAAAGATG GTGATGCCA TCCAGCGCAA TCGTCTGGGA 1740  
 20 CTTGCGCAATG AAAAGAAACC GATCGGTTCT TTCTTTTTC TCGGCCCCAC GGGGGTAGGC 1800  
 AAGACCTATT TGGCCAGAA GCTCGCCGAA TACCTGTTCC AGGATGAGAA TGCCATGATC 1860  
 AGGTGGATA TGAGCGAGTA TATGGAGAAG TTCTCCGTTT CCGCTCTCGT GGGTGCCCTT 1920  
 CCGGGATATG TGGGCTATGA AGAAGGCGGC CAACTGACGG AGCGCGTAAG ACGCAAACCC 1980  
 TATTCGTGG TTCTCTTGA TGAGATCGAA AAGGCGCATG CCGATGTCTT CAATCTGCTC 2040  
 25 TTACAGTGA TGGACGAAGG TCAGCTGACC GACAGTCTGG GACGCGCGGT GAATTTCAAG 2100  
 AACACCGTGA TCATCTACAC CTCCAACGTG GGTACACGCC AGCTCAAAGA CTTCGGGCAG 2160  
 GGTATCGGT TCCGTTCGGA AAAAGACGAG GAAGCGAACA AGGAGCATAG CCGTTCGGTG 2220  
 ATCCAAAAG CTCTGAACAA GACGTTACGC CCGGAATTTT TCAACCGTTT GGACGATATC 2280  
 ATCCTCTTCG ACCAACTGGG CAAGACGGAG ATTCGCGGGA TGGTGGACAT AGAGCTTAAA 2340  
 30 GCCCTCTTGG CGCGCATCCA TCGTGCCGGA TACGACCTCG TCCTTACCGA TGAAGCCAAG 2400  
 GATGTGATAG CGACGAAGGG ATACGACCTC CAAATACGGAG CACGACCGCT CAAGCGCACA 2460  
 CTCAGAAAG AAGTGGAGGA TCGCTCACG GATCTTATCC TCTCCGACA GATCGAGAAA 2520  
 GGCAGACGC TTACGCTCTC TGCTCGCAT GCGAGATCA TCGTACAAGA ACAAACA 2577

- 35 (2) INFORMATION FOR SEQ ID NO:165  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1251 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 45 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 50 (A) ORGANISM: PORPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 55 (B) LOCATION 1...1251  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:165

ATGAATTACC TGTACATACT GATTACACTT TTACTCTCCG GCTTTTTTTC CGGTGCTGAG 60  
 ATTGCTTTCC TTTCTTCGGA CAAACTGCGT CTGAGTTGG ACAGGAATAG AGGCGATCTC 120  
 ACAGGCGAG CGTTAAACTT GCTGTATCGA CATCCGGACC AACTGGTGAC TACTCTCCTT 180  
 GTGGGTAATA ATATCGTTTT GGTAGTCTAT GGTCTGCTGA TGGCGGGATT GCTGGCCGCA 240  
 CCTTTGGCGC AATGGATTGA TAACGATGCT ATGATCGTGG TTCTCCAATC TGTCTTATCC 300  
 ACTATCATCA TACTGTTTAC CGGGGAATTT CTACCCAAAG CCATTTTCAA GACCAATGCC 360  
 65 AATATGATGA TGAAGGTATT CGCCTCCCT ATCGTAGCGA TCTATTATCT GCTTTATCTT 420  
 CTGTCTAAAC TCTTACCGG TTTATCTCGC TCTTTTATTC GTCTGGTGGG CAAGAATTAT 480  
 GTGCCTACAA CAGTAGGGTT GGGGCGCGTA GATCTCGATC ATTATTTGGC AGAAAATATG 540  
 TCCGAGAGAA ACGAACAGAA CGACTTGACT ACCGAAGTGA AAATCATCCA GAATGCGCTG 600  
 GATTTTTCGG GTATTCAAGT GCGAGACTGC ATGATCCAC GCATGAGAT GATAGCATGT 660  
 70 GAGTTGAAA CGGATATTGA AGTACTCAA ACGACTTTTA TCGATACCGG TTTGTCCAAG 720  
 ATCATTATCT ACAGACAGAA CATAGATGAC GTAGTAGGAT ATATCCATTG GAGCGAAATG 780  
 TTCTGTTGGC AAGACTGGCA AAAACGTATC AATACTACTG TATTCGTACC CGAAAGCATG 840  
 TATGCCAATA AACTGATGCG ACTACTCATG CAGCGCAAGA AAAGCATTGC GATGCTCATC 900  
 GATGAACITG GAGGTACGGC CGGAATGGTC ACATTAGAGG ATTTGGTAGA AGAGATTTTC 960  
 75 GGTGACATTG AAGACGAACA CGACACTCGC AAGATCATAG CCAACACGCT CGGCCCTCAT 1020  
 ACCTATCTGG TCAGTGGTGG TATGGAAATA GATGATGTA ACGAACGTTT TGGGTTGTCC 1080

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TTGCCTGAST CTGACGACTA CTTACCGTG GCCGGATTTA TCCTGAATAG CCATCAAAAT 1140  
 ATCCCACAGG CCAATGAGGT CGTGGAGATT GCTCCTTATA CTTTACCAT TCTCAGATCT 1200  
 TCTTCCACCA AGATCGAACT GGTGAAAATG TCCATCGACG ACCAATCGAA C 1251

5

## (2) INFORMATION FOR SEQ ID NO:166

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 879 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...879

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:166

30 ATGAACAGA ACTACTTCAA AAGAGTCTGC TCACTGCTTT GGCTGGTTTT ACCCATGCTT 60  
 ATTATGCCAT TGAAGTAGC AGCTCAAGAG ATTATTCCTA ACGAAGAGGT GTTGGGAATCA 120  
 TTGACTTTTC TTGCACCGGT TGAGGAGACA GACGCAATAG AGGCAGAGGT AGAAGCTCTG 180  
 CAGGAGATAG TCGCTACTGA GGAGATTGCG GAGCAGGCTG TTCGTTCTTA TACCTACACG 240  
 GTCTATCGTG ATGGCGTGAA GATTGCTTCA GGATTGACTG AGCCCACTTT TCTCGATGAA 300  
 35 GATGTTCTG CCGGCGAACA TACCTACTGC GTAGAAGTAC AGTATCAGGG AGGCGTATCC 360  
 GACAAAGTAT GCGTGGACGT AGAGGTGAAG GACTTCAAAC CGGTTACCAA TCTCACGGGA 420  
 ACTGCTTCCA ATGACGAAGT TTCTTTGGAC TGGGACGGTG TGGAAGAGAA AGCTGAAGAG 480  
 CCGGCAAGTG ATAAAGCAGT CAGCTACAAC GTCTACAAGA ATGGAACCTT GATCGGTAAT 540  
 ACAGCTGAAA CTCATTATGT GGAGACCGGT GTAGCCAAATG GTACATACAT CTACGAAGTG 600  
 40 GAAGTAAAGT ATCCTGACGG TGTATCTCCG AAGGTGGCTG TAACCGTGAC CGTGACCAAC 660  
 AGCTCATTTGA GCAATGTAGA TGGACAGGCT CCTTACACAT TGGCAGTAGA AGGCAAGAAG 720  
 ATTATTGGGG AAGCCCATGG TATGATCAGG CTCTACGACA TCAACGGACG TACCGTGGCC 780  
 GTAGCCCGCA ATCGATTGGA ATACATGGCG CAACACGGTT TCTATGCAAT GCGCTTCGAT 840  
 GTGGGGAATA AACACCATGT ATCGAAAATA CAAGTAAGA 879

45

## (2) INFORMATION FOR SEQ ID NO:167

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 936 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...936

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:167

70 ATGATTCCTC TAAGCGAGAG TTTTGAATCA GGTATTCAG CTATATGGAA GACCAITGAC 60  
 GCAGATGCGG ATGGCTATAA TTGGATGCAT TTGACCAATT TCACGGGACA GAGTGGTCTC 120  
 TGTGTCTCTT CGGCTTCATA CATAGGCCGGC GTCGAGCTT TGACTCCGGA CAATTATCTG 180  
 ATAAACCCCG AATTAAACT ACCACAGAC GCGTTGCTGG AAATAATCTA TTGGGTATGT 240  
 ACTCAAGATC TCACTGCTCC ATCGAGGAC TATGCGGTTT ATTCCTCTTC TACAGGCAAT 300  
 75 AATGCTGCTG ACTTTGTTAA TCTCTTATAT GAAGAGACTT TGACTGCCAA ACGGATACAA 360  
 TCCCCCGAGT TGATCCGCGG AAATCGGACA CAAGGTGTTT GGTATCAAAG AAAGGTGGTA 420

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5 CTCCCTAACG ATACTAAATA TGTGCTTTC CGCCATTTTA ATTCCACGGA TAATTTCTGG 480  
 CTCAATTTGG ATGAAGTATC TATCCTGTAT ACCCCTCTTC CCCGAAGAGC TCCGTGTCCG 540  
 CATCCGGGTG GTTACACTTA TTCTGTATTC CGTGATGGAC AAAAGATAGC GAGTGGATTG 600  
 TCGGCATTGG CATATATCGA TACGGATGTA CCGTATGGGA CTCAGAGCTA TTGTGTCCAA 660  
 GTCAATTATC TGCAAGGAGA CTCGTATATA GTCTGCAAAA ATATAGTGGT GGCAAAATTCT 720  
 GCAAAATCT ATGGGGCGGA TAAGCCTTTT GCGTTGACCG TGGTTGGCAA GACCATTGTA 780  
 GCGAGTGCTT TCAAAGGAGA GATCACTCTT TATGACATTC GTGGCCGGCT GATAGCTTCC 840  
 GGCTGCGATA CGCTTAGGTA CAAAGCGGAA AATGGTTTTC ACCTCATTAA AATACAGGTA 900  
 10 AACGGAACCTG TCTATCTGA GAAATCCAA ATCCAA 936

## (2) INFORMATION FOR SEQ ID NO:168

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2529 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 20 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 25 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2529  
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:168

35 ATGAAAAA GTTTTCTTT AGCCATAGTA ATGCTCTTTC GCATTGCCAT GCAGGGACAT 60  
 TCTGCTCCGG TTACGAAAGA GCGAGCTTTG AGTCTGGCTC GGCTGGCTTT GCGACAGGTA 120  
 TCCTTGCGAA TGGGACAAAC AGCAGTATCT GACAAGATT CCATCGATTA CGTTTATCGG 180  
 CAAGGAGATG CTGAGAGGGG TATCAGATCA CAAGAGGAAG GCTCTCCTGC ATATTTTAT 240  
 GTAGCTAATC GTGAAATATA TGAGGGCTAT GCTCTTGTAG CAGCAGATGA CAGAATACCG 300  
 40 ACAATTTTAG CCTATTCACC CATTTGGCCGT TTCGACATGG ACAGTATGCC GGACAACTCT 360  
 CGCATGTGGC TACAAATTTA CGATCAGGAA ATAGGCCTGA TACTTTCCGG AAAAGCTCAG 420  
 CTCATGAAG AGATATTACG TACCGAGGGC GTACCGGCTG AAGTACATGC TCTGATGGAT 480  
 AACGGTCATT TTGCAACGA TCCCATGCGA TGGAAATCAAG GTTACCCATG GAACAATAAG 540  
 GAACCACTGC TTCCTAATGG CAATCATGCC TATACCGGCT GTGTTGCTAC TGCTGCAGCA 600  
 45 CAATCATGCG GCTACCATAG CTGGCCGCTT CAAGGTGAAG GCTCTTTCGA TTATCATGCA 660  
 GGTTCATTAG TTGGCAACTG GTCCGGCACA TTTGGTGAAA TGTACGACTG GATCAATATG 720  
 CCCGAAATC CCGACCTTGA TAATCTGACT CAATCTCAAG TGGATGCCTA CGCCACACTG 780  
 ATGGGTGATG TGAGTGCATC TGTTTCGATG AGTTTTTATG AAAATGGAAG TGGTACGTAC 840  
 50 AGCGTTTATG TAGTAGGAGC CTTCGGAAC AACTTTCCGT ACAAGCGTTC ACTGCAGCTA 900  
 CATGTACCGC CCTTATATAC CTCACAGGAG TGGCAGGATA TGATCCGCGG GGAACCTGCC 960  
 TCCGGAAGCC CGGTCTATTA TGCAGGGAAT AACCAGAGCA TAGGACATGC TTTGTTTGC 1020  
 GATGTTATG CTTCGGATGG TACTTTCCAT TTCVACTGGG GTTGGGGAGG TGTTCCTAAC 1080  
 GGCTTCTACA AACTAACACT CCTCTCGCG ACTTCGTTGG GTATCGGAGG TGAGGGAATA 1140  
 55 GCGGTACAG ATGCCCTGCC GATCTTGCCA CTGAAAGACA TAGAAGCCGA GTATAAAAGT 1200  
 GAATCCGGAT TGAACGTAGG GTATTTCGATA TATAATACAG GTGAAGAGCA ATCAATCTT 1260  
 GACCTCGGAT ACAGATTGAA CAAGGCTGAC GGAGAAGTCA TAGAGGTGAA AACTTCATCT 1320  
 ATCAATATCT CTTGTTACCG ATACGGAGAG CATCCGAGA GTTCTCATT GGCACCTAAT 1380  
 CAGTTGTAC CAGGAATCAA CACCATCACC CTACTTTATC GTCCGACAGG CACCGAACAG 1440  
 60 TGGGAGCGG TACGGCATGC ACAGGGAGGA TATGCAATA GCATTAAAGT AAATACGACA 1500  
 GACCCGAACA ATGTCGTAGT CACGGTAGAT AATAACGAAG GCAAGCTCAG TATCGTCCCC 1560  
 AACAGCTTTG TCGCAGATCT GAATTCCTAT GAACATAGTA CGATTACAGT ACAGTCAAT 1620  
 AGCGACAGCC CTGATGAGAT CCGTACACCC GTAGCCTTTG CTCTATCTAC AGGAGCTACT 1680  
 GCGCAGCAT TAATATCTTT GGGCTGGGTA ATGGCTGAAG TTCCGGGGCG TAGCAGCAAC 1740  
 65 TATCCGGTGG TTTGGTCTAA AGACGTTCTC ACTCTCTCGG AAGGCACTA TACATTGTGG 1800  
 TATAGATTTT CCATCAACAA CCAAAAGGAT GAATGGAAGA AGATCGGAAG CGTGTCTAGT 1860  
 AAACACCGA CAGAGTATAC GCACCCCTTA TTCGAATGG GCCATAATCA AACTCTACC 1920  
 TATACGCTGC ATATGGACA CAACAGAGTA TTGCCGACT TTACACTCAA AATCTCGSA 2040  
 70 TTGCCTTTCA ATGGTGAGTT GGTGTTGTT TTCCGCCAAA CACAATCCTC ATCGGGGTCT 2100  
 TTATGGGCGC CTCAGAAAC AGTACATATC AAGCAAGGAG AAATTTCTGT ATATAAACCT 2160  
 GTTGTGCAAG GCCCTATACC TGATGGATCC TATCGTGCGA CCTCCATGC ATTGTAAC 2220  
 GGACAACAAC AGTTGTACCT CAAGGGGAAA AGGAATACA CGGTGAAGAT CGTCAATGTT 2280  
 ACAGCGGTAG AAGCAATAGA ATCGTCAGAA GAGATCAGAG TATTCCTTAA TCCGGCACGC 2340  
 75 GATTATGTGG AAATATCGGC ACCTTGCAAT CCCCAGAAA CATCTATCAT TCTTTTCGAT 2400  
 CTGTACGGCA AGATTGTCTAT GAAGAATAGT TTATCAGCGG GGCATGGCAG AATGGATGTC 2460

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AGCCGACTTC CTAATGGGGC CTACATCCTT AAGGTGGATG GATATACGAC GAAAATAAAT 2520  
 ATAGTGAC 2529

5 (2) INFORMATION FOR SEQ ID NO:169

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 870 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature  
 (B) LOCATION 1...870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169

ATGAAAAAGC TATTTCTCTC GCTCAGAGT CTGTGAATGG TCTTCGCTGT TGCAAGTTGC 60  
 GATATAATCG ACAAGGATCA AACCTCTTGG CCGGCTCCGA CCAATGTGAC ACCCGATAAT 120  
 CGGGATGACA ATCCTTCGGA GATCGACATT ACGCAGACGC ACACAGAAAA ATATGTTTGG 180  
 GCTGAAGAAT TTACCGGCCA AAAATGTCTC AACTGTCCGA AAGGTGATCG CAAACTGGCG 240  
 GCTCTCAAGG AGCAATACGG TAAGAGATTG ACTGTTGTCG GTATACATGC CGGCCCTGGA 300  
 TCTCTCGTGC CACCTCTTTT CCGTACAGAA GCCCGAGACG CATATTATAG CAAGTTCGCC 360  
 AATAATACCC CTCTCCCTGC GCTGATGGTT TCGCGCAAAA AGTTGGGCTC TTCCTAGTTT 420  
 TATGATAAGA GCTACAAAAC GTGGGACGTG CCTATTGCCG AGCAGATGGA CCAAAGGCG 480  
 AAGATCAATA TCTTTGCCGT GGCCGAATAC ACCGATACCC AAAAGATCAA GGTGACTGTA 540  
 AAGGTAATAA TACTGGAGGG GAATACACTC CCGAAGTCCA TGGTTCAGGT GTATCTGTTG 600  
 GAGGATAAGC TGATCGCTCC GCAGGTGGAT GGCAATACGA CAGTCGAGAA TTACGAGCAC 660  
 AATCACGTGT TGGGTGGAGC CGTTAATGGT ATTTGGGGCG AAGAATTGT GAATCTCAA 720  
 GATTATTGT ATACTTACGC CGTTGAACCG CTCTCGGGTA TGTCCTTCGT AGCCGAGAAT 780  
 TATTCGATTG TGGCTTTTGT ATACGATGTG CAGACGTTG AAGTGTATGA CGTTGTGCAT 840  
 GTAAAGATCA ATCCGCAATC CGATGGCAAA 870

45 (2) INFORMATION FOR SEQ ID NO:170

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 669 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature  
 (B) LOCATION 1...669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170

ATGAAGAAAT CAAGTGTAGT AGCCTCAGTT TTGGCCGTGG CTCTCGTGTG CGCCGGTTGC 60  
 GCACTGAACA ATATGGCAAA AGGCGGCCTT ATCGGCGCGG GAGTAGGAGG TGCCATTGGT 120  
 GCCGGACTAG GTAACGTAGC CGGAAATACG GCTGTGGGTG CCATCGTCGG TACTGCAGTC 180  
 GGTGGAGCAG CCGGTGCTCT CATCGGAAG AAGATGGACA AGCAGAAAAA AGAACTGGAG 240  
 GCCCGAGTAC CCGATGCTAC GATTGAGACA GTAAATGACG GAGAGGCTAT TCTGGTTACT 300  
 TTCGATAGCG GTATCCTCTT TGCGACGAAC TCCAGCACTC TGAGTCCCAA CTCAGGCACT 360  
 GCGCTGACGA AGTTTGCTGC AAACATGAAC AAAAACCCCG ACACGGATAT TCGTATCGTA 420  
 GSCCATACGG ACAATACCGG CTCCGACAAG ATCAACGATC CTCTGTCTGA GAGACGTGCA 480

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GCCAGCGTAT ATTCTTCTCT GAATTCTCAG GGTGTGAGTA TGTGCGGCAT GGCAGCCGAA 540  
 GGGCGTGGGA GCCATGAACC GGTTGCAGAC AATAGCACAG TTGCCGGACG TTCGGCCAAC 600  
 CGCCGTGTGG AGGTTTATAT CTTGCCGAAT GCCAAGATGA TCGAACAAAGC ACAGCAAGGT 660  
 ACGCTGAAG 669

(2) INFORMATION FOR SEQ ID NO:171

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1011 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171

30 ATGTCGAAAA AATCGATCCT TCTGCTTTGC TGTTCGCTGT GCTTCATTTC TGCTACGAAG 60  
 GCTGTGACCC CCGTCAGAAA TGTGCGCAAT AGCCAAGTGA ACAGCAAAGC AAAGACCGAA 120  
 CGTACAAAGC CCTCGGACTC TGTACGGTAC ATTAGCAACA TGATTGCAGA TCGGCTGGAG 180  
 TTCCGCAACA AGATTCTTC CGAAAAAGAG GTAAGAAAAG CCGAATATGA AAATCGGCTG 240  
 GCGATGGAAG CACTCAATTA CCCTGCCATA GATTATATG GTGAAGATTG TTGGAGCGAG 300  
 35 TATGTAAACC CTTTCGTGGG TGCAGSAACC GATGTCGAAA TTCGGAATC CTATGACAIT 360  
 GATTGCTCTT CGTTCGTGAT GCCCGTCGAA GATAAGCAGG TCACCTCTCA ATTTGGCTAC 420  
 CGTCGSCGTT TCGGACGGAT GCACTATCGT ATTGATCTTT CAGTGAATCG TGGCGATACG 480  
 ATACGAGCAG CCTTTGACGG GAAAGTTCGT GTACGCAGCT ATGAAGCCGG TGGCTATGGC 540  
 40 TACTACATAG TCTTGCGCCA TCCGAACGGA CTGGAGACTG TGTACGGACA CATGAGTCGC 600  
 CAATTGGTAG ACGAGAATCA GATCGTTCGA GCAGGACAAC CGATCGGATT AGGAGGCAGC 660  
 ACGGGTCGAA GCACCGGTCC TCATCTTCAC TTGAGAGCCC GCTTCATGGG TATTCCCATC 720  
 AATCCGAGTA CCATTATAGA CTTCGATAAC GGAGTCCCGC TCCGAGACAT TTACACATTC 780  
 AAACGAGGGA GCAATTCTCG CTATGCAAAA GCCTCTAAGA CTTCTTCTCG CTATGCAAAA 840  
 45 AAAGGGAAGA AAGGCAGACA AGCTTCTTCT CCTATGACCT ATAGAATCAA AAAAGGCGAT 900  
 ACTTTGGAAA CAATAGCCAA AAGGCACGGC ACTTCTGTTC AGAAACTCTG TGCTACCAAT 960  
 GGCATTGGCA AGAGTAAAT TTTGACTCCG GGCAAAGCCT TGAGGATCAA A 1011

(2) INFORMATION FOR SEQ ID NO:172

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 453 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172

75 ATGSCAAAAA TCAATTCTA TGCTGAAGGC GTCAGCCTTC CTTCGGATCAG AAGACGGATC 60  
 GTCGGTAAGT GGATAGCCGA AGTATGCAGC CGATATGGGA AAGCGGTGGG AGAAATCTCC 120  
 TATCTTTTCT GTGATGACGA ATATATCTTG AAGCCCAATC AGGAATTCT CTATCATGAC 180  
 TACTACACCG ACATCATCAC CTTGATTCC TGCGAAGCGG ATACGGTGAA TGGCGACCTG 240

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5 CTTATCAGTC TCGATACCGT ACGCTCGAAT GCCCGTGCTC TTGATCTTCG ATACGAAGAC 300  
 GAACTGCATC GTGTCAATAT CCACGGCATA CTGCATCTTT GCGGATTGAA AGACAAGAGC 360  
 AAAAAAGGATG AAGCCCAAAT GCGTGCAGCC GAAGAGAAAG CCCTTGTTCAT GCTGCGAGAA 420  
 ACCATCGGAT CGGAGCTTTC CCTATTGCAT ACA 453

## (2) INFORMATION FOR SEQ ID NO:173

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1173 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1173

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:173

30 ATGAAGGTAA AGTACTTAAT GCTCACATTG GTTGGAGCAA TTGCACTGAA CGCAAGTGCA 60  
 CAGGAGAATA CTGTACCGGC AACGGGTCAG TTACCCGCTA AGAATGTTGC TTTTGCTCGC 120  
 AATAAAGCAG GCAGCAATTG GTTTGTAAACA CTGCAAGGCG GTGTTGCAGC GCAGTTCCTC 180  
 AATGACAACA ACAACAAAGA CCTCATGGAC CGCTTAGGAG CCATAGGTTT TCTTTCTGTC 240  
 GGAAAGTATC ACAGCCCTTT CTTTGCAACT CGTTTGCAAA TTAACGGAGG TCAAGCCAC 300  
 35 ACTTTCCTCG GAAAAAATGG CGAACAGAA ATCAACACCA ATTTTGGTGC AGCTCACTTC 360  
 GACTTTATGT TTGATGTGGT TAACTACTTT GCACCATATC GCGAAAATCG TTTCTTCCAT 420  
 TTAATTCCAT GGGTAGGTGT TGGCTACCAA CACAAATTCA TCGGTAGCGA ATGGAGCAAA 480  
 GACAATGTGG AATCACTGAC GGCGAATGTA GGAGTTATGA TGGCTTTCAG ATTAGGAAAG 540  
 CGAGTAGACT TTGTGATCGA AGCACAAGCA GCTCACTCCA ATCTCAATCT AAGTCGCGCA 600  
 40 TACAATGCCA AGAAAACCTCC CGTATTGAA GATCCGCGAG GACGTTATTA CAATGGATTTC 660  
 CAGGGGATGG CTACAGCAGG TCTTAATTTC CGCCTGGGAG CCGTAGGCTT CAATGCCATT 720  
 GAIICCAATGG ACTACGCACT TATCAATGAT CTGAATGGTC AGATTAAACG TTTGCCGAGC 780  
 GAGGTGGAAG AACTCTCAA ACGTCTCTGA TCATGCCCGG AATGTCCTGA AGTAACTCCT 840  
 GTTACTAAGA CAGAAATAT ACTGACGGAA AAAGCTGTAC TGTTCGTTT CGACAGCCAC 900  
 45 GTTGTGGACA AAGATCAATT GATCAACCTG TATGACGTAG CTCAGTTTGT AAAAGAACT 960  
 AACGAGCCGA TTACCGTTGT TGGTTATGCT GATCCTACGG GTAATACTCA ATACAACGAG 1020  
 AAATTGTCTG AGCGTCGGGC TAAAGCCGTT GTTGATGTTT TGACAGGTAA ATATGGTGTG 1080  
 CCTTCCGAAT TAATCTCTGT AGAATGGAAG GCGGACTCTA CGCAACCGTT CAGCAAGAAA 1140  
 50 GCTTGAATC GTGTTGTAAT CGTTCGCTCC AAG 1173

## (2) INFORMATION FOR SEQ ID NO:174

- 55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1155 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 60 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 65 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1155

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174

75 ATGACATACA GAATTATGAA AGCTAAATCT TTATTATTAG CACTTGCGGG TCTCGCATGC 60

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5 ACATTCAGTG CAACAGCCCA AGAAGCTACT ACACAGAACA AAGCAGGGAT GCACACCGCA 120  
 TTCCAACGTG ATAAGGCCTC CGATCATIGG TTCATTGACA TTGCAGGTGG AGCAGSTATG 180  
 GCTCTCTCGG GATGGAATAA TGATGTAGAC TTGTAGATC GTCTAAGTAT CGTTCCTACT 240  
 TTGGGTATCG GTAAATGGCA TGAGCCTTAT TTGGGTACTC GTCTCCAAT CACAGGATTC 300  
 GACATCTATG GATTCCCGCA AGGGAGCAAG GAGCGTAACC ACAATTACTT TGGAAACGCC 360  
 CACCTTGACT TCATGTTTGA TCTGACGAAC TATTTGCGTG TATACCGTCC CAATCGTGTC 420  
 TTCCATATCA TCCCATGGGC AGGTATAGGA TTTGGTTATA AATTCCATAG CGAAAACGCC 480  
 AATGGTGAAA AAGTAGGAAG TAAAGATGAT ATGACCGGAA CAGTTAATGT CGGTTTGATG 540  
 CTGAAATTCC GCCTATCAAG AGTCGTAGAC TTCAATATTG AAGGACAAGC TTTTGCCGGA 600  
 10 AAGATGAAC TATATCGGAC AAAGAGAGGA AAAGCAGACT TCCCTGTAAT GGCTACAGCA 660  
 GGTCTAACGT TCAACCTTGG CAAGACAGAG TGGACAGAAA TTGTTCTTAT GGACTATGCT 720  
 TTGGTCAATG ACCTGAACAA CCAAATCAAC TCACTTCGCG GTCAAGTGGG AGAGTTGAGC 780  
 CGTCGTCTGT TTTTATGCCC TGAATGCCCT GAGCCTACAC AGCCTACAGT TACTCGTGTA 840  
 15 GTCGTTGACA ATGTGGTTTA CTTCGTATC AATAGTGCAA AGATTGATCG TAATCAAGAA 900  
 ATCAATGTTT ACAATACAGC TGAATATGCG AAGACCAACA ACGCACCGAT CAAGGTAGTA 960  
 GATTACGCTG ACGAAAAAAC CGGTACTGCG GCCTATAACA TGAAGCTTTC AGAGCGTCGT 1020  
 GCAAAAGCGG TAGCCAAGAT GCTTGAAAAG TATGGTGTTT CTGGCGATCG CATTACAATT 1080  
 GATGGAAGG GCTCATCAGA GCAAATCTAT GAAGAGAAGC CTGGAATCG TATTGTAGTA 1140  
 20 ATGACTGCAG CGGAA 1155

## (2) INFORMATION FOR SEQ ID NO:175

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 570 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 30 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...570

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175

45 ATGGAATTTT TCATGTTATT CATAGCGGCG GTTTTCGTTA ATAACGTCGT GCTGTGCGAG 60  
 TTCTGGGTA TATGCCCAT CTTAGGCGTA TCGAAGAAGG TAGACACCTC AATCGGTATG 120  
 GGTGCAAGCG TGACATTGCT ATTGGCACTG GCTACCTTGG TTACCTTCCT GATTCAAGAAG 180  
 TTCGTTTGG ATCGTTTCGG ATTGGGCTTT ATGCACACCA TTGCATTTAT TTTGGTCATT 240  
 50 GCGGCTTGG TGCAATGGT GGAGATCATA CTCAGAAGAG TATCTCCTCC CCTCTATCAG 300  
 GCACTGGGTG TATTCTTGCC CTGTATTACG ACGAACTGCT GTGTGCTCGG TGTGGCTATT 360  
 TTGGTTATCC AGAAGGATTA TACCTGCTC CAGAGCTTCG TCTATGCAAT ATCCACGGCT 420  
 ATCGGTTTCA CCTTGGAAT GGTACTTTC GCAGGTATTC GAGAGCAACT CGATATGACC 480  
 AATCTCCCA AAGCTATGAA GGAATACCT TCGGCACTCT TGGCTGCCGG TATATTGGCT 540  
 55 ATGGCTTTCA TGGGCTTCAG CGGTATCGCC 570

## (2) INFORMATION FOR SEQ ID NO:176

- 60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 558 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 65 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 70 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature

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(B) LOCATION 1...558

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:176

5	ATGTTATTC	TAGCGGCGGT	TTTGGTTAAT	AACGTCGTGC	TGTCGCAGTT	CCTCGGTATA	60
	TGCCCATCT	TAGGCGTATC	GAAGAAGGTA	GACACCTCAA	TCGGTATGGG	TGCAGCCGTG	120
	ACATTCTGAT	TGGCAGTGGC	TACCTTGGTT	ACCTTCCTGA	TTCAGAAAGT	CGTTTTGGAT	180
	CGTTTCGGAT	TGGGCTTTAT	GCAGACCAAT	GCATTTATTT	TGGTCATTGC	CGCCTTGGTG	240
	CAGATGGTGG	AGATCATACT	CAAGAAAGTA	TCTCCTCCCC	TCTATCAGGC	ACTGGGTGTA	300
10	TTCTTGUCCT	TGATTACGAC	GAAGTCTGCT	GTGCTCGGTG	TGGCTATTTT	GGTTATCCAG	360
	AAGGATTATA	CCCTGCTCCA	GAGCTTCGTC	TATGCAATAT	CCACGGCTAT	CGGTTTCACC	420
	TTGGCAATGG	TTACTTTCGC	AGGTATTGCA	GAGCAACTCG	ATATGACCAA	TCTCCCCAAA	480
	GCTATGAAGG	GAATACCTTC	GGCACTCTTG	GCTGCCGGTA	TATTGGCTAT	GGCTTTCATG	540
15	GGCTTCAGCG	GTATCGCC					558

(2) INFORMATION FOR SEQ ID NO:177

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2499 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(1v) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...2499

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:177

40	ATGAACAAC	TAAACATTAT	CAGCTTCATC	ATTGCTTTCC	TATTCTTAGG	AACGAGCGCA	60
	TCGGCTCAGC	AATCGGGCGG	ATCCGTTACA	GGTACCGTAG	TGGACAAAAG	CTCAAAAGAA	120
	CCTATCGCAT	ACGTACAAGT	ATTCTGTCAA	GGAAACCACT	TCGGAACTTC	CACGGATGCA	180
	AACGGAAACT	ACTCGATCAA	GGGAATCCCT	TCGGGTAAAT	AAACTATCGT	AGCCCGACTC	240
	ATGGGTTACT	CCACTTGCGA	AGAAAAAGTA	CATATAGAAA	AGGGTGGTTC	CGGCCACGTA	300
45	GACCTCTATC	TGACCGAAGA	GATTCTCTCT	CTCGATGGGG	TAGTGGTATC	TGCCAATAGA	360
	AACGAGACTT	TCGCGCGTCA	AGCACCCCTG	TTGGTAACGG	TACTGTGCGC	GGAACTTTTC	420
	CTCAAAACCA	ACTCTACCAA	CCTGAGTCAG	GGACTTAAAT	TCCAGCCCGG	TCGCGCGGTG	480
	GAGGACAAC	CTCAGAACTG	CGGTTTCAAC	CAAGTTCTGA	TCAATGGACT	CGAAGGAGCC	540
	TATTCGCAAA	TTCTTATCGA	CAGCCATCCC	ATCTTCAGTT	CGCTTGCCGG	TGTCTATGGC	600
50	TTGGAGCAGA	TGGCTGCCAA	TATGATCGAA	CGTGTAGAAG	TAATTCGCGG	TGGAGGTTCC	660
	GCTCTGTTCG	GCTCTAATGC	TGTGGGAGGC	GTATCAACG	TAATTAAGAA	AGAAACCGCT	720
	CGCAATTCCG	CCGAGATCAG	CCATTCTACG	ATGACCTTCG	ACCACGCGAA	AGGGTGGGGG	780
	AGCTTCCAAA	ATACGACCCA	GTTCACCGGT	TCTATGCTGA	CGGAAGACCG	CAAAAGCCGGT	840
	GTCTGGTAT	TCGGCCAAAC	CAACTACCGT	CCCGGACAGG	ATATAGACGG	CGACAACCTT	900
55	ACCGAACTAC	CCAACTCTCG	CAACCGCTCG	CTCGGTTTCC	GCTCATACTA	TAAGACCGGT	960
	CTCTACAGCA	AAGCAACCOCT	CGAATATCAC	AGCATGCAGS	AGTACCGTGC	TGGTGGCGAC	1020
	AGACTGGACA	ATCTCTCTTT	CGAAGCCCG	ATAGCGGAAT	ATCTCCAGCA	CTATATCAAT	1080
	GGCGGAAGTT	TCAAATTCGA	TCAGGGCTTC	AGCGGTGGCA	AGGATTCTTT	CAGTCTGTAT	1140
	GCTTCAGCAC	AAGACGTTCA	GGTCTGTAGC	TACTACGGGG	GTGGCGACTA	TACCGAAAAT	1200
60	CTGCTGAACG	GAGCAGTTCA	GAGTGGAAAG	ACCGAATCGG	ACGAATACAA	CGATGCTTTC	1260
	ACGGCTCTTA	CTTCTACCGG	GACTACCAAG	GGATTCTGAT	TGCAAGGAGG	AGGTATGTAC	1320
	CGTCATACCT	TCGGAGAAAA	CTGGGACTTT	ACCGCGGAG	TCGAATATAT	CTACGGCCAA	1380
	CTCGATGACA	GAAGCGGCTA	CAGACCGAGC	AJATAGATC	AGAATACCTC	TACTTTTAGT	1440
65	CAGTACGACC	AGCTCGAATA	TAAGACGGAG	AAGTTAAGTG	CCCTTATCGG	AGCACGTATC	1500
	GACTATGTTT	TCTCAATCA	GGATGGCAAA	CGCTATATCG	ATCCGCTCTT	CATTTTCAGT	1560
	CCTAGAGCCA	ACGTACGATA	CAATCCCAAT	AAGAACTCTA	GCTTCCGACT	CTCATACAGC	1620
	GAAGGATTCC	GCGCTCCTCA	GTATTTCGAT	GAAGATCTGC	ACGTAGAGTT	GGCCGGTGGT	1680
	ACTCTCTATC	GCCGTGTCTT	TTCCDCAAT	CTGAAAGAA	AACGTTACAG	AAGCATCAGT	1740
	GCTTCTTTTG	ATTATTACCA	CAGAGCCGAC	GAATGGCAAT	TCAATATCAT	GGGAGAAAGC	1800
70	TTCTCCACCT	TTATCAGCAA	TCAGTTCAAA	CCATCCGATA	AGGTCGAAAC	CACGAGCGAT	1860
	GGCAAAGAAT	GGATCATTCG	TACCATCTAC	AACGACAAGG	ATGGAGTATC	GAGGTATAT	1920
	GCTGTGAATC	TGGAGGGAAG	AATCGCTTAC	AACAAATCGT	TCGACCTCCA	GCTCGGCGGT	1980
	ACATGGCAGA	GAAGCCGCTA	CGGAAGCATC	TATACCGCTG	TGGAAGCGGA	CAAAACCAACG	2040
	GGACAAGCCG	AGATCTCTGT	GAAAGACTAT	GTACGCACTC	CGAATCTGTA	CGGCTATTTC	2100
75	GTGTGCTACG	TACGTCCTAC	CGAGCACTTC	GCCATCAATC	TCTCCGGTAC	ATTCACGGGC	2160

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5 AAVATGGATG TAGTACACGA AGCCTATGAA GGCATATTG CCGCAGACA CATAGCTCCG 2220  
 GACGGATCGT TCGACTTTGA AATGAATGGT CAGCAATTCA AAGGTTTGGC CGAAGGTCAT 2280  
 GCCAAGCTCG TCAAGACTCC GGCCTTCGCC GATATAGACC TCAAGCTGAG CCACGACTTC 2340  
 CACCTTGCTT CCACTATGAC CTGGAATTG AATGCCGGA TACAGAACAT ATTCAACAGC 2400  
 TATCAGAAAG ACACGGACAA GGGACCGGT AGAGCTTCTA CTACGTATA CGGTCTATG 2460  
 CAGCCAGAA GGATTTTCTG CGGTACAAAG ATCAATTTT 2499

## (2) INFORMATION FOR SEQ ID NO:178

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2673 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 20 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 25 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...2673  
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:178

ATGTACAAAA AGATTATTGC CGTAGCAGCT CTCTTCTGCG CCAGCATAGG GATCCTGAAA 60  
 GGACAGTCCT CGGATCTGAC CCCTCAGGAT ACTATATATA GCCCTGAAAT ATCCTATGCC 120  
 AAGCCTATTC ATAAGACCAT AGCATCTATT GAGATCGAGG GAATGAGGTC TTTCGATGAC 180  
 35 TTTGTCTTGC GCAATCTTTC AGGCTTGGCT GTAGGTGATG AAGTCCTGAT TCCTGGAGAT 240  
 GCCATGCTCG CTGCCGTGAA TAGAATTATG CGTCAGGGCT ACTTCTCAAA TGTGCGAATC 300  
 ATCGCGGATA AATATGTCGG CAATAAAGTC TATCTGAPAA TCATTGTGAC TGAACGTCTT 360  
 CGCATCAGTA AGGTACTTTT TAGCGGGGTA AAGAAGTCTG AGAGAGAAGA TCTTGAAATG 420  
 AAAATCGGTC TTCCGCGAGG GATTGAGATG ACCAGAAATA ATGAAGACAA GGTCAGGCCAA 480  
 40 ATCGTACAGA AGTATTTTAC TGAGAAAGGT TATCGCGATG CCAGCATACG GATACGCCAG 540  
 GAACCGGATC TTTCGAAAGA TGGCTTTGTC AATGTGCTTA TCTCGATGTA GAAGAAAAGC 600  
 AAAACCAAGG TGAATGAAT TATTTTTC CCACAACAGG CCTTAGCAA TCATAAGCTA 660  
 AGAATGGCGA TGAAGAACAC CAATGCCCAA TTCAGTCTTA GAAAGCATAT TCGCTCATCT 720  
 TTCTTGAAC TTTTGTAGTAC TCATAAGTTT GTGGAAGAGA GCTACCGTGA AGATTGGTTC 780  
 45 CGATTGATAT AGAAGTATCA GGAATATGGA TATCGTGATG CTGAAATACT GACCGACAGT 840  
 TCGCTGAGGG CTCCTGACGG CAAAGAGATG GATATTTATC TCAACATCGA AGAGGGGCGAG 900  
 AAGTATTATA TTAAGGATGT CAACTTTGTG GGCAATTCAC AATATCCATC GGAGTATTTC 960  
 GAACGAGTGC TCGGATATAA ATCCGGAGAT GTGTACAATC AGAGACGATT GGCTAAGCGT 1020  
 CTCATGAAS ATGAAGATGC TGTGGGGAAC CTGTACTATA ACAATGGCTA TATTTTTCG 1080  
 50 TGGGTCTGAT CCGTGGAAC AAATGTAGTG GGGGATTCTG TTTCCCTTGA TATTCGTATA 1140  
 GCGGAGGGGA AGCAGGCCAA TATCAATAAG GTGATCATCA AAGGAAATAC TGTCTGTAC 1200  
 GAAGACGTAG TACGCCGAGA GCTTTACACA AAGCCCGGCC AGCTCTTAG TCGCGAGGAT 1260  
 ATCATTAAC CTATTCTGCT CATCAATCAG CTGCGGATT TCGATGCCGA AAAATCTATT 1320  
 CCCCCTCGGA TTCCCAATCC CGAAACAGGA ACAGTGGATA TAGAGTATGA TTTGGTGGCG 1380  
 55 CGTAGCAGTG ACCAATTGGA GCTTCTGTC GGTGAGATC AGTCCGACT TCTGTCCGA 1440  
 GGAGCCATTA AGTTCACGAA CTCTCTGTC GGCAACTTGC TCCATCCCTC GATGTATAAG 1500  
 AAAGGGATCA TTCCGCAAGG GATGGGCAA AACTATCAC TGAGTGCTCA GACCAATGGA 1560  
 AAGTACTATC AGCAGTATAG TGTACATTT ATGGATCCAT GGTGTTGGGG CAAGCGGCCG 1620  
 GATACTTCA GCTTCAGTGC ATTCTATTCC AAGACTACGG CGATTGACTC CAAGTTCTAC 1680  
 60 AATAGCAATG CCGGCAACTA CTATAATGCC TACTATAATA GCTACTACAA CAACTATAAT 1740  
 AGTTATTACA ACGGTATGTC GAACTATACC GCGGACCTCT ATACTCAGGC CAGCGATCCG 1800  
 GATCGTTCCG TTGAGATGTT AGGTACTTCG ATCGGTTACG GTAAGCGTTT GACTTGGCCG 1860  
 GACAATGGT TCCAGATTTA TACTTCTCTG AACTACACCT ACTATAGACT GCGAAATTGG 1920  
 AGCTACAAAT CCTTCCAAA TTTCCATCAT GGTCTGGCTA ATGATCTCAA CTGGAGCTG 1980  
 65 CGTCTCTCTG TACTTCCAT CGATAATCCT ATTTATAACA GAAGCGGATC GGATTTCATG 2040  
 GTTCTGTGTT CTGCTACTCT TCCTTATTCT TTGTTGGACA ATCATGACTA TGCCAGCCAG 2100  
 AACCTCAGCG TAAGCGATCG TTACAGATTJ ATCGAGTATC ACAAGTGGAA GTTTAGAGGA 2160  
 CGAGTTTTTA CTCCATTGCT CAATCCTGCT ACSCATAAAT ATACACCGGT GCTCATGAGT 2220  
 70 CGAGTGGAGG GAGCAGTTCT TGGTTCGTAT AATTCCAAFA AGAAATCTCC TTTCCGTACT 2280  
 TTCTATATGG GAGGTGATGG TATGTCCAGC TATTATGGTG GCTACATGAA TGAGACTATA 2340  
 GGTTTGGGTG GTTATAAGAA CGGATCTATT GCCGGTAATA ACTACGACTA TGCATATGCT 2400  
 TATATCGGCG TTACGATGGA ACTACGTTTC CCGATTCTGT TTGAAAACCT ATTCAATGCG 2460  
 TGGCTCTTAT CTTTTCGCGA AGCAGGCAAT GCGTGGCGCA GTATCGACAA TTATAATCCC 2520  
 75 TTTAACTCTA AGCGATCGGC CGGTGTAGGA TTGCGTGTAA CGTTACCGAT GGTGGAATG 2580  
 CTCGGTATCG ATTGGGGATA TGGCTTTGAC CGTCCGGACA ATTCCTCTAC GCGAGGAGGA 2640

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AGCAATGTCC ACTTTGTGCT CGGACAGGAG TTC

2673

## (2) INFORMATION FOR SEQ ID NO:179

- 5 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 522 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- 15 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 20 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...522
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179

ATGAATGGCG ATATGAAACG GTTTTGTGATT TTGATCGGCT TTGCACTGGC GGTAGCTTTC 60  
 TCCGGTTTTT CCCAAAAGTT CGCTTTGGTA GATATGGAAT ATATCCTCAG GAATATTCCT 120  
 GACTATGAGA TGATGAACGA ACAGCTGGAA CAGGTGTCCA AGAAATGGCA AAATGAAATC 180  
 GAAGCTCTCG AAAATGAAGC CCAATCTATC TATAAGAAGT ATCAGAGCGA TCTCGTATTTC 240  
 TTGTCTGCTG CACAGAAGAA AACCCAAAGAA GAGGCTATCG TAAAGAAAGA GCAGCAAGCA 300  
 TCCGAGCTCA AGCGGAAGTA TTTCCGGCCCG GAGGGGGAGC TGTATAAGAA ACGCTCCGAT 360  
 CTGATGAAGC CTATTCAGGA TGAGATTGG AATGCTATCA AAGAGATTGC CAAGCGTAAC 420  
 AACTATCAGA TGGTGCTTGA TAGAGGTACG TCCGGAATTA TCTTTGCCAG TCCGTCTATT 480  
 GACATTAGCG ACCTTGTACT GAGCAAGATG GCCTTTAGCA AG 522

## (2) INFORMATION FOR SEQ ID NO:180

- 40 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 510 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 45 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 50 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 55 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...510
- 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180

ATGAAACGCT TTTTGATTIT GATCGGCTTT GCACTGGCGG TAGCTTTCTC CGGTTTTTCC 60  
 CAAAAGTTTCG CTTTGGTAGA TATGGAATAT ATCCTCAGGA ATATTCCTGA CTATGAGATG 120  
 ATGAACGAAC AGCTGGAACA GGTGTCCAAG AAATGGCAAA ATGAAATCGA AGCTCTCGAA 180  
 AATGAAGCCC AATCTATGTA TAAGAAGTAT CAGAGCGATC TCGTATTCTT GTCTGCTGCA 240  
 CAGAAGAAVA CCCAAGAAGA GGCTATCGTA AAGAAAGAGC AGCAAGCATC CGAGCTCAAG 300  
 CGGAAGTATT TCGGCCCCGA GGGGGAGCTG TATAAGAAAC GCTCCGATCT GATGAAGCCT 360  
 ATTCAGGATG AGATTGGAA TGCTATCAAA GAGATTGCCA AGCGTAACAA CTATCAGATG 420  
 GTGCTTGATA GAGGTACGTC CGGAATTATC TTTGCCAGTC CGTCTATTGA CATTAGCGAC 480  
 CTTGTACTGA GCAAGATGGG CTTTAGCAAG 510

## (2) INFORMATION FOR SEQ ID NO:181

- 75 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 489 base pairs

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

5 (ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO  
10 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
(ix) FEATURE:  
15 (A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...489  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181

20 ATGAAGAAAT TTTTCTCAT GCTTCTGATG GCTCTTCCTT TGAGCCTCTT GGCACAAAAG 60  
GTGGCAGTGG TAAACACTGA GGAGATCATT TCCAAAATGC CGGAACAAGT AGCTGCTACC 120  
AAACAGCTCA ACGAATTGGC CGAAAAGTAT CGCCTTGATC TCAAGAGTAT GGACGATGAG 180  
TTTGCCAAAA AGACAGAAAG ATTGTAAAG GAAAAAGACT CTCTACTGGA GAACATCCGC 240  
AATCGTCGTC ACCAGGAACT TCAGGATATT CAAACTCGTT ATCAGCAGTC ATACCAAACG 300  
25 ATGCAGGAGG ATTTGCAAAA GCGCCAACAA CAGCTTTTTC CTCCTATCCA ACAAAGGTG 360  
GCTGATGCCA TCAAGAAAGT GGGTGACGAA GAAAACTGTG CCTACATCAT GGAGGCCGGT 420  
ATGATGCTTT ACACCGGAGC TACTGCTATT GACTTGACCG CAAAGGTAAA AGCGAAACTC 480  
GGAATCAAG 489

30 (2) INFORMATION FOR SEQ ID NO:182  
(1) SEQUENCE CHARACTERISTICS:  
35 (A) LENGTH: 2481 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular  
(ii) MOLECULE TYPE: DNA (genomic)  
40 (iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO  
45 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
(ix) FEATURE:  
50 (A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...2481  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182

55 ATGAAGGAAG CTATTCCCCG AAAGAACAAG TATATAAAGC TCAACGGTAT ATACAGATTG 60  
TCATTCAATC TGCTATGCTG CCTGCTATGC TCTCAGGCAG CTATGGCACA AGGCGTCAGG 120  
GTATCGGGCT ATGTGCTCGA CCGTGGGGAA AAGCCGATCC CGTTCGCCGG AGTCAAAGTG 180  
CGTGTACGGG GGACAGGGCGC AACGACGAAT CTGAAAGGAT ACTACGAGTT TCGGATGAAG 240  
GCCACGACGG ACAGCATCAC GATCGAGTTC AGCTCCATGG GGTACCAAGG GGTAAGTCGC 300  
60 AGCTTTCCGT CTCTGACCAA GGACACTCGG CTGAATGTTT GTTTGGCAGA GGCCGAGATG 360  
GASCTTTCGA GCGTGACGGT ACAGGCCACA AAACGCAGAC TCAACACGAT GGAGCGCGTC 420  
AATACCCGAG ACCTTCGTGT CAATGCAGGG CCTACGGGAG GGGTGGATC GCTCATCAGT 480  
ACCTACGAG GAGTAACGCA GAACAATGAA CTAAGCTCGC AATACTCGGT TCGCGGAGGA 540  
AGCTACGATG AGAATATGGT CTATGTAAAC GGAGTGGAGG TTTATCGCCC GCTGCTGGTT 600  
CGCTCTGCAC AGCAGGAAGG TCTGAGCTTC GTCAAACCGG ATCTGACACA ATCCGTACAG 660  
65 TTCTCCGCGG GAGGGTTCAC GGCCGACTAT GGCGACAAGA TGTCCTCGGT ACTGGATATT 720  
CGCTACAAGC AACCGCAGGA GAAGGAAGGA GCGGTACTCC TCGGGATGCT ACAATCGAAT 780  
GCCTACTATG GCAGCAGTGC CGGAGCCTTC AGCCAAATCA CGGGTGTACG CTACAAGAGT 840  
GCCAAATCGC TCTTGGGCAC TACGGACACG AAAGCCGAAT ACGATCCGAT CTATGCGGAC 900  
GACAGACAT TCATGACGTA CCGTTTCAGC CCCAAGCTGT CGGTAGTTT CCTCGGCAAT 960  
70 ATTTGCAAAA CTGCTACAA GTTTGTCCCT CAGACCCGTG AGACGAGCTT CGGTACACTG 1020  
AGCGATGCCA AAAAGTTGAA GATCTTTTTC GACGGTCAGG AACAGATOS TTTCTGACC 1080  
TACTTCGGTG CCTTCAGCAT GAACTTCGTG CCGGACGACA AACAGCGGCA TACGGTTACG 1140  
CTTTCGGGCT TCAACAGTAA CGAACGGGAG ACCTACGATA TTCAGGGAGA ATACTTTCTG 1200  
AACGATGTGC AGCTGGGGGC GGACGGAAT GCTTCGATGG CTTTCGGGTC AGAGAACTCC 1260  
75 AACGGCTTGG GCATCGGGCG CAATCACGAG CATGCGCGCA ACAGGCTGAG CTACCCGCTG 1320

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5 CTGAACATGG GTTACAGAGG GGAGATGAAG CTGAACGAGA AGCATCGCCT GCAAGCCGGC 1380  
 GTATCGGCAC AGATGGAGAA AATAGCCGAC CATATCAGCG AATGGGAACG GAGGGATTTCG 1440  
 GTAGGATACA ACCTACCTCA CTCGGAGACC GTATTGCTGA TGTACAATAA CCTATATGCC 1500  
 10 GATACGACAG TGAGGGGAAC GCGCTTGTGG GCATTCTGTAC AGGATCGATT CAACCTCAGC 1560  
 ATGGGAGGAG GTACATTTTC TCTCATTCGG GGTATCAGAG CTTCGTGGTG GAGCTTCAAC 1620  
 AAGGAGTTGC TCGTCAGCCC ACGTATCAGC GTGGGTATT CTCCGGAAAG CAACCCGGCT 1680  
 TTGGTACTGC GTGCAGCCGC CGGACTTTAT TATCAGGCAC CGTTTACAA AGAGCTAAGG 1740  
 CAGAGCATA AGGATGCCGA AGGCAATAAC GTGGTGTCC TCAACGAGAA GATCCGCTCT 1800  
 CAGGGAGCTT TTCACATTCT CGCAGGAGCA GACTATACCT TCGAAATGGG GGGCGGAAAA 1860  
 15 TACAAGTTTA CGGCAGAGGC TTAACAAG AGCCTGTTC ACATCAACCC GTATATAATA 1920  
 GAGAACGTGA AGATCCGCTA TCTGGGCGAA AACATCGGTT CGGTTATGC TCGGGGTATC 1980  
 GATCTCAAGC TCTTCGGCGA ACTGGTACCC GGAGTGGATT CGTGGCTGAC GGCTTCCATT 2040  
 ATAAAAGCCC GTCAGAAACT GGATGGCTAC GGTCTTTTAC CACTGATGAA CGCACCCACT 2100  
 20 TACAATTTCT CCTTCTTCTC TCAGGAGTAC GTGCCGGGCA ATAAACGCAT CACAGCCACC 2160  
 CTGCGGGCTG CACTAAGCGG AGGATTGCCC CAGCTCAATC CGAGCAAAGG GCTTAGCTCG 2220  
 CUGGCTTTTA CCGCACCGGC CTATAAGCGT GTCGATCTGG GGGTAATGTA CAAATGGCTC 2280  
 CACCCGGATG ACTCCTTTGC CGGCCGAAGC AAATGGCTAA TGGGAGTAAA AGGGGCTTAC 2340  
 ATAGGGGCTG ACCTCTTCAA TCTGTTCGAC ATGACCAACG TCAATTCTTA CTACTGGGTG 2400  
 25 TCGGATGCTC ACCAACAGCA ATACGCCGTA CCGAATACC TGACACGCCG CCAATTCAAC 2460  
 CTGCGTCTCC TCGTCGAATT C 2481

## (2) INFORMATION FOR SEQ ID NO:183

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2016 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 35 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GIUGIVALIS  
 40 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2016  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:183

50 ATGTACAGCG GACATCATAA AATCCATTAT CCTTTTCTTA TCCTGTTGGT ATGCTTGGCT 60  
 TTTGCTGCCT GCAAGAGCGT GAAGTTGAAA GATGCGGAGA AGGCACATGA TCGCCAAGAG 120  
 TATACCAAGG CTGCCGATAT GTACAATACA TTATACAGGC GTACCCGAGC AAAGCAGGTG 180  
 GAGATGAAAG CTTATACGGC TTTCCGATCC GGTGAAACT ATCGTGCCGC CGGCAGACAA 240  
 55 GCCAAAGCTT TGGGTGGCTA TCTGAATGCC AGACGCTACG GGTATCCGGA TTCTGTGGTA 300  
 CTGCTCCGTT TGGCAGAGAC TTATCAGCAA GGAGGTAAC ATAAAGGAAGC CGAGGTACTC 360  
 TTCCGTGGAT ATCTGGAAGC TTATCCGAAA AGTTATTTTG CAGCTATCGG TTTGGAGGGG 420  
 TGTCTCTTTG CCGGCCAGCA AAAGGAATAT CCTACACGTT ACCGGATAAG GCGAGCTGCC 480  
 GAGTGAATTT CGGCACGGGG CGACTTCGGC CCGGCTATG CACCCGATGC TTCGGCTCTC 540  
 60 TATTTACAT CGAGCAGAAG CAAAGACGAC GGTTCGATA ATAGCAGCAT AACGGGACTG 600  
 AAACCAACG ACATTATAT CATCAAACGA GATGCACAAG GACGATGGGG ACGTCCCGAT 660  
 AGCGTGTCCG GAGGAATCAA CACTCCATGG GATGAAGGCG TGCCAACGAT CACGCCCGAT 720  
 GGTAGTACCA TATATTATAC GTTGGCGCAG CAAGGAGCCG ATTACGACCG TACGGTACAG 780  
 ATCTATTCCG CCGCTCGGAG CGGAGAAGGC GGTGGAGCA ACGGTTCCGT CGTGGACATT 840  
 65 ATGCGCGATT CGCTCCGTAT GGCTGCTCAT CCCTCTATGT CGGCATCCGG CGATTACCTG 900  
 TATTTCGTCA GCAATATAGG CGGTAGCTAT GCGGCAAGG ATATTTATCG TGTCAAGGTG 960  
 TCGGATCGTT CTTATGGTTC ACCGGAGAAT TTGGGGCTTG ATATCAATAC GCGGGGGGAC 1020  
 GAAATGTTTC CCTTCATAGA TGGGGATAGT ACCCTTTTCT TCGCTTCGGA CGGACACGCC 1080  
 GGTCTGGGAG GACTGGATAT TTTCAAAGCC ACGCTGGACT CTACCGGCCA ATGGCATGTA 1140  
 70 GTCAATATGG GACRAACGGT CAATTCCTCT GCCGATGATT TCGGCTTGGC TGTGGAGCCT 1200  
 AAAGGCAAAA ACAAGAAGA AGCTTTGCCG GACAACGGAG TCAAAGGTGT ATTTGTGTTCC 1260  
 AACCGAGGCG ATGCACGCGG ATGGCCGCAC CTCTTCCATT TCGAACTGCC GGCTATCTAC 1320  
 ACCGAGATTG AAGGTTATGT GATGGACAGA GAAGAAAATC CCATAGCCGG AGCCACTGTC 1380  
 AGGATCGTAG GCGAACGCGG CCCCGTAGGA CAGGATTCG TGAATCTCG TGACGATGGC 1440  
 75 TCCTATAAGA TGAGCGTGCA GGGCGATACT CGCTATGTAA TGCTTGGCG AGCATCGGGT 1500  
 TATTGAAATC AGTAGCTAGA ACTCAAGACC GATACCGCCA ASCAGAGTGA GACCTACTAT 1560  
 GTGGACTTTT TCCTTGCAAT CGGTGAGAAA GCGAGGGGCT TGCAAAATAT TTTCTATGAT 1620  
 TTCGATAAAG CTACTCTTCG CCCGAAAGC ATGAAGAGCT TGGACGAAT GATTCGTATC 1680  
 CTCACGACA ATCCGATAT TCGGATCGAA TTGGGTTCSC ATGCCGACG GAAGGCCCC 1740  
 GATGCTTACA ACCTCGGACT ATCTGACCGG AGAGCCAAAT CCGTGGTGGA TTACCTCAGC 1800

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AGTCGTGGCA TAGCGGCCGA CAGGCTTACG TGGAAAGGCT ACGGTAAGTC TGTCCCCAAG 1860  
 ACGGTGACAG CCAAAATTGC CGAACGGCAC GATTTCCTGA AGGAAGGCGA TGTGCTCACC 1920  
 GAGGAATTGG TAGCACCTTT GACCGAGGAG CAGCAGTCAG TCTGCGACCA ACTGAACCGT 1980  
 CGTACCGAGT TCCGTGTGAT CGAAGAAGAG TTGCGT 2016

5

(2) INFORMATION FOR SEQ ID NO:184

10

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2124 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

15

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

20

(111) HYPOTHETICAL: NO

(111) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORPHYROMONAS GINGIVALIS

25

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...2124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184

30 ATGAAAAAGT TTTTCTTCGC GCTACTATCG ATTGGTATTT CAGCGCAGGC TTTTGCCAAG 60  
 ACGGACAAAG TCCCCGACAGA TTCGCTACGA GTACACAATC TTCAGACCGT CACGGTCTAT 120  
 TCTACACGCA CGGCCGTACC TCTGAAAAAG ATACCGGCCA AGATGGAATC CATCTCATCG 180  
 CGCAACATCA AGCAGTCCGG CTTTAAACAAC ATGACCGACA TCCTCAAGAC GCAAAAGTTG 240  
 CTCGATGTCA TACAATACCC GGGCTTTAGT TCGAACATCG GTATCCGCGG TTTCAAGCCC 300  
 TCCGCAAGT ATGTAACCGT ATTGGTAAAC GGCATCCCTG CGGGAACGSA CAATATCTCT 360  
 ACGCTCAACA CGAGCAACAT CGAACAATC GAGATCCTCA AAGGCCCGTT CTCTTCCATC 420  
 TACGGCACCA ATGCCATGGG CGGTGTGGTG AACATCATCA CCCACAAATC CAAGGACAAG 480  
 ATCCATGGCA ACGTTTCTCT CTTCGGCGGT AGCTACCAGA CCATGGCCGG ATCATTCAAC 540  
 TTGGGTGGCC GCTTCGAGGA TATTCTTCTA TTCGATCTTA GTCTGGGCTT GGACAAGCAG 600  
 40 AACAGGACT ATAAGACCGG ATCAAAACAT TFCCTATCCC TGAGCAAACT GGAAGAAGCT 660  
 ATAGTAGATG TAAATGCTAC CAAAAACAG AAAATGAAGG GGAGCGACTA TACTGTAGCA 720  
 ACGGGACGTC TGGCTTTCGG TATCGACTTC ACGCCCGAAT GGTCCCTGAA TCTGTATCAA 780  
 AACGTATTCC TCGGAGATGC GATCCCCGTA GGAGGATCTA TATGGGGCGT TTACGGAGAA 840  
 TCCAAAAAAA ATCTGAATCG TTCTTCGACC TCTTTCGAGC TGCTCGGCAA ACATGGGTGC 900  
 45 CACACGCTTC AATCTCCCC CTACTTCAAC ATAGAGAAAT CGGAGAACTA TAACAATGCC 960  
 GATCCACCCG GTTTCATCAA CTACAAAAGC GACTACTACA CCTATGGTGC CCTACTCCAG 1020  
 GACAAGATTT CCTTTGGAGG ACAAATATC GTACTCGGTG TCGACAGCCG AAACATGACG 1080  
 ATGGAGTCAG AAAGATTGCA GCAGGCAGGA GTGAATACAA AGCCATACAA CCCCAGATAT 1140  
 GGCACGAACA ATATCGGTTT GTTCGGACAG GCCAATTCTT ACCTGCTGAA CGATGCTCTA 1200  
 50 TCGATATCTG CCGGTGCACG TGGCGACTTC ATGTTCTTTG ACCTGAAAGC GAACGAGTAT 1260  
 CTCACAAATG AAGCCAAACA GGAACCTCAT AACGTAATCA ATCCGAATGT CGGAATCAAA 1320  
 TATGAGTTTG TGAAGGCCCT TACAGCTCAT GGTACATTCG GTAGTGCAAT CAGTGCTCCC 1380  
 GATGCTTTCC AAAAAGCAGG CCAATACGTA GGCCCGTTCG GCACGACCAT AGGCAATCCT 1440  
 GACCTGAAAC CCGAAAGTC CATGACCTGG GACTTCGSTA TCGGATACAG CAATGCACCG 1500  
 55 TGGCGGATCC AAGCCGACGT AACCTTAACC TATTTCACA CCGACCACAA AGATCTGATC 1560  
 TTGTCCAGCC CTGACTATGC TAATAATATC ACCACATACA TCAATGCCGA CAAGGCTCGT 1620  
 ATGAGCGGTA TCGAGGCCCT TTTGCTTAT GACTTCGGCA GCTCTTTGC CAACAAGTTC 1680  
 TCTCTCCGCG CATTTGCGAA TGCCACGATC ATGCTCAATT CCGAGATGAA GAAAGGCCAG 1740  
 ACCGATGCCC CTTGGAGCGA AATGTACTAC GTTCGCAAGC AGAACATCAC CTTCCGTATC 1800  
 60 GAATATCGTG GCAAGAAGG ACTTGAAGTG ATGCTCAAGC GTGCTTCAT GGCACGCAGG 1860  
 ATCGAGCAAA ACTGGTATGC TTAATACCCC GAAGTTCGCC CCGAATCTCA GCAACTGCTT 1920  
 GCAGCAGNAG AGCCTGAATT GGCTGCTCAG GGACTGCTCC GTCATCCGCA AGCAATGGTG 1980  
 TTCAATGCTT CTGCTTACTA CCNATGAAC AAGTATCTCA CTTTCGGTGT GAACITGAAC 2040  
 AACATCTTGG ATGAGCTTTA TACGGAGAAA GACGGCTACC ACATGCCCGG ACGTAACATC 2100  
 65 ATGGGTAAAG TTATGTCATA CTTC 2124

(2) INFORMATION FOR SEQ ID NO:185

70

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1386 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

10 (ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...1386

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:185

ATGAACAGGT	TTTCAAATCA	TGGCCCTG	ATCCTCGTGG	GSTTTGTACT	CTGGTTTGTA	60
TGGGCGAGTC	GGACTGTGGC	ACAAAACGCC	TCCGAAACGA	CGGTATCGTA	CGATACGGAT	120
ACCGCCGTAC	TCTCCGAAGC	CGATGTGCTT	CGGATCGCTC	TTAGTGAGAA	TGCCACAGTG	180
AAAGTGGCCG	ATATGGATGT	GGGCAAAACAG	GAATATGCAC	GTAGGGCAGC	ACGTGCCGAT	240
CTCTTCCCGA	AAGTAGACCT	CAATGGCGTT	TACAGCCATA	CGCTAAAGAA	GCAGGTCTTA	300
TATATAGATA	TGCCCGGTTT	CAGCAGTAGC	GAAGGTATCG	AAATGGGGCG	TACACACAAT	360
ACGCAAGGAG	GGGTGAACGT	CTCCATGCCA	TTGGTGTCCG	CACAGCTTTG	GAAGAGCATT	420
GCCATGACCG	GAGAACAGCT	CGATCTGGCT	CTGGAGAAAG	CTCGCAGCTC	CCGAATCGAT	480
TTGGTGGCCG	AGGTGAAGAA	GGCTTACCTC	AGTGTATTGT	TGGCCGAGGA	CTCTTATGSC	540
GTATTCAAGC	GCAGCTATGA	CAATGCTCTG	GCCAATTATA	AGAACATATC	CGACAAGTTC	600
GATCGTGGAC	TTGTGGCCGA	GTATGATAAG	ATTCGAGCCA	ATGTACAGGT	ACGCAACATC	660
GAGCCTAACC	TCTTGCAAGC	GCAGAACTCC	GTAGCCCTTG	CTCTCTGGCA	GCTCAAGGTC	720
CTGATGACCA	TGGAAGTGGA	AACTCOGATC	AGACTCTCCG	GTTCAATTGC	CGACTATAAA	780
GAACAAGTCT	ATACCGGCTA	TTTTGCCGCC	GATACGGCTA	TTTCCAACAA	CTCCTCCCTG	840
CGTCAGCTCG	ATATACAGCG	TCGTCTGGCT	GTCAAGTGAG	ACAAGCTGAA	CAAGTACAGC	900
TTCTTGCCTA	CACCTCAATCT	GGGAGGGCAG	TACACCTATT	CGCTCAACAG	CAACGACATC	960
AAATTCGCG	GCGAGGGACA	ACGCTGGACG	CCTTCTCCA	CCATATCGCT	CAGCCTGTAC	1020
ATTCCTATAT	TCAATGGAGG	CAACGCTCTG	TACAAGGTGA	AGCAAAGTGC	TTTATCGATC	1080
CGTCAGATCG	ATCTGCAACG	ACGCCACATA	GAGCAATCCA	TCCGAATGGG	AATCAAGAAC	1140
CAAAATGACC	GTCTGCGTAC	CTGTATGCAG	AGATTTGTGG	CCTCGGAAGA	GGCTGTCCGA	1200
AGTGCAAGAA	AGGGCTATCA	GATAGCAGAG	AAACGCTATC	AGACAGGCGA	AGGCACTCTC	1260
GTGAGCTCA	ACGATGCCGA	TGTGGCTCTT	TTGCAGGCTC	GACTCAATTA	TAATCAGGCC	1320
ATATTCGACT	TTATGACCGC	AAAGGCCGAA	TTGACAAGA	TGAACGGCAT	GGGGATTCCC	1380
GAACAA						1386

(2) INFORMATION FOR SEQ ID NO:186

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1476 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

50 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

55 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...1476

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186

ATGTGGGGGG	ACAGCCATGG	AGTGGCGCGG	AACCAAGTGC	GCCGAACGCT	GGTGAAGGTA	60
GCCTTAAAGTG	AATCCCTTCC	TCCGGGTGCA	AAACAGATTG	GTATCGGATT	CTCTCTCCG	120
AAAGAAACGG	AGGAAAAAGT	CACCGCCCTA	TATCTCCTTG	TGAGTGATTG	TTTAGCGGTG	180
CGCGACTTCC	CGGACTACAA	AGGGCGAGTC	TCTTACGATA	GCCTCCCGAT	CTCAAAGGAA	240
GATCGTACCA	CAGCCCTTTC	TGCGGATTGG	GTAGCCGGAC	GCCGCTTCTT	TTATTTGGCT	300
GCGGATATAG	GGCCTGTTGC	TTCTTTTTC	CGATCCGATA	CGCTGACTGC	CCGTGTGGAA	360
GAGGTGGCTG	TCGATGGCCG	CCCTTTGCCG	TTGAAACAGC	TGTGCGCTGC	CTCCCGTCGT	420
CTGTATAGGG	GGTATGAGGC	CCTCTTTGTA	CCCGGTGATG	GCGGATCGCG	GAACATATCGT	480
ATCCCGGCCA	TTTTGAAAC	GGCTAATGGA	ACACTCATAG	CGATGGCCGA	CAGACGAAAA	540
TATAATCAGA	CGGATCTGCC	GGAGGATATA	GATATAGTCA	TGCGGCGCAG	TACGGACGGA	600
GGGAATCGT	GGAGCGATCC	CAGGATTATC	GTACAGGGAG	AGGGGCGCAA	TCATGGCTTT	660

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5 GCGGATGTAG CCTTGGTGCA AACCCAAGCA GGAAAGCTCC TGATGATCTT TGTGGGTGGA 720  
 GTAGGCTGT GGCAGTCTAC CCCCAGTCGT CCTCAGCGCA CTTATATATC GGAAAGTCGG 780  
 GACGAAGGAC TGACTTGGTC GCCTCCTCGG GATATAACCC ATTTTCATCTT CGGCAAGGAT 840  
 TGTGCGGATC CGGGACGACAG TCGCTGGTTG GCCTCCTTTT GTGCTTCGGG ACAAGGGCTT 900  
 GTGCTGCCAT CCGGTCGTAT CAGGTTTGTG GCTGCCATCC GCGAATCAGG GCAGGAGTAC 960  
 GTCTTGAACA ACTATGTCTT CTATAGCGAC GATGAGGGCG ATACATGGCA GCTTCCGAC 1020  
 TGTGCATACC GCCGTGGCGA TGAGGCAAAG CTTTCATTGA TGCCCGATGG CAGGGTACTG 1080  
 ATGAGCATAC GCAATCAGGG ACGGACGAGG AGCCGACAGC GTTTCCTCGC TCTTCTCTCC 1140  
 10 GACGATGGCC TTAATTGGGA GAGAGCCAAG CAGTTCGAGG GCATCCATGA CCCCGLTGT 1200  
 AATGAGGCTA TGCTCAAGT GAAAGGAAC GGAAGGGATC AAGTGTCTGA CTCCTGCTT 1260  
 CTCGCCCCGG ATGGGCGTCG CGATGGAGCT GTCTATCTCT TCGATCATGT CTCGGCCGC 1320  
 TGGTCCGCTC CCGTTGTGT CAATTCAGGA TCGAGTCCCT ACTCGGATAT GACTCTGCTG 1380  
 GCGGATGGA CGATCGGTTA TTTCGTGAA GAGGGCGATG AGATCTCATT GGTTCATT 1440  
 15 CGGTTCTGCC TTGACGATCT CTTCGATGTC CGGCAA 1476

## (2) INFORMATION FOR SEQ ID NO:187

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 735 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 25 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 35 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...735

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:187

40 ATGAAAAAAG AAAAAGTTTG GATTGCGATC GTCGCCGGTT TGGCTTTCGT ATTGGGCCTT 60  
 TATGCTCTTG GCCGAGTGT CGCTCAGCTA CGCCGCTCTC AGCCTTCGGT GACTGTGACC 120  
 GGTATGGCCG AGCGTAATTT CAAATCCGAT CTGATCGTTT GGACTGCTTC GTACCAGCTC 180  
 CAGATGATGG ATCTCGAATC GGCCTACAAG GCTTTGAAGG AAAACAGAT ATTGGTAGCA 240  
 45 GACTATTGGA AAAACAAGCA GTCGCCGAT TCGTCTTATA TCTTCTCAAG CGTAGCCATC 300  
 TCTAAAGAA ACACACTACTA TTACGATCCT CGGCAGGAAC AAAACGTCAG GACCTTTGCC 360  
 GGGTATCTGC TCAGCCAGAC AGTTACGGTG ACCTCAGAGG ACATCGAACA TGTGGAGAAA 420  
 ATATCTCGCG ATATAACGGA GCTGATCAAT CAGGGGGTAG AGATTACCTC CGACCGTCCG 480  
 GCCTATTACT ACACCAAGCT CAATGATCTG AAGGTGGAGA TGCTGCGCAA TGCCTCCGAA 540  
 50 GACGCTTCA ATCGTCTTC GGTCAATGG GAGGGGAGCG GTTCTCCGT GGGTAAGATG 600  
 CTATCTTCTT CGATGGCGT GTTCCAGATA GTGGGGCTCA ACTCGAACGA AGATTATAGC 660  
 TGGGGAGGTT CGTTCAATAC GTCTTCCAAG ATGAAGACGG CAAGCATAAC GGTTAAGGCT 720  
 TCTTTCGCTT TGAAG 735

## (2) INFORMATION FOR SEQ ID NO:188

- 55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 828 base pairs  
 60 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 65 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 70 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 75 (B) LOCATION 1...828

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:188

5	ATGAAAAA	CAATTGCAAT	TATCGCCTCA	GCCCTCTTGG	CTTTAGGAGC	CGTCGGCTGT	60
	AAGAAAAATG	CTGACACTAC	CGCTGTCTAGT	GAAAAGGATA	GCATAGCCTT	GTCCATGGGT	120
	ATTTTGTACG	GACAGGATTT	TGCCAATCAG	TTGGAATGT	CCCGCTTGCA	AGGCCAGCCG	180
	ATTGATTCGG	TAGCTTTCTT	GGACGGTTTC	AAATATGGTA	TCGATACGAC	GCGCTTCTCG	240
	TACAATCTGG	GAGCCATCTA	TGCTTCCAAT	ATAGCTCGTC	AGCTGGCTCA	TGATTCCATC	300
	GATATCGACA	AGTTCTATGC	AGCCATGCGT	GCGGCTCTTC	TTAAAGACAC	CGTATCTATC	360
10	GCCATGAAGC	CTGCAGATGC	ACAGGCTTTC	ATGCAACGAA	TCCAAGCCAA	AAAGCAGCGA	420
	GAAAAAATA	TGAAGCAGTT	TGGCCAGAAC	ATCGAAAAGG	GTAAATGAATA	CATCGATACC	480
	TTTAAAAAAG	AAGATGGTGT	AACTGTTACG	ACAACCTGGT	TGGCATACAA	GACTCTTCAG	540
	GAAGGTACGG	GAGCTACTCC	CTCTTTGGCC	GATACTGTAC	GTGTCAAGTA	TGTGGGTACT	600
	CTGGTCTGATG	GTAAGAGATT	CGACAAAAAC	GAAGAAGGAA	TGCAATTTCG	CGTTACCGGT	660
	GTGATTAAAG	GCTGGACGGA	GATGCTCCAA	CTCATGAAAG	TGGTTCAGAA	AGTTCGCGTG	720
15	GTAATCCAC	AGGAGCTGGC	TTATGGGGAG	ACCGGCAACT	ATACCATCGA	ACCGTTCTCT	780
	ACCGTACGCT	TCGAGATGGA	ACTTATCGGG	ATCAAGCCCG	GGAAAAAG		828

## (2) INFORMATION FOR SEQ ID NO:189

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...2325

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189

45	ATGAAAGTAT	TACGGCAAGT	ATTCCTCCCC	ATCCTTTTGG	TCCTACTGAC	AGGTGCCTGC	60
	TCCACCACAA	AGAATCTGCC	GGAAAGGCGAA	CAGCTGTATA	TCGGAAATGGG	CAAGACACAG	120
	ATACTCCGGC	AGGACAAGAG	CCACGCCGGC	CAACAGGCTC	TGACCGAAGT	GGAGAGTACA	180
	CTGAAAGTTA	CACCCAATGG	AGCTATTTC	GGCAGTGCAA	GTGCCTCCTT	ACCCAAGATA	240
	CCATTCCGGC	TATGGCTATA	CAACAGCTTC	GTGGGGGATT	CCACTGTCTAT	TTGGAATGG	300
	ATATTGCGCA	AGTTTGCAAG	CAAGCCGGTT	TTCATCAGTC	AGGTCAAATC	CGTAGCCGG	360
	GCTAAGAGTG	CGACGAACAT	OCTCCGCGAA	CACGGGTACT	TCGATGCTAA	AGTAAAAAGC	420
	AGTGTGACCA	CTCTGAAAAA	GGACTCGCTC	AAAGCCAAAA	TCTCCTATAC	GGTGGATATG	480
50	GCCTCTCCTT	ATCATTACGA	CAGCATCATT	CCCTTACCGA	TCAGCACTTT	CCCCGACAGC	540
	ATTCTGGCTT	ACAGGCAGAC	TCCGTCTTTG	ATCAGGAAAG	GAGACCAAGT	CAATTTGGCA	600
	AAGCTGCACG	AAGAGCGTCA	GACCATCAGT	GCCCTGCTGA	GAGACAATGG	TTACTACTAC	660
	TTCCGCCCCAC	AGGATATTAT	CTACGAAGCC	GATACCTCC	TCGTAAGAGG	TGCGGTATGC	720
	CTGCGAGCCA	AGCTCTCGGA	AGATACTCCA	CCCCAAGCCA	TGCGCCCGTG	GAGGATAGGG	780
55	AAACGGACAG	CAGTCTGTCT	CGGAATGAAC	GGAGAAAGCC	CGACAGACTC	GCTCGAAGTG	840
	GAGGATATGA	AAGTCCTTTA	CTATCGTAAA	ATGCCGGTTC	GCCCAAGAT	TTTGGCCAAA	900
	CGCTTTCGTT	TCTTCTCCGG	CAATCTGTAT	CGGCAGAAAG	ACGATGAGAC	GACACGCCAA	960
	TCCTTGGCTC	GTTTGGGAGC	CTTCTCCGTT	ATCGATCTCA	ATTTTTTGCA	ACGCGATTCC	1020
	ATTTCCGGCC	TTTTGGATGT	GCGACTGCTA	ACCACCTCG	ACAAACCTTG	GGATGCATCA	1080
60	TTAGAGACCT	TGTTACGAG	CAAAAGCAAT	GACTTCATCG	GTCCCGGACT	GAATTTTGCT	1140
	CTTGCTCGGC	GCAATGTATT	CGGCGGAGGA	GAAATCTTT	CTTGAATAT	CGGTGGATCG	1200
	TATGAGTGGG	AGACCGGCAA	TCGTCCCGAA	AATAGCAGCA	ATCGGCTGAT	CGATATAAAT	1260
	TCGTACAACA	TGAATACGGC	CGTGAACCTC	TCGTTTCCCT	CGATTGTATT	TCCCGTCTG	1320
	CTGGATAAAT	ACTATTACTA	CCCCACGACT	ACGACTTTTC	AGGCTTCTGC	CACCGCGCTG	1380
65	AACAGGGCAC	ACTACTTTAG	CATGTACTCT	TTGGGCTTTT	CGACCACTA	CGAATTTCAG	1440
	CCCTCCAAGG	AACACCGGCA	TGCTATTTC	CGCTCAAGC	TCAACTACAA	CCTCCTGGGG	1500
	CATCAGACAG	AAACTTTCCA	GGCCATTACG	GCGAACAATC	CGCCCTGCT	GCTCAGCCTT	1560
	CAGAGTCAGT	TCCTTGCTCA	AATGGGGTAT	ATCTATACGT	TCAACAAATC	CGTTTCAGAG	1620
	AAAGTCTCTC	ATCATCTTTG	GATGCAATTC	GGACTATCCG	AGGCAGGCAA	TCTCCTGAAT	1680
70	CTGATCTATC	TGGCAGCCGG	CAAGAAGTAC	AGCGACACCA	AGAATTTCTG	CGGCGTCCCC	1740
	TTCTCTCAGT	TCATCAAAGC	CACGGGAGAA	CTGCGCTATT	CCTATACCAT	AGACCGCAAT	1800
	CAGTCACTGG	CAACCGTTT	CGGACAGGCG	GTGATATATA	GCTATGGCAA	TATGCGAGTG	1860
	GCACCTTATA	GCGAGCAGTT	CTATGTAGGC	GGTGCCAATA	GTATCAGAGC	TTTCAACGTC	1920
	CGTAGCATCG	GCCCCGGACG	GTTCATCCCG	GATTCCGACA	ATCAGTATTC	CTATTGGGAT	1980
75	CAGGTGGGCG	AATTCAAAC	CGAAGCCAAC	GTGGAATATA	GAGGCAAGCT	TTTCGGGGAT	2040

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CTCCACGCAG CCGTTTTCCT CGATGCGGGC AACGTTTGGC TCTTGAGGGA GGATTCTTCC 2100  
 CGTCCGGGCG GTGCTCTGTC CGAAGTGGA TCGGTGAGCA ATTTCCGTGA TAGCATCGCT 2160  
 CTCGGCACCG GTGTCGGGCT TCGCTACGAT CTGGCATTTT TCGTGGTTTC TGTGATGTC 2220  
 GGCTTCGGTC TCCACCTTCC TTACAATACG GGTAAGAAAG GTTACTACAA TATCCACGC 2280  
 5 TTTAAGGATG CCATCGGTTT CCATTGGCT GTCGGTATC CCTTC 2325

## (2) INFORMATION FOR SEQ ID NO:190

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2322 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2322
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190

30 ATGTCCTCGC ATTCCGTTTC GTATCTAATC GGCATTGCCG GCTGCTTGCT CCTCATGCTT 60  
 GCTTCCTCCT GCTCGGTCAC CCGTTATGTG CCGGACGGTA GCAGACTATT AGACAGGGTA 120  
 ACATCGCAA GCGAAACGGG CAGTATCGCT CTGCCGGAAG ATATTGCGGA CTATACCCCTC 180  
 35 CAGCAACCCA ATTACAGACT GTTCGGGATG ACTCGCTGGC TACTGCGCGT CTATAGCAGC 240  
 TCGAATCCGA ACAGCAACAG CTGGTGAAC CGTTCGCTCC GGAAATGGG CGAACCGCCT 300  
 GTCTCATCG ATTCTGTCCT CACGATCGT ACTGCCAACC GTCTGGCAA GGCGATGGCC 360  
 GGGCATGGCT TTCTCGATGC TACTGCTCGT GCGTGGTAG ACACCGGCTT GTACAGAAA 420  
 GCTCGCATT CTATCTGAT TCAGCCCGGA AGCCGTTATT ATATACGCA TATGGCTTTG 480  
 40 GATGTGAAGA ATCCACTCCT TCCTCCCGTT GCGCTTGGCA ATTCGCTTC TTCCGCATAC 540  
 AAGTTCGGGA TCAGCGAGGG TTCTCCCTTG TCGCCCATCG TACTCGATGA AGAGAGAAAG 600  
 GCGATAGCTC GTCATATGCG CAACAACGGC TTCTGGAAGT TCTCCGCCGA GGATGTTTAT 660  
 TATGAAGCAG ATACTACCGT TTCAGGAGGA TCGGGTACGA AATCTGCCGA TCTGAAATTA 720  
 GTGGTCAATG GCATCGGGCG TTATCCATAT CGGATCGGCA GGGTATTCTT TCATGCCGAT 780  
 45 TATGATCCTC TCGAATCGGA CTTCAGAGTT CAGGAGCTGC CAGGTATCGA TTCGATTTCG 840  
 CTGGCGGATT ACAGTGTTTA CTATGGGAGT AGGGGACGTT ATATCCGGGC ATCGGCTCTC 900  
 ACCCGGTCGG TGTCCGTTAC ACCGGGAGCT TTTTCTGCG AGGATGATGT GGAACGCTCT 960  
 TATATCAAGC TGAATGCGCT CCTATCGTT CCGAACGTGA ATATCCGATT TGTGGAGCAC 1020  
 AATGGTAAGG ATGAGATTGC TCTGGCGGAT AGCTCTCGCC TTGTGGACTG CTATATTCTT 1080  
 50 ACCGTTCCGG CCAAGAGCAA ATCGTTCGAA GCGCAAGTCC TCGGCACCAA TTCGCTGGA 1140  
 GACTTCGGGG CGGCTTTGTC TCTCGGTTTC ACCGATCGCA ATTTGTTTCG TGGGGCGGAG 1200  
 ATGTTCAATA TCAAACTCAA GGGTGGCTTAC GAAGCCATTG GCAAGGGTTC GCACAGCTTC 1260  
 ATGGAATATG GGGTGGAAAG CTCGCTCCGT TTCCCTCGTC TCCTCTTCCC ATTCATTCTT 1320  
 GACGAAACGC GCGGGCGGCT ACGGGCATCC ACGGAATGGA AGATCGGGTA TAATTACCAG 1380  
 55 ACAGTCCCG AGTTTGATCG GGTGATTCTC TCCGCTCAAC TCAATTATTC ATGGCAGACC 1440  
 TACCTGCACA ATCGTCTCGG TCATACGATC CGCCTGCTGG ATGTGATTA TCTCCATCTC 1500  
 CCGTACATCG ATCCCGACTT CGCCCAATCC CTTCGCGCTA CGACTGCATG GTATAACTAC 1560  
 ACGGAGCAGT TTATCTCGG CTCGGCATAT ATACTGAAT ATACCAACGC TTCGTCCATG 1620  
 GAGCGTACCG TATCCAATCC TTTACGGCA CGGTTCACTA TCCAGACAGC CGGCAACCTG 1680  
 60 CTGCAAGCCA TTCTTATCT GACCGATTCT CCGAAAGACG AACACGGGTT GTATAAATG 1740  
 TTCGGTCTGC ACTATGCTCA GTTCGTCAGG CTGATCTCG ATCTGGCTAA AACCGTTCTT 1800  
 CTCGAAAAGG ACAATACTTT GGCAGTGCAT CTGGGTTTCG GACTGGCTTT CCCTATGGC 1860  
 AATGCTCGCC ATATACCTT TGAGTTACGT TACTTTGCG GAGGATCGAA CAGCGTTCGC 1920  
 GGCTGGAGTG TCCGTACCTT CGGCCCGGG AGTATGAAGA TGACTCCGGA CAAGACCTTC 1980  
 65 TTCGATCAGA TGGGTGATAT TCGTCTGGAT CTGAATGTCG AATACAGGAC AAAGCTGTTT 2040  
 TGGAAGTTTC GCGCAGCAGC TTTTGTGAT GCGGCAATG TCTGGACGAT AAAGGATAT 2100  
 GAGAATCAGG AGGACGGTCT CTTTGTGTTT GATCGCTTCT ACAAGGAAAT AGCTTTGGCC 2160  
 YACGGTCTGG GGCTTCGTCT CGACTTCGAT TATTTCTTGT TCGGGCTGGA TCGCGGACTG 2220  
 AAAGCTACG ATCCTCAGCA GACAGGCGGT TACAAATGGG CTATCACAG CCCAAACCTT 2280  
 70 TCTTCCAATT TCGCTTGGCA CATTGCAGTA GGCTATCGGT TC 2322

## (2) INFORMATION FOR SEQ ID NO:191

- 75 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2601 base pairs

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

5 (ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO  
10 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
(ix) FEATURE:  
15 (A) NAME/KEY: misc feature  
(B) LOCATION 1...2601  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191  
20 ATGAGAAAAA GAATTCTACA ACTTTTCCTG ACCGCATTGC TGCTGGCATT AGGCTCCTCT 60  
CTCGCCATAG CGCAAAACAGT GGTGACCGGT AAGGTGATCG ATTCAGAAAC GTCCGAACCG 120  
CTCATCGGTG TATCGGTAAG CACCGGTGAG GGAGCATCCC TCCGCGGTGT AACCAACCGAT 180  
ATGGATGGTG GCTTCGGATT CGAAGTACCG GCCAAATCTG TCTTGACTTT CCGTTGCGTA 240  
GGTTATGCTA CCGTAACTCG CTCTATAGGC AGAGTTTCTC AAGAAGACCT CGGTACGATT 300  
25 CTCCTCGATC CCGAGGCCAT CCGCTTGGAT GAGATTGAGG TAATAGCTC TGTGGTGCCC 360  
AAGACCGTA TGACCGCGGT ACCGTTTTC AATATCCGTG TGGCTGATAT TCAGGCAGCA 420  
TCGTTGAATG TCGAATTTC CGAACTGGTT AATCCACTC CCTCTACCTA TACGACAAA 480  
GGAAGCGGAG GTTTCGTGA TGGTCGTACC AATGTGCGTG GATTGACAC TTACAACCTC 540  
GGTGTACTCA TCAACGGAGT TCCTGTCAAT GGTATGGAAG ACGGGAAGT ATATTGGAGC 600  
30 AATTGGAGTG GTCTGATGAA TCAAGCCAGT ACCATTGAGA TTCAGCGCGG ACTCGGAGCC 660  
TCCAAGCTCG GTATCAGCTC GGTAGGTGGT ACGATGAACA TTATCAGCAA GACTACGGAC 720  
GCCAACACCG GAGGTTGCGG TTATGTGCGT ATGGGTAATG ATGGATTGCA CAAAGAATCG 780  
TTCCTCATTT CTACGGGTAT GAACGACGGT TGGGCTATCA CCATTGCAGG CTCCTATATG 840  
ACGGGCTGCG GTTATGTGAA GGGGCTGAAG GGACGTGCAI TCTCTTACTT CTCACACGTT 900  
35 TCGAAGAAGT TCAATGAACG TCATACCCCT TCTCTTACCG GATTGCGTGC ACCACAATGG 960  
CACAAACCAAC GTTCTTCCAA ATATTCTGTA GCCGACTATG ACAAATACCG CATCCGTGAC 1020  
AATCAATCCT TCGGCTATCT GCGAGCGCAA CTAAGTCTTA CCGCTTATGC TTACAATACG 1080  
TACCACAAGC CCCAGTTCTC GCTGAACCA TCTGGAAGA TGGATGAAAA TACCTCTCTT 1140  
TATACGCGAN CCTACGCATC TTTGGCTACC GGTGGAGGTC GTCCGCTTA TGGAAAGAAC 1200  
40 AGTAAGTGGG TATTGATCAA CTACACACC GGACAACCCT ATGAACAAAC AAAGGTGACT 1260  
CCCGATGGAC TTATGSACTA CGATGCGSTA CTGGCTGCCA ATGCTGCGGC GAGCAATGGC 1320  
TCGGAGACAA TTTTTCGCCCT TGGCTCCAA TCTCACAAGT GGTTCGGTCT ACTCTCTTCA 1380  
TTCAAGVAGA AACTTAATAG TTCGTGACT TTGACAGCG GATACGATGG GCGTTACTAC 1440  
CGTGGCGGAG ACTATGACAA GATCACCAGT CTGCTCGGCG GTAGCTACTA CATAGAGGAT 1500  
45 CCCAAGACAA AGCTCGCATA CCATGCGGAA GGTGAGCAAC TGAAAGTGGG TGACATTGTA 1560  
AATCGGACT ACACAGGCGA ATCATGTGG CACGGCCTCT TCGCACAGAT GGAGCATTGG 1620  
TCCGAATGGA TCGATGCATT CGTATCAGGA TCTATCAACT ACGAACTATA CCGCAATCAC 1680  
AACTATGGCG GTAGCAAGTC CACCGGCTAC CTGCCCCGGG TATCGCGGTG GAAAGGCTTC 1740  
CTTCCGTGGA GTGGCAAGGC AGGTCTGAGC TACAAGTTGG CACAGGGACA CAATGTATT 1800  
50 GCCAATGGCG GTTCTTCCAC ACGTGCAACA CTCTTTGGCA ATATCTATGC TGGGGGGGCT 1860  
ATCATTCCCA ATGACAAAGC CAATATGGAA AAGGTGCTTA CAGGAGAGGT CGGCTATGGA 1920  
TTCAGGAATC ACAAACCTT CGAGTTCAAT ATCAACGGAT ACTATACGAA GTGGATGGAT 1980  
CGCGTGACCT CGAAGAGAT CCGAAACGAG TATGTTTATC TCAATGGCGT TGATGCTGTT 2040  
CACTGTGGGG TAGAGGCTGA GGTGAGCTAT CGTCTATTTC GTGAGATGSA CCTTCGCGGT 2100  
55 ATGTTCTCTC TCGGTGACTG GACTTGGCAA AACAATGTAA GTTACACTTC TTACGACGAA 2160  
GCCGGCAATG AGACAGGCGA GGAATATAAC TATATCAAGG GTCTTCAGT CCGAGATGCA 2220  
GCACAGATGA CCGCTGCTGT ATCGGCAGAC ATAGAGCTGT TCAAGGGTTT CCATGTCATA 2280  
GGTAAGTACA ACTTCCTTGG CAAGAATAT GCAGGATTCA ACCCGCAAC CGGTAATGCA 2340  
CAGCAGTACG AAGCGGATGG CAAAGAAATC GTGGAATCAT GGAAGTTGCC CGATGTAGST 2400  
60 CTGTTGATC TGTCTGCATC CTACAATTC AAGCTTGGTT CACTGAGCAC CACATTCTAT 2460  
TTCAACATGG ACAACGTAGC CGACAAGCGA TATGTAGCG ATGCCGACCA CAATATCATC 2520  
GGTAAGAAAC ACGATGAGGC TTGGGCTCTC GTATGGTACG GTTTCGCGCG CACTTGGTCT 2580  
ACCGGTATTC GTGTAACCT C 2601

(2) INFORMATION FOR SEQ ID NO:192

(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1293 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
10 (B) LOCATION 1...1293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192

15	ATGAAGTTT CAATCGGCT TTCTCTGTC ATCATCTTC TCCTCTGTC ATTTATCCTG	60
	CCTGCTCTCG GACAAAAATC CAAGCAGGTA CAGCGACTTG AGAAGCAACG TAAGGAGGCC	120
	CTCAAAGCCA TCGAAAAAAC CGATCGCGAA CTACGAAATA CCAAGAAAGA CAAGCAAGAC	180
	AAACAAAGC ATCTCAACCT CCTGAACAG CAGGTTGCTC AACGCAAGCA GATCGTACAA	240
	CTCTGGACA ATGAGGTCAA AGAGTTGCAA TCCGACATTG ATCCATGAC GGGTGTATGT	300
20	CATCAGTCT CTGTAGAAGA GAAAGCCCGA TCCGATGAAT ATGCCCAAGC TCTACAGTCT	360
	ATGCAAAAGC GGAAACGCTC GTTGGATGCG ATCCTTTTCA TTTCATCGGC CAAGAGCTTT	420
	GACGAAGGCA TGGCAGGGAT GCGTTTCTTG GAACAATACG CTTCTGCATA CAAGCTGGCA	480
	TCTGTCCGGC TGGCGGATAC ACGTAGCAAG TTGGAGACTG AACGTGCGAC TGTAGAAGAC	540
	GCCAAAAGG AGAAAGGACA TCTCTTAGTC ATCAGAGAAG AGGAAAAAAA GAAACTCGAA	600
	GGACAGCAAG CCGAGCAACG TCGGCAGGTG CAGGCTTTGG GAGCCAAACA AAAAGACTTG	660
25	GAAGCGCAGC TCGGAAGCA GAAAAAGCAA GCGGAAGCTC TGAACAGAAA GATCGAGAAA	720
	CAGATTGCCA AGGAATAGA ACCTGCCGAA CGTCGTGCTC GAGAAGAAGC TGAACGGTTG	780
	GCACGCGAAG CCAAAAGCCAA GGGTAAGCCG GTTCTTGCAG AACCGGAACG GAAGGCGGAC	840
	ACCAAGGGCG GCTATGCTAT GGATGCCCTC GAGCGTGCTC TCTCGGGCAG CTTTGACACG	900
	AACAAAGGTC GCCTGCCCGG CCCGTTTCGC GGCAGATACC GAATCGTAAG CGACTTTGGC	960
30	GTGCATCAGC ACAGTGAGCT GAAAAAGTA CAAGTTAATA ATGGAGGTAT CGACATCGCT	1020
	GTAGCAACAG GATCCGATGC TACCAGCGTA TTCGATGGTG TAGTGTCCAG TGTATTCTGT	1080
	ATACCGGTTT ATAATTCCGC CGTAATGGTT CGTCACGGTA ACTATATCAC GGTTTATGCG	1140
	AATCTGAGCA AAGTGATATG AAATTCCGGC ACTCGTGTTA AAACGGGTCA GGCTCTTGGT	1200
35	CGTGCTTATA CGGATCCTTC CAACAACCAG ACCATTATTC ACTTCGAAAT CTGGAAGGAA	1260
	CGCAGCAAAC AAAACCCAAG ACTATGGTTA CGA	1293

(12) INFORMATION FOR SEQ ID NO:193

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 999 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

45 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

50 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

55 (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193

60	ATGAAAAAGT ATTTGTTATA TGCCTCGTTG CTAACGAGTG TTTTGCTCTT TTCCTGTTCA	60
	AAGAACAATC CTAACGAGCC GGTGGAAGAC AGATCCATCG AAATTTCTAT AAGGGTAGAT	120
	GATTTACCCA AAACGGGTGA GGCAGTACGC TATGAAAGGA ATCAAGGAAG TGTGCGCGAA	180
	AGGCTCATTA CCAATCTTTA CCTCTTGTIG TTCGATCAGT CAGGGGCGAA TCCGCGGAAA	240
65	TACTATATTA CCGGTAACAC TTTCACCGGA GGGACCTGGC TTCCTGACGA TATGAAGGTG	300
	AAGTTGGATA TGACACAATC CGAGGCCGGA GAGCGCAAAG TATATGTGCT AGCCAATGTT	360
	GATAATCGCG TTAACACGGC TCTTGATGCT GTCGCTAACG AAAGCGATTG GCAGACTGTA	420
	AAGAGGACGA CTGCAATGCC GTGGTCGACC GATATAGCCT CTCCTTTCTC GATGTCCGGA	480
	AACAGACAC ACAGACTCTT GGCCAATCGT CTTTGGACA ATGTGCCCTT TGTGCGTGCC	540
70	ATTGCCAAGG TGGAGCTGAA TATCTCGCTG AGTGAGAAAT TTCAGATTGT GCCGATAATT	600
	GTCAATCGTA GTTTGAGTGA GTTCAAGTTC AGATACGTAA ACCTCGACAA GGAGACCTAC	660
	GTAGTGANGC CAACGACCAA GCCGGACAAT CTCATTAGTT CTGCTAATGG TGTTTGGCCT	720
	CAGATTACAG ATTGGACTGT ATGGGGTGCT TCCTTAAATA CTTCTCTGTC TCCGGATGCG	780
	GGCAGAGGTT ATACATTGGA TGCAAATGGC AAGGTAACGG CACTACGGAT TGTACCTAT	840
75	CTGAATGAGC GCGATAGCAA ACGGGCTACG GTAGAGGTG CATTGCCCTG TGTGGATGAT	900



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GGCACCCCTTC CTCCTCCGGA ATTCCGGTCCG GAGCTTTATC GTTTCCTTT GCCGGACVAG  
ATCCTGCCGA ATCATTGGTA CAAGTATGAA GTCGAGATT

960  
999

5 (2) INFORMATION FOR SEQ ID NO:194

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 945 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

15 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...945

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:194

ATGATCAGAA CGATACTTTC ACGATATGTA TCCTCGAACT TTTGGAGTCG GGGAGCTACC 60  
TTTTTTTCA CGATTTTCCC GGCCTTCATC CTCGCCGCTA CTGCTTTGCC GGCTTGTTGA 120  
GGGGGTACTG CTTCAGGCTC CGATCGTACG CTGGCTGTGA CCATCGAGCC ACAGAAATAC 180  
TTCATCGAGT CCATTGCCGA TAAGTCGGTG CAGGTGGTGG CATTTGGTACC GGCCGGCAGC 240  
AATCCGGAGG AATACGACCC TTGCGCTACC GTGATGAAGC GTTTGTCCGA AGCAGATGCC 300  
TACTTCTATA TAGGAGGACT GGGGTTTCAG CAAAGAAATC TCGCTGCCAT TCGGGACAAAT 360  
AACCCTAAGC TCCTCTTTT CGAAATGGGC AAAGCCTTGG CGGATGCCGG AAGTGCAGAT 420  
CTCCACGGCT CCTGCACAGA TCATTCTCAI ACAGACCTGC ATGCCATGA TCCGCACTAT 480  
TGGAGCAGTG TGGTAGGGGC AAAGGCACTC AGTCGTGCTG CATACGACGC GCTTGTGGAG 540  
CTTTATCCGA ACGAGAAAGA CAAATGGGAC AAAGGGCAGG ACCGTCTCAA CGGACGTATC 600  
GACAGCGTGA AGAGACTCGT CGATACCATG TTTGCCAATG GCAAAGCAGA CAAAGCCTTC 660  
GTCATATATC ACCCATCGCT CAGCTTTTTC GCCCAAGAGT TCGGCCTGCG GCAGATCGTC 720  
40 ATAGAGGAAG ATGGGAAAGA GCCTACGGCT GCCCACCTTC GTCGTGTGAT CGATCAGGCA 780  
CGTGCCGATG GTGTCAGAAAT CGTATTATC CAACCCGAAT TTGAAACGCG TCAGGCGGAG 840  
GACATCCGAC GCGAGATCGG TGCTCGTCCG GTAAGGATCA ATCCTCTGCG CAGCTCGTGG 900  
GAGGAGGAAA TTTTACATAT TGCTCGCGCT TTGGTCATG AACGG 945

45 (2) INFORMATION FOR SEQ ID NO:195

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 2544 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

55 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

60 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- 65 (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...2544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195

ATGATCGGAA AAAAAATCTT TTTTATCTTG CTGGCGCTCA TTGCGTTCAG TGGGCTGAAC 60  
GCAGCGACAG AACTGAGTT CAAGTACCG ACCGATGCCA ATATCATCGG TCACGTCAAA 120  
GACAGCAAGA CGGGTGAACA CCTTGTGGT ATCACTATTG CTATCAAAGG CACTACCTTT 180  
GGTACATCTA CAGATGCAAC CGGGCACTAC TATCTTCGTA ACTTGCCTCC GGGTGAGATC 240  
ACTTTGATTA TGGTGGCAT GGGCTATAAG AGCCAGGAGC GCGTAGTCCG CGTAGAAAAG 300  
GACAGACTA TCGAGGTGAA TTTTGAAGCA GAAGAGGATG CCATCAATCT GGACGAAGTC 360  
75 GTGATTTCGG CCAACCGGA ACTGACGCTT CGCCGTCTTG CTCCTACTCT GGTAAATGTA 420

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TTGAACGAAA AAGTCTTCTC GCAAGTCAAT GCTTCTAACC TGGCTCAAGG CTTGTCAATC 480  
 CAGCCGGGAC TTGGTGTAGA GAACAACTGT CAGAACTGTG GTTCAATCA AGTTCGTATC 540  
 AATGGACTGG ATGGTGGTGA TGACAGATC CTCATCGACA GCCGTCCCAT CATGAGTGCC 600  
 CTTGCCGGTG TTTACGGTCT GGAGCAGATC CCTGCCAATA TGATCGAACG TGTGGAGGTA 660  
 5 GTACGTGGTG GAGGATCGGC CTTGTACGGT TCTTCTGCTA TTGCCGGAGT GGTGAATATC 720  
 ATCACCAGG AACCTTCTCA CAATTCTTTC ACATTCAATG AATCTCTGAG CTTTACCGGT 780  
 TTCAGCAAGC TGGATAACAA CACGAACCTC AATGCCTCCA TCGTCAGCGA TGACAACCGT 840  
 GCCGGTGCCA TGGTATTCCG GCAGGCTCGT TACCGCAACC ATTGGGATGC TAACAATGAC 900  
 GGTATTCCG PATTGGGTAA AATAGATGCC CGCTCGCTGG GAGCGCATTC TTATTGCGC 960  
 10 TTGAGCGACT ACAGCAAATT GACGGGAGAG TTTCACACGA TCAGTGAATT CCGCCGTGGT 1020  
 GGCGATCGTA TCGATTGCCC TCCTCACGTA GTGGGTGTAG CTGAACAAAC TGACCATAGC 1080  
 GTATTAGCG GAAACTTGAA ATACGATCTC TTCTCTTCCA ACTATAACA CCACTTCCAG 1140  
 GCTTATACTT CCGGACAGAT CGTAAATCGC AAGAGCTATT ACGGAGGTAT CGGAGAGATT 1200  
 GACGTCAATG CCCACCCGGG TGGTACGGAA GGCTACCCTA TCCCTCAAGA TCAATACGGC 1260  
 15 AATAATTATG GCGTGACCAA AGGCAAGACA TATATGGGCG GTATCCAGTA CAGTACGAC 1320  
 TTGGACAAAT TCCTCCTCAT GCCTTCGCAA CTTTGTGTCG GAGCCGAATA TACCGTGAT 1380  
 GAACCTCAATG ACGTGATGCC CATCCTTCA TGGCAGACCG GCGAGGATGC CAATGGGAAT 1440  
 ACCATTCCCC TCTATCCCGA ATTGGATCAG AATATCAACA ACTACAGCCT ATTCCGTCAG 1500  
 AACGAATGGA AAAATGACAG ATGGAGCATC CTTGTTGACG CTCGCTTGA CAAGCATAGC 1560  
 20 GAAGTCAAGG ATATGATTCT GAGTCTCTGT ACCACACTGC GTTCAACGT GAATCCGGAC 1620  
 ATCAACCTGC GCGCTACATA TGCAAAAGGG TTCCGCGCAC CGCAGGTATT CGATGAAGAC 1680  
 TTGCACGTAG GGGTTGTAGG CCGTGAGGCA CAGAAAGTAT TCRAACGATCC GAACCTCAAG 1740  
 CCTGAAATTT CTCTGTGATT CAGTTTGTAGT GCCGATATGT ATCATCGTTT CGGTAACGTC 1800  
 25 CAGACCAACT TCCTTGTGGA AGGCTTCTAT ACTCGTTTGC TGGATGTATT CACCAACGAG 1860  
 GAGGAGCCTG ATCAGCAGCA TGGCATCAA CGCTACACGC GTATCAACGG TAGCGGAGCC 1920  
 AAGTATTTCG GTCTCAATCT GGAAGGTAAG GTGCGATACA AGTCCTTCCA GCTCCAGGCC 1980  
 GGTCTTACCC TGGCCAGCAA CAATACGAC GAAGCACAGG AGTGGGTCT GAATACGGTG 2040  
 AAGACACCA ACGGAGCTTT TGTACCGAG GCCAATGCAA ATGGACAAAC GGAATACAAG 2100  
 30 AACGAATCCA TGACGGATAC GCAGATCACC CGTACCCCCA GCGTATACGG TTATTTTACT 2160  
 TTGGCCTACA ATCTGTCTCA CTCATGGAAC ATAGCCCTTA CGGGAGCATA TACCGGTCAG 2220  
 ATGTATGTAC CCCACGCTAT CGAATATGGT GTGAAGTCTG CCGAACTGGA TATTATGACG 2280  
 AACAACTCTG AGATTACCGA CGAAACCGGA AAGGCTCCCC GTATTGATGA GCTGAAGAAG 2340  
 ACACCTGCAT TCTTCGATTT GGGCTTGAAA GTGGGTATG ACTTCCACGT ATTCCAGGCT 2400  
 35 ACTGAGGTTT AACTCTATGT AGGTATGAAC AATATCTTCA ACTCTTCCA GAAGGACTTC 2460  
 GATCGTGGAG CTGCACGTGA CAGCGGATAT ATCTATGGTC CTACGCAGCC GCGTACAGGC 2520  
 TACATGGGCT TGGTAGTGAA GTTC 2544

- (2) INFORMATION FOR SEQ ID NO:196
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 606 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PORPHYROMONAS GINGIVALIS
- (ix) FEATURE:
- (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196

ATGACAGTAA AGCGCGCAGT GCGAATAGCA CTTCTCACGC TGATAGGCAT TCTTTTTC 60  
 TCACCTTCTC TTGTTCCGGC GCAAAGTCTT TTCAGCACCG AACATGTCTT GCAACTATAC 120  
 AACCAAGATAC TCTATGGAGA GTCGCGCGCG GATACCGTGG CAGAGAAAAC GGCAGGTGAG 180  
 65 TCGGCATTTT CTTTATAGA CAAACTCATC AATCTCGGCC GCACTTTCCT CGGCAAAACCA 240  
 TATCGCTATC GCGGTCTTTC CCCATGGCGG ATGGAAGTGT CCGGCTATGT GTCTTACCTC 300  
 TACTCCAAAT TCGACATCAA ACTCCACGT GGTGCGGCAG CACAGAGCCA ATATACGAAT 360  
 CCTATCGAGC GCGAGGATGT TCGTCCGGGC GACCTCCTTT TTTTCAAAGG CGCAATGCA 420  
 70 CGCAGCAACC GTATCGGGCA TGTAGCTTTG GTCGTATCTG TCGATGAAGA TGATATTACC 480  
 ATGATGCACA GCGCAATTC GCGAGCGATC GTGATCGAAA AACTCAATCG CAGTGCATAC 540  
 TTCTCCGCTC GCTTGGTGAG CTATGGCAGG GTACCCGGAG CCAAGAGAGT GATCCACGA 600  
 AAAAGT 606

- (2) INFORMATION FOR SEQ ID NO:197

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1365 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197

ATGAAACGGA	CAATCCTCCT	GACGGCACTG	ACCGTCCTAT	CTTCGGCTCTC	CTTGCTTGGT	60
GCACAAAATG	AATCGGAAGC	ATCAACCAAT	CCGATGTCAG	GCCTCTCCCT	GGAAGACTGT	120
ATCCGGATAG	CCAAGGAGCG	CAACCTGAAT	CTGCGCAGAC	AGGAGATCGA	ACAAGAAAAC	180
CGAATCATTA	GTCTCGATGC	AGCACGACAC	AGTTTCCTGC	CCTCGGTCAA	TGCAGGCATC	240
GGACACAAC	ATAGCTTGGG	ACGTTGAAA	GACAAAACGG	GAGTAACUGT	AGATCGCTCC	300
TCGATGATA	CCAATCTCAG	CATCGGAGCT	TCGGTGGAA	TATTGAGCGG	CACACGTGGT	360
CTGCACGACC	TCAAGCAGCA	AAAGTACAAC	GTGGAGGATS	GTATAGCCCG	ACTTCAAAAA	420
GCGCGTGAAG	ACCTCAGCCT	GCAAAATCGCG	GCTCTCTATA	TCAATTGTCT	CTTCCGTCAG	480
GAAATGACTC	GTACGGCAGA	AACACAGTTG	GCACTGATTC	GCGAGCAACG	CAATCGCACG	540
GCCGAAATGG	TTCGCGTAGG	TAAATGGGCA	GAGGGTAAGC	TCCTCGACAT	AAATGCCGAG	600
ATGGCCAAGG	ACGAACAAC	TCTCGTACAA	TATCGTTCCG	AGGAGGAGCT	GGCTCGTCTG	660
GACTTGGGGC	AAGCCCTCGA	ACTGGAGCAC	CCCGAAAGCA	TTGCAGTCAA	GGCTCCCGAC	720
ACAGACGTTT	TCGTAGCAGA	AAGGTTGGGA	TCTCTCCTTG	CTCCCGAAGA	GATCTATCGC	780
ACGGCTCTCG	GCTTGAAACC	GGCACTGCAT	TCGAGCGAGC	TGCAAAATAGC	TTCCGCACGC	840
GAAAGTCTGG	CCTCGGCTCG	TGCGGCATAC	TTCCCGACGC	TCAGCCTCTC	TGCCGGATAC	900
AGCAACGGTT	ACTTCGCGA	CCTCGGCAAG	GAGTATGCCG	CCATCAACCC	CTCCTTCTCC	960
GAACAGTGGG	AGAACAACGG	CAGCTACAGT	ATCGGACTCT	CTTTGAATAT	CCCCATCTTC	1020
TCTGCCATGC	AAACGCAAGA	TGCGGTTCCG	AGCAGTCGCC	TGCAAAATAGC	CTCAAGCGAG	1080
CTTCGACTCG	TCGAAGAGAA	AAAAGCCCTC	TATTAAGAGA	TCAGGCAAGC	ATACAGCAAT	1140
GCCGTGGCAG	CGGATAAGGC	CATCGCAGCA	GCCGAAAACA	GCAAGGCCGC	TACGCTCAAG	1200
GCAIACGAAT	ACGCTCGCGA	CAGCTTCGAG	GCAGGGCGCT	TGTCTGCCTA	CGAATATGCC	1260
GAGGCAAAAA	CAAAATACGC	CCTCAGCCAA	GTGGAAGAAC	TTGCTGCCAA	GTATGACTTC	1320
ATATACAAAG	CCAAAGTTT	GGATTCTCTAT	CAGGGCAAG	ACTTC		1365

(2) INFORMATION FOR SEQ ID NO:198

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1332 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198

ATGCGTTTCC	AACATTATCT	CATCTGTACG	GCTGCCGTAG	CGGCTTTGGC	TGCGAATCCC	60
CTTACGGGCC	AATCGAATAT	GACCTCGAA	GAGTGACATG	ACTATGCACG	CCGGCACAGT	120
TCGGCCGTGG	CGCTGTCCGC	TGCGGAAC	GAGCAGTCCA	AGGCCGATTA	CCTTCAGGCC	180
GTCGGCAATT	TTCTGCCCCG	TGTATCGGCC	GGAACCGGTG	CTTCGTGGAA	TTTCGGACGC	240
GGATTGGATG	CCGAGACGAA	TACCTACACC	GACATCAACA	GCTTCAACAA	TTCTGACAGC	300

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	ATACATGCCA	CGATGACCT	TTTCGACGGT	TTGCAGAGTG	TCTATCGACT	GCGGATGGGS	360
	CATGCACGCC	GGGAGGCTTC	GCGCCTCTCC	GTTCGCGAGC	AGCAGGAGCT	GGCAGCTCTC	420
	GGCACCACCG	AGGCCCTACTA	CGACCTCGTC	TATGCGCGCC	AAATGCAAGA	GCTGGCCATG	480
	CAGAAGTACG	AGGAGAGCAG	CCGCCCTCCAC	CGGCAGACGG	CTCGAATGGA	AGAGCTGGGG	540
5	ATGAAGAGTC	GTCCCGATGT	CCTCGAGATG	CAGTCGCGAA	TGGCCGGTGA	CCGTTTGGCC	600
	CTGACTCAAG	CGGACAATCA	GTGCATCATC	GCTCTGATCC	GGCTCAAAGA	AAAAATGAAC	660
	TTCCCATCG	ATGACGAACT	CGTCGTAGAC	GATATGCCGG	CTGACAGTCT	CTCCGCCGAC	720
	ATGGCCGAAT	CGGACAGCTC	GGCCGGCGTC	TTGCCCGGTG	CTGCCCATCA	TCATCCCGTC	780
10	CTCCTCGGTG	CCAAACTCGA	CGAGCAGGCT	GCCACCGACC	GTTCGCGAGC	CGCGCGAGGT	840
	GCATTCCTGC	CGAGTGTGTC	GGTATCCGGA	GGATGGAACA	CGGGATTCTC	ACGCTTTTGG	900
	AATGGATCGG	ACTATACGCC	CTTCAGCGAG	CAGTTTCGGA	ACCGTCGGGG	GGAAATACGTC	960
	AGTCTGAATC	TGAGTATCCC	CATCTTTTCC	GGATTCAGCC	TTGTGAGCCA	TCTGCGTCAG	1020
	GCGCGTGGCG	AACGCAGGGC	GGCAATCGTC	CGACGGGGCG	AAGCGGAGCG	CAGGCTCTAC	1080
	AGCGAGATCG	CCCAAGCCAT	GGCCGACCGG	GATGCCGCTC	TGGCTTCTTA	CCGCCAGGCG	1140
15	AAGGAGCATA	CCGACGCCAT	GCAAAACCGCT	TACGAAGCCG	TCTTGACGCG	TTATGAGGAG	1200
	CGGCTGAATA	CGGCCATCGA	CCTGACCACT	CAGGCCAATC	GGCTCCTGGA	TGCCCGGTGTG	1260
	CAGCGACTGA	GAGCGGCCAT	GACCTACCGG	CTCAAATGCA	AACTCATAGC	CTATTACGGC	1320
	TGCCTTTCCG	AC					1332
20	(2) INFORMATION FOR SEQ ID NO:199						
	(i) SEQUENCE CHARACTERISTICS:						
	(A) LENGTH: 2820 base pairs						
25	(B) TYPE: nucleic acid						
	(C) STRANDEDNESS: double						
	(D) TOPOLOGY: circular						
	(ii) MOLECULE TYPE: DNA (genomic)						
30	(iii) HYPOTHETICAL: NO						
	(iv) ANTI-SENSE: NO						
35	(vi) ORIGINAL SOURCE:						
	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS						
	(ix) FEATURE:						
40	(A) NAME/KEY: misc feature						
	(B) LOCATION 1...2820						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199						
45	ATGAACAAAT	TTTACAAATC	ACTTTTGCAG	TCAGGACTGG	CTGCCCTTCGT	GTTCATGGCA	60
	ACTGCACTGA	CGGCTTCTGC	ACAGATTTCC	TTCCGAGGGG	AACCCCTTGG	TTTCTCTTCA	120
	AGATCCGTCG	GAACGCATTTC	ATTTCGACGAT	GCAATGACTA	TCCGCCTTAC	TCCGGATTTC	180
	AATCCGGAAG	ACCTGATCGC	ACAGAGCCGT	TGGCAATCGC	AAAGAGATGG	CCGGCCCGTC	240
	CGGATAGGAC	AAGTAATACC	GGTGGATGTG	GACTTTGCAT	CCAAGGCTTC	GCACATCTCT	300
50	TCCATCGGAG	ACGTAGATGT	ATATCCGCTG	CAATTCAAGT	TGGAAGGAGC	CAAAGCCATT	360
	ACGCTTTATT	ACGATGCATT	CAATATTCCG	GAGGGCGGAC	GCCTCTATAT	CTATACCCCC	420
	GACCATGAAA	TTGTCTTGGG	AGCATATACG	AACGCCACTC	ATCGCCGCAA	CGGAGCTTTT	480
	GCCACAGAGC	CGGTACCGGG	GAGTGAGCTT	ATTATGGATT	ATGAAGTGTG	TGCGGAGGGG	540
	ACTTTGCCCTG	ACATCAAGAT	CTCCGCTGCG	GGTTATATAT	TCGACAAAGT	CGGCGGACGC	600
	CCCGTAAACGG	ATAACCAATTA	CGGGATCCGGT	GAGGACGATT	CCGATTCCGA	TTGCGAGATC	660
55	AACATCAATT	GTCTGAAAGG	TGCAGACTGG	CAGGCAGAGA	AGAACGGTGT	GGTGCAAAATG	720
	ATCATGGTAA	AAGGACAGTA	TATCTCAATG	TGCTCAGGCA	ACCTGCTCAA	TAATAAGAAA	780
	GGAGACTTIA	CTCCGCTGAT	CATTTCGCCC	GGACACTGTG	CTTCCATAAC	AACCAATTTC	840
	GGTGTAAAGC	AATCCGAGTT	GGATAAGTGG	ATCTTCACCT	TCCACTATGA	MAAAGAGGSA	900
60	TGCAGCAATG	GTACATTGGC	CATCTTCOGT	GGCAACAGTA	TCATCGGAGC	TTCCATGAAG	960
	GCTTTCTTCC	CGATCAAAGG	TAAATCCGAT	GGTCTCTTGC	TGCAACTCAA	CGATGAAGTC	1020
	CCTCTGCGCT	ATCGTGTCTA	TTACAAATGGA	TGGGACAGTA	CGCCCGATAT	TCCCTCGAGC	1080
	GGTCCCGGTA	TTATCATCC	GGCCGGAGAT	GCCATGAAGA	TTCCCATCCT	AAAGAAGACT	1140
	CCGCTCTGTA	ATACATGGAT	CTCCTCCAGT	GGTCCGGAG	GGACTGACGA	TCACTTCTAT	1200
65	TTCAAATACG	ATCAAGGTGG	TACGGAAGGA	GGATCCTCCG	GTCTCTCTCT	CTTCAATCAG	1260
	AATAAGCAGC	TGGTCGGCAC	ACTGACCGGA	GGTGCCCGCA	ATTGTGGCGG	GACGGAGTTC	1320
	TACGGCAGAC	TGAACAGTCA	TTGGAACGAG	TATGCATCCG	ATGGCAATAC	GAGCGCATG	1380
	GACATCTATC	TGGATCCCCA	AAACAATGGC	CAGACGACCA	TCCTCAACGG	AACGTATCGT	1440
	GACGGTTATA	AGCCTTTGCC	CTCTGTGCC	CGGCTATTGT	TGCAGTCTAC	AGGCGATCAG	1500
70	GTGCAATTGA	ATTGGACGGC	TGTTCTCTGCC	GATCAATATC	CATCATCTTA	TCAGGTGCGA	1560
	TACCACATAT	TCCGAAATGG	AAAGGAAATA	GCTACGACAA	AGGAGTTGTC	CTATTCCGGAT	1620
	GCCATCGAGC	AAAGTATTAT	CGGTAGCGGT	ATCATTTCGAT	ACGAAGTAA	CGCACGCTTC	1680
	ATTATCCCTT	CGCCGTTGGA	TGGAGTGGAA	TCTTATAAGG	ATACGGACAA	GACTTCTGCC	1740
	GACCTTGCCA	TAGGAGACAT	TCAGACCAAG	CTGAAGCCGG	ACGTAACACC	TGCCCCGGA	1800
75	GGAGGAGTAT	CATTAAAGCTG	GAAAGTTCCT	TTCTTAAGCC	AGTTGGTTTC	CCGATTCCGA	1860
	GAAAGCCCCA	ATCCTGTGTT	CAAPACCTTT	GAAGTGCCCT	ATGTTCTGCG	CGCAGCCGCA	1920

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5 CAAACCCCA ATCTCCCGT TGGCGTAGTC ATTGCAGACA AGTTTATGGC CGGTACATAT 1980  
 CCCCAGAAAGG CTGCTATGCG TGCCGTTTAT GTAATGCCAT CCGCTCCGGA CTCTACTTTC 2040  
 CACCTCTTCC TCAAGAGCAA CACAAACAGA AGATTGCAGA AGGTGACAA CCGCTCCGAT 2100  
 TGGCAGGCCG GAACATGGTT GAGGATCAAT TTGGATAAGC CGTTCCCGGT GAATAATGAC 2160  
 CATATGCTTT TTGCCGGTAT CAGAATGCCT AATAAGTACA AGCTCAATCG TGCTATCCGT 2220  
 TATGTAAGAA ATCCGGATAA CCTTTCTCC ATTACCGGTA AGAAGATTTC ATATAACAA 2280  
 GGAGTCTCTT TCGAAGGCTA CGGAATACCC TCGCTCTTGG GCTATATGGC TATCAATAT 2340  
 CTGGTGGTAA ATACCGATGC TCCGAAGATC GATATGTGCG TTGTACAGGA GCCTTATGCT 2400  
 10 AAGGGAACGA ATGTGGCTCC ATTCGCCGAA TTGGTCGGCA TATATGTCTA TAAGAACGGA 2460  
 ACATTTATCG GCACACAGGA TCCATCCGTC ACAACTTATT CGGTTTCAGA CGGAACAGAG 2520  
 AGCGATGAAT ACGAAATAAA ACTGGTATAT AAGGGATCGG GCATTTCGAA TGGCGTTGCT 2580  
 CAGATTGAGA ATAACAATGC TGTCGTTGCA TATCCGTCG TTGTAACAGA TCGTTTCAGC 2640  
 ATTAAGAACG CTCATATGGT TCACGCTGCC GCCCTCTACT CATTGGATGG CAAGCAGGTT 2700  
 CGTTCITGGA ACAACCTCCG CAATGGCGTG ACATTGAGTG TTCAAGGACT TACGGCCGGT 2760  
 15 ACTTATATGC TCGTTATGCA GACGGCAAC GGCCTGTGA GCCAAAGAT CGTGAAGCAG 2820

## (2) INFORMATION FOR SEQ ID NO:200

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2010 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 25 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 30 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 35 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2010  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200

ATGAATATC TTATCAGACT CTCTTATCA TTGATGTTAC TCTCTCTCG GACGGGCTGT 60  
 ACACACGAGG AGCTCTCTAT TTGCGATGGC GAGAATACGC TTGTTTACG CGTAGAGACC 120  
 GGTAAAGCCC CAAATGCTCG TGCCACAGAA CCGGTCAGG GCATATACAA TGAGAATAAA 180  
 GTAGGCTCCA TTTCTGTGCT CTCTATTTA GAGGGACAAC TTCGTTGGCA GGTGAAGTCT 240  
 45 ACAGACTATC AAATCCATGA AGGGGCGCTAT ATCATTCCGG TCAAAGAGCA AATGCGACCA 300  
 CTATTCATG GCAACAACAA CTTCAGCATC TATGTAGTGG CCAATCTCGA TTTCAATGCT 360  
 CCGGCCACAG AAGCTGCGCT TTCTCAATTT GTGGTAGAGA AATCTATTGA AGTCTCTTCT 420  
 ACGACAGCCC CTGCCGATTT CGTAATGCTT GTCATGGCA ATAAGCAGAT CAATATGGCT 480  
 ACGACAGAGG SGAAACTGTT GGGGGATTAT AAATCAAAC GAGTGGCAGC AAAGATTCCG 540  
 50 ATGATAAAAC CCACCATCAA TGTGCAAGGA TATGAAGTGG TCGGAAATAT ACAGGCAAG 600  
 TTTGCAATTT CGGTAACGAA GGGGTTCTTT ACCACAGAAG CTCGAAGAT CUCAGCTGCT 660  
 GCATCCTATA AGACATCGGA ATATCTTGAT ATTGCAGAGT CGGCACCTGC CAATTCTATC 720  
 CATTCTATT CTACTATAA CAAATGGACA CTCTCCACAC CGGAGAAGCG ACCGGAATTC 780  
 55 TTATCATGTT TCAAATTCAA AAAGACAGGA CAGCCGACAC ACACAGCCAA ACCGTACTAC 840  
 TACAGAGTGC CCTCGAATC TCAGGACAAT CAGGTCAAGA GCAATGTCTT CTATAATCTG 900  
 AATGTGAAAA TCGAATCTTT GGGTTCTTTA CAAGAGCCGG AAGCTGTTTC TGTAAACGGC 960  
 ACACTGCGAA TAGAAGAATG GATTCTCCAT CAGGATGCAT TCAATCTGCC TGCCACCAAT 1020  
 TACTTGATAG TGGACAGCA CGAATCTTC ATGAATAACG TGAACACATA CTCGGTGAAA 1080  
 60 TATCAAACTT CGCAGAAACC AATCAGCATT AGCATACAGT CAGTTACCTT TAGCTAOGTC 1140  
 TCTTCTGATG GCACTCAGCA CAATGATCTT GTAGCAAGTA GTAGCGACCA GTATCCTACG 1200  
 ATTACAAGCG ATAATACAAG CATCATAATC ACTTCCAAGA TACCGGTTAA TAACGTACCA 1260  
 AAGAAGATCG TTTTGTAGGT AACTAATGGG GTAGCCGTTT TGAAGAGAC TGTCACAGTA 1320  
 CTCCAATATC CTGCACAATT TATTGTCAAT ACACTTGGCA CAGCATCGGC ATGGAGACCA 1380  
 GACGGATCTT TGGCTCCGGG GCTTAACAAT AAAGCGATTT ACCATGTCGT AGTACTGGTT 1440  
 65 CCACCCGAGA ATTTATTTGA AGATGGGACA CAGACAATCA TCGTTATCC CCCCCTGAA 1500  
 ACAATTTCTT TTCATAAGAA AGAGAACAAT ACCTATCCGA TAGTATGGTC TGACACAAAT 1560  
 ACGACAAAC AGGACCTTGA GACATCAAGA ATGATTTCAC CTTCCTTTGA GTTAGCCTCC 1620  
 CAACCTGGGG CTACTCTCCC GATGCCCTAT CTCGAGTATT GGCCAGGGAC ATCATATCTC 1680  
 70 CTGTGACTATT CGGGAACTA TAATAATAAG AGATACGCTT TGTTAATTG CGCTTTTAC 1740  
 TGGGAGAAAA GAAAAGTTAA TAACGAAGAA ATTAATTCG ATGACTGGCG TTTGCCGACA 1800  
 GAAGCTGAGA TCAAATTGAT AGATAAGCTG CAACATAATG AGCAGAGTGC TGTCCAAGCT 1860  
 ATCATGACAG GGAATTATTA TTGGGATAGT TACTCTGCAA ATGGGTCTTA TAAATGCAA 1920  
 GGAGGAGGGG GCAAGGAAA TTCTCCAAA GCCTATGTTT GTTGGCTGCG GGATGTGAAA 1980  
 75 AAGCCGATTC GTGACAACAA GTCAGGTAAG 2010

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## (2) INFORMATION FOR SEQ ID NO:201

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3846 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...3846

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:201

25	ATGCGAAAAA	TTTTGAGCTT	TTTGATGATG	TGCTCTCTGC	ATTTAGGTCT	ACAATCTCAG	60
	ACTTTGGCATG	GAGATCCGGA	CTCAGTGGCA	GCCCTACCTT	CTATCGGTAT	TCAAGAGTCA	120
	AGTTGTACCC	GAATCACGTT	CGAGGTTGTT	TTCCCGGGAT	TTTATAGTGT	GGAAAAACGA	180
	GAAAGGCAACC	AGTCTTTCA	GCACATTTC	ATGCCGGGTT	GTGGCTCCTT	TGGGAATCTG	240
30	GGCGAAGCTG	AATTGCCTGT	TTTGAAGGAG	ATGATAGCCG	TTCCGGGAAT	TTCAACAAGT	300
	AACGTTGCTG	TAAAAATCAA	AGAGACGGAG	ACATTCGACA	ATTATAATAT	CTATCCTAAT	360
	CCTACCTATG	TCGTAGAGGA	GTTGCCTGAG	GGGGGGACTT	ATCTGGTAGA	GGCTTTCCGG	420
	ATAAACAATG	ACTATTATAG	CCAAAATGTA	AGCCTCCCTT	CTACTCACTA	TGCTATTCTT	480
	CAAGACGGGT	ATTTTCGCTC	ACAAAGATT	ATCGAAGTTA	CCCTGTATCC	TTTTCGATAC	540
	AACCTCTGCC	GACAAGAAAT	TCTATTGCGA	AAAAAATCG	AGGTTACAAT	AACCTTCGAT	600
35	AATCCTCACC	CACCTTTACA	AAAAACACC	GGCATATTTA	ACAAAGTAGC	CTCCTCTGCA	660
	TTTATTAAAT	ATGAAGCTGA	TGGCAAATCG	GCGATAGAAA	ATGATATGGT	GTTCACTGCT	720
	GGTACAACAA	CGTACATAAG	CGGAAATGTT	GCCAGCAACC	TCCCTCAGAA	CTGTGACTAC	780
	TTGGTTATTT	ACGATGATAT	GTCAACGTA	AATCAACAAC	CACACGACGA	AATCAAAACGG	840
40	CTGTGCGAAC	ATAGAGCCCT	CTACAACGGC	TTTGATGTAG	CTGCTGTAAG	TATAAAGGAC	900
	GTATTGAATA	GCTTCCCATC	AAATGCCACC	TCATACATCA	ACGAAACTAA	ACTGAAAAAT	960
	TTCAITCGCT	CAGTTTACAA	CCAAAGCAAT	GCGAAGAGGA	CTTTAGATGG	CAAACTGGGA	1020
	TACGTGCTAC	TGATCGGAAA	ACCATTGAGC	AAATATTGGG	CTGACACTGA	TAATACAAAA	1080
	GTCCCAACCT	CTTTTATTCA	TAATGTCTCC	TTAATTCCAA	GTCACTCAAC	TTTTGGTTCC	1140
45	ATATGCGCCT	CGGACTATTT	TTTTAGTTGT	GTTCGCCCCC	TTGATACTGT	CGGCCGATTG	1200
	TTTATCGGCT	GATTTAGCGT	CACCAATGCT	CATGAATTGC	ACAATCTGAT	TGAAAAGACT	1260
	ATCAACAAAG	AAATCTCATA	TAATCCTATT	GCACACAAAA	ATATTCTTTA	CGCAGAAGGG	1320
	AAAGGCTGCC	ATGCTCCAAT	CTTACGTTTA	TTCTTAAAG	AAATCGCCTC	TGGTTACACA	1380
	GTCAACTCTA	TCTTAAATCT	TAATCAGGTC	TCTGCAATAG	ACTCGATATT	TGACTGCTTG	1440
50	AATAATGGTT	CCCATCATTT	TTATTTAAAC	ACTCATGGAA	TGCCGACTGT	TTGGGGGATA	1500
	GGGCAGGGAC	TCGACGTCAA	TACTCTAACA	GCCCGATTGA	ACAATACATC	TTCGACGGGA	1560
	TTATGTACGA	GTCTATCATG	TAGTTCCGCT	GTAGCAGATT	CAACTATTAG	ATCGCTTGGA	1620
	GAAGTCTCTA	CCACATACGC	ACCTAACCAAG	GGATTCTCGG	CTTCTTAGG	AGGAAGCAGA	1680
	GCCACCCCAAT	ATGCCGTTTA	TTTAGAAGGC	CCCTGTCTCT	CGTCAGAATT	TTATGAATAT	1740
55	TTACCTTATT	CTTTATATCA	CAATCTCTCG	ACTGTTGTG	GCGAAATGTT	GCTATCATCC	1800
	ATTATCAATA	CTAATTCTGT	TGATACGTAT	TCGAAATTCA	ACTTCAATTT	GCTTGGCGAC	1860
	CCTGCACTAA	ACATTATGGC	TCATGGCATG	GAGGTTAGTA	ATTGTATTAC	ACTACCAAAC	1920
	AACACCATTA	TAAGCAGTCC	GATAACAATA	AAAAATGGTG	GCTGCCTAAA	AATACCGGAA	1980
	AAAGGAGTTT	TGCATTTTAC	TAATAATGGC	TCCATACAAG	TCATGTCCCG	AGGAACCTCTG	2040
60	GAAATAGGCA	ATCAGGCTAA	AATATCCGGA	GAGACCGGTG	CTAACCCAC	CTTTATTACC	2100
	GTTTACG3CG	ATGGTCTTGC	GATTAAACAAG	CAGGTAGAGA	TAGACAATAT	AGACCGACTT	2160
	AACTGTGTTT	CTACGCATTC	GGTCATGCC	AAATTTCAAT	TTGACAGTGT	GAAATTC AAC	2220
	AGTGCCCGCG	TGTATACAA	GAATGTGAC	CTAAGCGTTG	AAAACAGTAT	GTTTAGCAAT	2280
	CGAATGACA	TTATTTCAAA	GAATTTGAC	CTAAGCGTTG	AAAACAGTAT	GTTTAGCAAT	2340
65	TCCGGGATAA	CGGTATTTCA	GCCTATGGCT	ACAAGCTCCA	TCACCGGATT	ATCTACAAAA	2400
	GCAAAGATTA	CCGACAATAC	TTTTTTTCG	ACAGGAAACT	TCCCTACCA	TATCACAAAC	2460
	ACGCCAGGCT	TAACAGCAAC	CTCCATGCT	GCCATCAAGT	TAGACAATAT	TCCTGAGTAT	2520
	TACATTTCCG	GTAATAAAAT	AGTCAATTGC	GATGAGGCTC	TTGTACTAAA	TAATAGTGGC	2580
	AACAGAACGA	ACAGACTCCA	CAATATCACA	CGGAATGTGA	TAAAAAACTG	TAGGATTGGG	2640
70	AGCAGCGTTT	ATAATTCCTA	TGGTATTTAC	AACCGAAATA	AGATCAGTAA	CAATCATATA	2700
	GGAGTACGTC	TCCTCAACAA	CAGTTGTTTT	TATTTGATA	ATGCTCCTGT	AATCAATGAA	2760
	GAAGATAAGC	AGACGTTTAT	TTCTAATAGG	ACTTGGCAGC	TCTATTATC	AAACGGTACA	2820
	TTCCCTCTCA	ACTTCCATTA	CAACAGCTTC	CAGGGGGGAG	ATACAGATAC	ATGGATTTAC	2880
	AACGACACGT	ATACGAATCG	CTATATTGAC	GTTTCAATA	ATCACTGGGG	CAACAATGAT	2940
75	TTGTTTGATC	CGAATCAGGT	TTTCAATACG	CCAGACTTGT	TCATTTGGAT	ACCTTTTGTG	3000
	GATGGATTGC	CAAAATGGGAG	ATCGGGCAAT	AGCTCTGCTG	AAGCAGTAGA	ATTCCAAACA	3060

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5	GCATTGGACT	GTATTGGCAA	TAGCGATTAT	CTTTCGGCAA	AAGTGGCTCT	CAAGATGATG	3120
	GTTGAAACCT	ACCGGGAATC	CGACTTTGCA	ATAGCTGCCT	TGAAGGAATT	GTTTCAGGATA	3180
	GAGAAAATGT	CAGGCAACGA	TTACGAAGGC	TTGAAAGAAT	ATTTTCAGATC	CAATCCAACC	3240
	ATCATCTCTT	CCCAGAACTT	GTTCCCGACA	GCTGATTTCC	TGCTGCGCG	ATGCGATATT	3300
	GTGTGTGAAA	ACTATCAGTC	TGCCATCGAT	TGGTACGAAA	ATCGCTTGAA	TAGTGAATC	3360
	TCCTATCAGG	ACAGTGTTTT	TGCAGTCATT	GACCTTGGTG	ACATTATATG	GAATATGCAG	3420
	TTAGACTCAC	TCAGAGGGAC	TGGTATAGAT	TTGAACATAC	TTTCCTGTGA	ACAAAGGAAA	3480
	TCGCTCGAAA	GCCATCAAAA	TGTAATAAAT	TATTTGTTGT	CAACTCTTCC	CGAATCAACA	3540
	GGTACTCTCC	TGCTCCATT	AGAATGCAAC	AAATCAAGCC	TTGATAAATC	CAAGATAATC	3600
10	TCTATTTGCG	CCATTCGGGC	GAAAGCTGTT	GTAACAATAA	TCTACTATAC	CGATAACCCCT	3660
	TCTGTCTCTG	TAATAAAAAAT	ATATGGAATA	AATGGAGCCT	CGGCTGATAT	AACCGGGTTG	3720
	CCCAACATC	TATCCGAAGG	TTATTACAGC	ATACAGTTCA	ATACATCCAA	CTTTGATCCC	3780
	GGTTTCTACC	TGGTAACGCT	AAATGTTGAT	CAGAAAATTA	TAGATACGGA	AAAATTACGA	3840
15	ATCAAA						3846

## (2) INFORMATION FOR SEQ ID NO:202

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 3822 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: circular
25	(ii) MOLECULE TYPE: DNA (genomic)
	(iii) HYPOTHETICAL: NO
30	(iv) ANTI-SENSE: NO
	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PORPHYROMONAS GINGIVALIS
35	(ix) FEATURE:
	(A) NAME/KEY: misc feature
	(B) LOCATION 1...3822

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202

40	ATGATGTGCT	CTCTGCATTT	AGGTCTACAA	TCTCAGACTT	GGCATGGAGA	TCCGGACTCA	60
	GTGGCAGCCC	TACCTTCTAT	CGGTATTCAA	GAGTCAAGTT	GTACCCGAAT	CACGTTCCGAG	120
	GTTGTTTTCC	CCGGATTTTA	TAGTGTGGAA	AAACGAGAAG	GCAACCAAGT	CTTTCAGCGC	180
	ATTTCCATGC	CGGGTTGTGG	CTCGTTTGGG	AATCTGGGCG	AAGCTGAATT	GCCTGTTTTG	240
	AAAAAGATGA	TAGCCGTTC	GGAATTTTCA	ACAGCTAACG	TTGCTGTAAA	AATCAAAGAG	300
45	ACGGAGACAT	TCGACAATTA	TAATATCTAT	CCTAATCCTA	CCTATGTCGT	AGAGGAGTTG	360
	CCTGAGGGGG	GGACTTATCT	GGTAGAGGCT	TTCGCGATAA	ACATGACTA	TTATAGCCAA	420
	AATGTAGCC	TCCCTTCTAC	TCATATGTC	TATTTCTCAG	ACGGGTATTT	TCGCTCACAA	480
	AGATTTATCG	AAGTTACCCT	GTATCCTTTT	CGATACAACC	CTGTCGACA	AGAAATCTA	540
	TTTGCAAAAA	AAATCGAGGT	TACATAACT	TTGATAATC	CTCAGCCACC	TTTACAAAAA	600
50	AACACCGGCA	TATTTAACAA	AGTAGCCTCC	TCTGCATTTA	TTAATTATGA	AGCTGATGGC	660
	AAATCGGGGA	TAGAAAATGA	TATGGTGTTC	AGTCGTGGTA	CAACAACGTA	CATNAGCGGA	720
	AATGTTGCCA	GCAACCTCCC	TCAGAACTGT	GACTACTTGG	TTATTTACGA	TGATATGTTT	780
	AACGTAAATC	AACAACCACA	CGACGAAATC	AAACGGCTGT	GCGAACATAG	AGCCTTCTAC	840
	AACGGCTTTG	ATGTAGCTGC	TGTAAGTATA	AAGGACGTAT	TGAATAGCTT	CCCATCAAAT	900
55	GCCACCTCAT	ACATCAACGA	AACTAACTG	AAAAATTTCA	TTGCTCAGT	TTACAACCAA	960
	AGCAATGCGA	AGAGGACTTT	AGATGGCAAA	CTGGGATACG	TGCTACTGAT	CGGAAAACCA	1020
	TTGACCAAT	ATTTGGCTGA	CATGATAAT	ACAAAAGTCC	CAACCTCTTT	TATTCATAAT	1080
	GTCTCCTTAA	TTCCAAGTCA	TCCAACCTTT	GGTTCCATAT	GCGCCTCGA	CTATTTTTTT	1140
	AGTTGTGTTT	CGCCCTTGA	TACTGTGCGC	GATTGTGTTA	TCGGTGGATT	TAGCGTCAAC	1200
60	AATGCTCATG	AATTGCACAA	TCTGATTGAA	AAGACTATCA	ACAAAGAAAT	CTCATATAAT	1260
	CCTATTGCAC	ACAAAATAT	TCITTAACGA	GAAGGGAAAG	GCTGCGATGC	TCCAATCTTA	1320
	CGTTTATTCT	TAAAAGAAAT	CGCCTCTGGT	TACACAGTCA	ACTCTATCTT	AAAATCTAAT	1380
	CAGGTCTCTG	CAATAGACTC	GATATTTGAC	TGCTTGAATA	ATGGTTCCCA	TCATTTTAT	1440
	TTTAACAATC	ATGGAATGCC	GACTGTTTGG	GGGATAGGGC	AGGGACTCGA	CGTCAATACT	1500
65	CTAACAGCCC	GATTGAACAA	TACATCTTCG	CAGGGATTAT	GTACGAGTCT	ATCATGTAGT	1560
	TGCGCTGTAG	CAGATTCAAC	TATTAGATCG	CTTGAGAAAG	TCCTGACCA	ATACGCACCT	1620
	AACAAGGGAT	TCTGCGCTTT	CTTAGGAGGA	AGCAGAGCCA	CCCAATATGC	CGTTTATTTA	1680
	GAAGGCCCT	GTCTCCGTC	AGAAATTTAT	GAATATTTAC	CTTATCTTTT	ATATCACAAT	1740
	CTCTGACTG	TGTTTGGCGA	AATGTTGCTA	TCAATCCATTA	TCAATACATA	TTCTGTTGAT	1800
70	ACGTATTGCA	AAITCAACTT	CAATTTGCTT	GGCGACCTG	CACATAACAT	TATGGCTCAT	1860
	GGCATGGAGG	TTAGTAATTG	TATTACACTA	CCAAACAACA	CCATTATAAG	CAGTCCGATA	1920
	ACAATAAAAA	ATGGTGGCTG	CCTAAAAATA	CCGGAAVAAAG	GAGTTTTGCA	TTTTACTAAT	1980
	AATGGCTCCA	TACAAGTCAT	GTCCGGAGGA	ACTCTGGAAA	TAGGCAATCA	GGCTAAAAATA	2040
	TCCGGAGAGA	CCGGTGCTAA	CCCCACCTTT	ATTACCGTTT	ACGGCGATGG	TCTTGGGATT	2100
75	AACAAGCAGG	TAGAGATAGA	CAATATAGAC	CGACTTAAT	TGTTTTCTAC	GCATTCGGTC	2160

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5	ATGCCCAAAT	ITCATTITGA	CAGTGTGAAA	TTCAACASTG	CCCCGCTGTA	TACAACGAAC	2220
	TGTATITGTGG	AGATAAGCAA	TTGCGAATTT	ACCAATCGAA	GTGACATTAT	TTCAAAGAAAT	2280
	TGTGACCTAA	GCGITGAAAA	CAGTATGTTT	AGCASTTCGG	GSATAACGGT	ATTCAAGCCT	2340
	ATGGCTACAA	GCTCCATCAC	CGGATTATCT	ACAAAAGCAA	AGATTACCGA	CAATACTTTT	2400
	TTTGGGACAG	GAACCTTCGC	CTACCATATC	ACAAACACGC	CAGGCTTAAC	AGCAACCTCC	2460
	AATGCTGCCA	TCAAGTTAGA	CAATATTCCT	GAGTATTACA	TTTCCGGTAA	TAAAATAGTC	2520
	AATTGCGATG	AGGCTCTTGT	ACTAAATAAT	AGTGGCAACA	GAACGAACAG	ACTCCACAAT	2580
	ATCACACGGA	ATGTGATAAA	AAACTGTAGG	ATTGGGAGCA	CGCTTTATAA	TTCCTATGGT	2640
10	ATTTACAACC	GAATAAGAT	CAGTAACAAT	CATATAGGAG	TACGTCTCCT	CAACAACAGT	2700
	TGTTTTTATT	TGATAAATGC	TCTGTAAATC	AATGAAGAAG	ATAAGCAGAC	GTTTATTTCT	2760
	AATAGGACTT	GGCAGCTCTA	TTCATCAAAC	GGTACATTCC	CTCTCAACTT	CCATTACAAC	2820
	AGCTTGACAG	GGGGAGATAC	AGATACATGG	ATTTACAACG	ACACGTATAC	GAATCGOTAT	2880
	ATTGACGTTT	CAATAATCA	CTGGGGCAAC	AATGATTTGT	TTGATCOGAA	TCAGGTTTTC	2940
15	AATACGCCAG	ACTTGTTCAT	TTGGATACCT	TTTTGGGATG	GATTGCCAAA	TGGGAGATCG	3000
	GGCAATAGCT	CTGCTGAAGC	AGTAGAATTC	CAACACAGCAT	TGGACTGTAT	TGGCAATATC	3060
	GATTATCTTT	CGGCAAAAGT	GGCTCTCAAG	ATGATGGTTG	AAACCTACCC	GGAATCCGAC	3120
	TTTGAATAG	CTGCTTTGAA	GGAATTGTTC	AGGATAGAGA	AAATGTCCAG	CAACGATTAC	3180
	GAAGGCTTGA	AAGATTATTT	CAGATCCAA	CCAACCATCA	TCTCTTCCCA	GAACCTGTTC	3240
20	COGACAGCTG	ATTTCTCTGC	TGCGCGATGC	GATATTGTGT	GTGAAAACCTA	TCAGTCTGCC	3300
	ATCGATTGGT	ACGAAAATCG	CTTGAATAGT	GAAATCTCCT	ATCAGGACAG	TGTTTTTGCA	3360
	GTCAITGACC	TTGGTGACAT	TTATTGGAAT	ATGCACTTAC	ACTCACTCAG	AGGGAGTGGT	3420
	ATAGATTTGA	ACATACTTTC	CTGTGAACAA	AGGAAATCGC	TCGAAAGCCA	TCRAAATGTA	3480
	AAAAATTATT	TGTTGTCAAC	TCTTCCCGAA	TCAACAGGTA	CTCTCTGCC	TCCATTAGAA	3540
	TGCAACAAAT	CAAGCCTTGA	TAAATCCAA	ATAATCTCTA	TTTCGCCCAA	TCCGGCGAAA	3600
25	GCTGTTGTAA	CAATAATCTA	CTATACCGAT	AACCTTCTCT	GTTCTGTAAT	AAAAATATAT	3660
	GGAATAAATG	GAGCCTCGGC	TGATATAACC	GGGTTGCCCA	AACATCTATC	CGAAGGTTAT	3720
	TACAGCATAC	AGTTCAATAC	ATCCAACTTT	GATCCCGGTT	TCTACCTGGT	AACGCTAAAT	3780
	GTTGATCAGA	AAATATATAGA	TACGGAAAAA	TTACGAATCA	AA		3822
30	(2) INFORMATION FOR SEQ ID NO:203						
	(i) SEQUENCE CHARACTERISTICS:						
35	(A) LENGTH: 2775 base pairs						
	(B) TYPE: nucleic acid						
	(C) STRANDEDNESS: double						
	(D) TOPOLOGY: circular						
40	(ii) MOLECULE TYPE: DNA (genomic)						
	(iii) HYPOTHETICAL: NO						
	(iv) ANTI-SENSE: NO						
45	(vi) ORIGINAL SOURCE:						
	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS						
	(ix) FEATURE:						
50	(A) NAME/KEY: misc feature						
	(B) LOCATION 1...2775						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203						
55	ATGGCTATCA	TGATGAAAAG	TATTGTTTTT	AGAGCATTTC	TAACGATTTT	GCTCTCGTGG	60
	GCAGCGATCA	CGAATCCGAC	TGCTCAAGAG	ATCTCAGGCA	TGAATGCATC	CTGTCTGGCT	120
	GCTCOCGCTC	AACCGGATAC	TATCTTATAT	GAAAGTTTTG	AGAATGGACC	TGTTCCCAAT	180
	GGCTGGCTTG	AGATAGATGC	TGATGCTGAT	GGTGCCACTT	GGGGAAGCCC	ATCAGGCTCT	240
	TTCTCTGTAC	CTTACGGACA	CAATGGCCTT	TGCACCTACT	CCCATATACG	TTCCGGTATC	300
60	TCAACAGCGG	GCAACTATCT	GATTACACCC	AATATAGAAG	GAGCCAAACG	GGTCAAGTAC	360
	TGGGTATGCA	ATCAGTATAG	TACCAATCCG	GAACATTACG	CAGTAATGGT	ATCGACAACG	420
	GGGACTGCCA	TTGAAGACTT	TGTTTTGTTG	TTTGATGATT	CCATAACAGG	GAACCCGACT	480
	CCTCTTGTAT	GGCGTAGACG	AATCGTGGAC	TTACCGGAAG	GGACCAATAA	TATTGCATGG	540
	CGACATTACA	AACTCACCGA	CTCACACACA	GAATTCCTGA	AATTGGATGA	TGTCACTGTG	600
65	TATAGTTCGA	TCGAAGGGCC	CGAACCTGCT	ACCGACTTCA	CAGTAATCAA	TATTGGTCAG	660
	AATGTGGGAC	GATTGACTTG	GAACATCCG	GAGGATTATC	AACCGGAAGG	AAAGGGGAAT	720
	GAAGAGTTGC	AGCTTAGCGG	CTACAAACATC	TATGCCAAGC	GTACACTACT	GGCACAATAA	780
	AAAGATGTCT	CCATACTCGA	GTATGTGGAC	AGCACTTACT	CTTTGCGAGA	CAATCCCTTG	840
	CAAGTGGAGT	ACTGCGTTAC	AGCCGTTTAC	GATGAAAGCA	TAGAATCTTC	GACCGTATGT	900
70	GGCACGCTGC	ATTACGCCAC	GGATGCCATC	CTTTATGAAA	ATTTTGAGAA	TGGACCTGTT	960
	CCCAATGTTT	GGCTTGTGAT	AGACGCTGAT	GGAGATGGAT	TATAGCTGGG	ACACTATTTG	1020
	AATGCATACG	ACGCTTTTCC	CGGCCATAAT	GGAGGCCATT	GTCCTTGTGC	GGCTTCTTAT	1080
	GTTCCGGGTA	TAGGCCCGGT	GACTCCCGAC	AACTATCTGA	TTACCCCAAA	GGTTGAAGGA	1140
	GCCAAACGCT	TCAAAGTACTG	GGTAAGCACG	CAGGATGCCA	ATTGGGCAGC	GGAACATTAC	1200
75	GGGGTGATGG	CTTCGACNAC	GGGGACTGCT	GTCGGAGATT	TCGTCTATAT	GTTCSAAGAA	1260
	ACCATGACAG	CGAAGCCGAC	CGGCCCATGG	TATGAAAGAA	CCATCAACTT	ACCTGAAGGG	1320

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	ACTAAATACA	TCGCATGGCG	GCATTACAAC	TGTACCGATA	TATATTTCTT	GAAGTTGGAC	1380
	GATATCACTG	TATTCGGGAC	TCCTGCATCA	GAGCCCGAAC	CTGTTACCGA	TTTCGTTGTC	1440
	TCGCTTATTG	AAAACAACAA	GGGACGATTA	AAGTGGAAAT	ATCCTAACGG	CTACGAACUC	1500
5	GATAAGACTG	ATGATAAAGA	CCCAATTGCAG	CTTGCCGGCT	ACAATATCTA	TGCAAAACGGC	1560
	TCGCTCCTTG	TTACATACA	AGACCCGACT	GTITTTGGAGT	ATATCGATGA	GACTTATTCT	1620
	TCACGAGACG	ATCAGGTGGA	AGTGGAAATAT	TGTGTCACTG	CCGTTTATAA	CGACAAATATC	1680
	GAGTCCCAAT	CGGTTTGGCA	TAAGCTGATT	TATGATTCTC	AATCGGACAT	TATCTTATAT	1740
	GAAGGCTTTG	AGGCCCGAAG	TATTCCTGAA	GGCTGGTTGT	TGATTGATGC	TGATGGCGAC	1800
10	AATGTTAATT	GGGACTATTA	TCCTTGGACT	ATGTATGGAC	ATGACAGTGA	GAAGTGATT	1860
	GCATCCCTT	CGTACTTACC	GATGATTGGC	GTITTAATC	CGGATAACTA	TTTGGTTACA	1920
	CCCAGACTCG	AAGGAGCCAA	GCTTGTCAAG	TATTGGGTAA	GTGCGCAAGA	TGCTGTTTAT	1980
	TCGGCTGAGC	ATTATGCTGT	GATGGTTTCT	ACTACGGGAA	CTGCTGTTGA	AGATTTTGTC	2040
	CTCTTGTTCC	AAGAGACAAT	GACCGCTAAG	GCTAACGGTG	CATGGTATGA	GCGAACTATT	2100
15	ACATTGCTTG	CAGGAACAAA	ATATATTGCC	TGGCGGCATT	ATGATTGCAC	CGATATGTTT	2160
	TTCTTGCTCT	TGGATGACAT	TACGGTTTAT	CGTTCTACTG	AGACTGTTCC	CGAGCCTGTT	2220
	ACTGATTTCT	TGTCTCTGCT	TATTGAGAAT	AACAAGGGTC	GCCTGAAATG	GAATTATCCT	2280
	AACGGCTAGC	AACCGATAA	GACTGATGAT	AAAAAACCAT	TGCAGCTTAC	CGGCTACAAC	2340
	ATCTATGCAA	ATGGCTCGCT	CCTTGTTCAC	ATACAAGACC	CGACTGTTT	GGAGTATATC	2400
20	GATGAGACTT	ATTCTTCACG	AGACGGTCAG	GTGGAAATGG	AATATTGTGT	CACTGCCGTT	2460
	TATAACGACA	ATATCGAGTC	CCAATCGGTT	TGUGATAAGC	TGAACATATC	TATCACATCC	2520
	TTGGATAATA	TTCAATCTGA	TACAAGCTTG	AAAATATATC	CTAATCCGGC	ATCGTATGTS	2580
	GTAAGGATAG	AGGGATTGAG	TCGGAGCAAG	TCGACAATCG	AGTTGTATAA	TGCGCTGGGA	2640
	ATTTGCATAT	TAAGGGAAGA	GACTCATTCA	GAGAAAAACGG	AAATCGATGT	TTACGCTCTC	2700
25	AATGACGGAG	TCTACTTGAT	TAAAGTAGTC	GGTGGAAATA	AAACAACAAC	CGAAAAGGTA	2760
	GAGATAAAGA	GGCCG					2775

## (2) INFORMATION FOR SEQ ID NO:204

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2766 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 35 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 40 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 45 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2766

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204

50	ATGATGAAAA	GTATTGTTTT	TAGAGCATT	CTAACGATT	TGCTCTCGTG	GGCAGCGATC	60
	ACGAATCCGA	CTGCTCAAGA	GATCTCAGGC	ATGAATGCAT	CCTGTCTGGC	TGCTCCGGCT	120
	CAACCGGATA	CTATCTTATA	TGAAAGTTTT	GAGAATGGAC	CTGTTCCCAA	TGGCTGGCTT	180
	GAGATAGATG	CTGATGCTGA	TGGTGCCACT	TGGGGAAGCC	CATCAGGGTC	TTTCTCTGTA	240
55	CCTTACGGAC	ACAATGGCCT	TTGCACCTAC	TCCCATATAC	GTTCGGGTAT	CTCAACAGCG	300
	GGCAACTATC	TGATTACACC	CAATATAGAA	GGAGCCAAC	GGGTCAAGTA	CTGGGTATGC	360
	AATCAGTATA	GTACCAATCC	GGACATTAC	GCAGTAATGG	TATCGACAAC	GGGGACTGCC	420
	ATTGAAGACT	TTGTTTTGTT	GTTTGATGAT	TCCATAACAG	GGAAACCGAC	TCCTCTTGTA	480
	TGGCGTAGAC	GAATCGTGGA	CTTACCGGAA	GGGACCAAT	ATATTGCATG	GCGACATTAC	540
60	AAAGTCAACG	ACTCACACAC	AGAATCTTGG	AAATTG3ATG	ATGTCACGTG	GTATAGGTGG	600
	ATCGAAGGGC	CCGAACCTGC	TACCGACTTC	ACAGTAATCA	ATATTGGTCA	GAATGTGGGA	660
	CGATTGACTT	GGAACTATCC	GGAGGATTAT	CAACCGGAAG	GAAAGGGGAA	TGAAGAGTTG	720
	CAGCTTAGCG	GCTACAACAT	CTATGCGAAC	GGTACACTAC	TGGCACAAAT	AAAAGATGTC	780
65	TCCATACCTG	AGTATGTGGA	CAGCACTTAC	TCTTTGCGAG	ACAATCCCTT	GCAAGTGGAG	840
	TACTGCGTTA	CAGCGTTTGA	CGATGAAAGC	ATAGAATCTT	CGACCGTATG	TGGCAGCTG	900
	CATTACGCCA	CGGATGOCAT	CCTTTATGAA	AAATTTGAGA	ATGGACCTGT	TCCCAATGGT	960
	TGGCTTGTGA	TAGACCGTGA	TGGAGATGGA	TTTAGCTGGG	GACACTATTT	GAATGCATAC	1020
	GACGCTTTTC	CCGGCCATAA	TGGAGGCCAT	TGCTCCTTST	CGGCTTCTTA	TGTTCCGGGT	1080
70	ATAGGCCCGG	TGACTCCCGA	CAACTATCTG	ATTACCCCCA	AGGTTGAAGG	AGCCAAAAGT	1140
	GTCAAGTACT	GGGTAAGCAC	GCAGGATGCC	AATTGGGCAG	CGGAACATTA	CGCGGTGATG	1200
	GCTTCGACAA	CGGGGACTGC	TGTGGGACAT	TTGCTCATAT	TGTTGGAAGA	AACCATGACA	1260
	GCGAAGCCGA	CCGGCGCATG	GTATGAAAGA	ACCATCAACT	TACCTGAAGG	GACTAAATAC	1320
	ATCGCATGGC	GGCATTACAA	CTGTACCGAT	ATATATTTCT	TGAAGTTGGA	CGATATCACT	1380
75	GTATTCGGGA	CTCTGCATC	AGAGCCCGAA	CCTGTTACCG	ATTTGTTGT	CTCGCTTATT	1440
	GAAAAACAAC	AGGGACGATT	AAAGTGAAT	TATCCTAACG	GCTACGAACC	CGATAAGACT	1500

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5 GATGATAAAG ACCCATTCGA GCTTGCCGGC TACAATATCT ATGCAAACGG CTCGCTCCTT 1560  
 GTTCACATAC AAGACCCGAC TGTTTTGGAG TATATOGATG AGACTTATTC TTCACGAGAC 1620  
 GATCAGGTGG AAGTGGGAATA TTGTGTCACT GCGGTTTATA ACACAAATAT CGAGTCCCAA 1680  
 TCGGTTTGGC ATAAGCTGAT TTATGATTCT CAATCGGACA TTATCTTATA TGAAGGCTTT 1740  
 GAGGCCGGAA GTATTCTGTA AGGCTGGTTG TTGATTGATG CTGATGGCGA CAATGTTAAT 1800  
 TGGGACTATT ATCCTTGGAC TATGTATGGA CATGACAGTG AGAAGTGTAT TGCATCCOCT 1860  
 TCGTACTTAC CGATGATTGG CGTTTAACT CCGGATAACT ATTTGGTTAC ACCCAGACTC 1920  
 GAAGGAGCCA AGCTTGTCAA GTATTGGGTA AGTGCSCAAG ATGCTGTTA TTCGGCTGAG 1980  
 CATTATGCTG TGAATGGTTC TACTACGGGA ACTGCTGTTG AAGATTTTGT CCTCTTGTTT 2040  
 10 GAAGAGACAA TGACCGCTAA GGCTAACGGT GCATGGTATG AGCGAACTAT TACATTGCCT 2100  
 GCAGGAACAA AATATATTGC CTGGCGGCAT TATGATTGCA CCGATATGTT TTTCTTGCTC 2160  
 TTGGATGACA TTACGGTTTA TCGTTCTACT GAGACTGTTT CCGAGCCTGT TACTGATTTC 2220  
 GTTGTCTCGC TTATTGAGAA TAACAAGGGT CGCCTGAAAT GGAATTATCC TAACGGCTAC 2280  
 GAACCCGATA AGACTGATGA TAAAAAACCA TTGCAGCTTA CCGGCTACAA CATCTATGCA 2340  
 15 AATGGCTCGC TCCTTGTTCA CATAACAAGC CCGACTGTTT TGGAGTATAT CGATGAGACT 2400  
 TATTCTTAC GAGACGGTCA GGTGGAAATG GAATATTGTG TCACTGCCGT TTATAACGAC 2460  
 AATATCGAGT CCAATCGGT TTGCGATAAG CTGAACATA CTATCACATC CTGGATAAAT 2520  
 ATTCAATCTG ATACAAGCTT GAAATATAT CCTAATCCGG CATCGTATGT GGTAAAGGATA 2580  
 GAGGGATTGA GTCGGAGCAA GTCGACAATC GAGTTGTATA ATGCGCTGGG AATTGCGATA 2640  
 20 TTAAGGGAAG AGACTCATTC AGAGAAACG GAAATCGATG TTTCACGTCT CAATGACGGA 2700  
 GTCTACTTGA TTAAGTAGT CCGTGAAAT AAAAAACAA CCGAAAGGT AGAGATAAAG 2760  
 AGGCCG 2766

25 (2) INFORMATION FOR SEQ ID NO:205

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 2763 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

35 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

40 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

45 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205

50 ATGAAAAGTA TTGTTTTAG AGCATTCTA ACGATTTTGC TCTCGTGGGC AGCGATCACG 60  
 AATCCGACTG CTCAGAGAT CTCAGGCATG AATGCATCCT GTCTGGCTGC TCCGGCTCAA 120  
 CCGGATACTA TCTTATATGA AAGTTTGGAG AATGGACCTG TTCCCAATGG CTGGCTTGAG 180  
 ATAGATGCTG ATGCTGATGG TGCCACTTGG GGAAGCCCAT CAGGCTCTTT CTCTGTACCT 240  
 TACGGACACA ATGGCCTTTG CACCTACTCC CATATACGTT CCGGTATCTC AACAGCGGGC 300  
 AACTATCTGA TTACACCCAA TATAGAAGGA GCCAAACGGG TCAAGTACTG GGTATGCAAT 360  
 CAGTATAGTA CCAATCCGGA ACATTACGCA GTAATGGTAT CGACAACGGG GACTGCCATT 420  
 55 GAAGACTTTG TTTTGTGTT TGAATGTTCC ATAAACAGGA AACCGACTCC TCTGTATGG 480  
 CGTAGACGAA TCGTGGACTT ACCGGAAGGG ACCAAATATA TTGCATGGCG ACATTACAAA 540  
 GTCAUCCACT CACACACAGA ATTCTTGAAT TTGGATGATG TCACTGTGTA TAGGTGATC 600  
 GAAGGGCCCG AACCTGCTAC CGACTTCACA GTAATCAATA TTGGTCAGAA TGTGGGACGA 660  
 TTGACTTGA ACTATCCGGA GGATTATCAA CCGGAAGGAA AGGGGAATGA AGAGTTGCAG 720  
 60 CTAGCGGCT ACAACATCTA TCGCAACGGT AACTACTGCG CACAAATAAA AGATGTCTCC 780  
 ATACTGGAAT ATGTGACAG CACTTACTCT TTGCGAGACA ATCCCTTGCA AGTGGAGTAC 840  
 TGCGTTACAG CCGTTTACGA TGAAGCATA GAATCTTGA CCGTATGTTG CACGCTGCAT 900  
 TACGCCACGG ATGCCATCCT TTATGAAAAT TTTGAGAATG GACCTGTTCC CAATGGTTGG 960  
 CTTGTGATAG ACGCTGATGG AGATGGATT AGCTGGGGAC ACTATTTGAA TGCATACGAC 1020  
 65 GCTTTTCCCG GCCATAATGG AGGCCATTGC TCCTTGTGCG CTCTCTATGT TCCGGGTATA 1080  
 GGCCCGGTGA CTCCGACAA CTATCTGATT ACCCCCAAGG TTGAAGGAGC CAAACGTGTC 1140  
 AAGTACTGGG TAAGCACGCA GGATGCCAAT TGGGCAGCGG AACATTACGC GGTGATGGCT 1200  
 TCGACAACGG GGAATGCTGT CCGAGATTTT GTCATATTGT TCGAAGAAAC CATGACAGCG 1260  
 AAGCCGACCG GCGCATGGTA TGAAGAACC ATCAACTTAC CTGAAGGGAC TAAATACATC 1320  
 70 GCATGCCCGC ATTACAACG TACCGATATA TATTCTTGA AGTTGGACGA TATCACTGTA 1380  
 TTCGGGACTC CTGCATCAGA GCCCGAACCT GTTACCGATT TCGTTGTCTC GCTTATTGAA 1440  
 AACACAAGGG GACGATTAAA GTGGAATTAT CCTAACGGCT ACGAACCCGA TAAGACTGAT 1500  
 GATAAAGACC CATTGCAGCT TGCCGGCTAC AATATCTATG CAACCGCTC GCTCCTTGTT 1560  
 75 CACATACAGG ACCCGACTGT TTTGAGTAT ATCGATGAGA CTATTCTTC ACGAGACGAT 1620  
 CAGGTGGAAG TGGAAATATG TGTCACTGCC GTTTATAACG ACAATATCGA GTCCCAATCG 1680

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5	5	GTTCGCGATA AGCTGATTGA TGATTCTCAA TCGGACATTA TCTTATATGA AGGCTTTGAG 1740
		GCCGGAAGTA TTCCTGAAGG CTGGTTGTGG ATTGATGCTG ATGGCGACAA TGTTAAATTGG 1800
		GACTATTATC CTGGGACTAT GTATGGACAT GACAGTGAGA AGTGTAITGC ATCCCCITCG 1860
		TACTTACCGA TGATTGGCGT TTTAACTCCG GATAACTATT TGGTTACACC CAGACTCGAA 1920
		GGAGCCAAAGC TTCTCAAGTA TTGGGTAAAGT GCGCAAGATG CTGTTTATTC GGCTGAGCAT 1980
		TATGCTGTGA TGGTTTCTAC TACGGGAACT GCTGTTGAAG ATTTTGTCTT CTGTTCGAA 2040
		GAGACAATGA CCGCTAAGGC TAACGGTGCA TGGTATGAGC GAACATATTAC ATTGCTTGCA 2100
		GGAAACAAAT ATATTGCTTG GCGGCATTAT GATTGCACCG ATATGTTTTT CTGTCTCTTG 2160
10	10	GATGACATTA CGGTTTATCG TTCTACTGAG ACTGTTCCCG AGCCTGTTAC TGATTTGTTT 2220
		GTCTCGCTTA TTGAGAAATA CAAGGCTCGC CTGAAATGGA ATTATCCTAA CCGCTACGAA 2280
		CCCGATAAGA CTGATGATAA AAAACCATTC CAGCTTACCG GCTACAACAT CTATGCAAAAT 2340
		GGCTCGCTCC TTGTTTACAT ACAAGACCGG ACTGTTTTGG AGTATATCGA TGAGACTTAT 2400
		TCTTCAGGAG ACGGTCAGGT GGAAATGGAA TATTGTGTCA CTGCCGTTTA TAACGACAAT 2460
15	15	ATCGAGTCCC AATCGGTTTG CGATAAGCTG AACTATACTA TCACATCCTT GGATAATATT 2520
		CAATCTGATA CAAGCTTGAA AATATATCCT AATCCGGCAT CGTATGTGTT AAGGATAGAG 2580
		GGATTGAGTC GGAGCAAGTC GACAATCGAG TTGTATAATG CCGTGGGAAT TTGCATATTA 2640
		AGGGAAGAGA CTCATTGAGA GAAAACGGAA ATCGATGTTT CACGCTCAA TGACGGAGTC 2700
		TACTTGATTA AAGTAGTCGG TGGAAATAAA ACAACAACCG AAAAGGTAGA GATAAAGAGG 2760
20		CCG
		(2) INFORMATION FOR SEQ ID NO:206
25		(i) SEQUENCE CHARACTERISTICS:
		(A) LENGTH: 1779 base pairs
		(B) TYPE: nucleic acid
		(C) STRANDEDNESS: double
		(D) TOPOLOGY: circular
30		(ii) MOLECULE TYPE: DNA (genomic)
		(iii) HYPOTHETICAL: NO
35		(iv) ANTI-SENSE: NO
		(vi) ORIGINAL SOURCE:
		(A) ORGANISM: PORPHYROMONAS GINGIVALIS
40		(ix) FEATURE:
		(A) NAME/KEY: misc_feature
		(B) LOCATION 1...1779
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206
45	45	ATGAACAGCA TCATGAATA TCAATTATAT ACGGCCGTCA TAATGGCTCT CTCTGTATCA 60
		TCGGTTTGGG GTCAAACCCC ACGAAATACA GAAACCAAAC GCCCGACAC GCTGCGCAGG 120
		CACCTTACTA TCGTTAATGA CCAGACTGTG GAGATGGAGC ATGCCGATCC GCTTCGGGCT 180
		GCATACAAGG CCATCGAACC TCGATTAAAA CCTTCCGTC CGGAATATAA CAAGCGTACA 240
		TTCCGAATTG TCCTCGAAGT TTCTCTTCA GGCAGGAACA ATCTTCCGAA TATCCTGCCG 300
50	50	ACGGAAGGTC ATATGAAGCA CCGGGGGTAC CTGAATATCG GTATCGGCCA TACGCTAAAC 360
		CAGCGAATGG ATGCCGGCTA TCGTCTGATA GATGCAGAGC AGGAGAGACT GAATCTTTTC 420
		CTCTCTATC GTGGGATGAA ATCGGCTTTC AATACCGGTG ACTTCGACGG CGACAGAAAG 480
		GATAGACGAA TGATGGCAGS AGTGGACTAC GAGCAGCGCA GGCCTTCCTT TGTGCTTGCT 540
		ACCGGCTTGT ATTATTCGAA CCATTATTC AATAACTACG GACGGGGAGC TACCACCAAT 600
55	55	GTGGGCGACA TCCCTCAGCT ATCGACACCT GTTACTCCTC AGATGGACAA CGGGACCCAC 660
		AACGTCCTG TATACTTGGG TGCAAAAAAT GATGTGATCG ATGCCAGGAT CGACTATCGT 720
		TTCTTCGGTT CTATTCCTTA TCTGGGTACC GATCCGATGA AGGCTCTCAC AGAACATACG 780
		CCTGAACGTA ACGTGACGAT GAGTAATGAG TTGTCCGATG ATATTAAGCT CCGGTGTCGAA 840
		GTTCGTACGG GAGGATTGTT TTTTGCCAAA AACAGCGAAA TGATTCAAAC GGGCGTTCTG 900
60	60	TCCGAAACCG ACCGCAACCT GTATTATGTG GAGGGCGGCG CCACAATCGG ATTTGTCCGA 960
		GACTCGGACA ATATGCAATG GAACATACAC GCCGGAGTAG GGATTTCCTC CCATTTCGGA 1020
		GCCAAAGGGA GGTGTGTTTT CTGGCCATAA CTGGATGCTT CGCTTAGTAT CTTCCTTTCA 1080
		TGGCGTGTGT ATGCGAAAGC CTTCGGCGGT GTGATTGGA ATGGTCTCGC CGATGTTATG 1140
		CRAGAGGAGA TGCCCTACCT GATGCCCAAT ACGATTGTAC TCCTTCGCG CAATGCTTTG 1200
65	65	ACUGCCCAAT TAGGGGTGAA GGGGAATATA GCCGATGTG TACGTATGGA GGTTTATGGC 1260
		GACTTCTCCA AGCTGACAGG TGTGCTTTTC TATACTCCGA CTCTACCTTT ATATAATCCA 1320
		TCCGACTTGT ATCAGTATAA TGTGAGTTTC TTGCCGATAT ATGCCGACGG CAGCGCTGG 1380
		CGCGCAGGTG GTAAGCTGGA ATACTCTTAT CGCGATATGC TCCGCTTTCT GGTAGACGCA 1440
		TCCTATGGCA AGTGGAAATT GGATGGAGGA CTGTGCGCCT CCATGCAGCC CGATCTTATA 1500
70	70	TTGAAGGCAG AAGTAGGTGT TCATCCCATG GCCCATTTGG ATGTGAGACT CCGGTATACA 1560
		CAGCTGAACG GACGGTATCG GTATTCTTTC GGCTCGGCTG GCTCGGAAGC CTGGGATATC 1620
		GGTAATGTAC ATCTTCTTAG TGCGGATGTT TCATACAAGC TGAAAAAGAA CTTGAGCCTT 1680
		TATCTCAAAA TCGATAATAT GCTGGCGGAA ACGACAGAGC TTATCGGTTA TTATCCTATG 1740
75		CAGCCGTTCC ATTGTTTCCG CGGTTTTAGC TGGACTTTC 1779

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## (2) INFORMATION FOR SEQ ID NO:207

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1767 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...1767
- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:207

25 ATGAATATC AATTATATAC GGGCGTCATA ATGGCTCTCT CTGTATCATC CGTTTGCGGT 60  
 CAAACCCAC GAAATACAGA AACCAACGC CCGACACAC TGGCAGGGA GCTTACTATC 120  
 GTTAATGACC AGACTGTGGA GATGGAGCAT GCGGATCCGC TTCCGGCTGC ATACAGGCC 180  
 ATCGAACCTC GATTAAACCC TTTCGGTCCG GAATATAACA AGCGTACATT CGGATTGTG 240  
 CCTGAAGTTT CCTCTTCAGC CAGGAACAAT CTCCGAATA TCCTGCGGAC GGAAGSTCAT 300  
 30 ATGAAGCACC GGGGGTACCT GAATATCCGT ATCGGCCATA CGCTAAACCA GCGAATGGAT 360  
 GCCGGCTATC GTCTGATAGA TGCAGAGCAG GAGAGACTGA ATCTTTTCTT CTCCTATCGT 420  
 GGGATGAAAT CGGCTTTCAA TACCGGTGAC TTCCGACGGC ACAGAAAGGA TAGACGAATG 480  
 ATGGCAGGAG TGGACTACGA GCAGCGCAGG CCTTCCTTTG TGCTTGCTAC CGGCTTGAT 540  
 TATTGGAACC ATTAATTTCAA TAACTACGGA CGGGGAGCTA CCACCAATGT GGGCAGCATC 600  
 35 CCTCAGCTAT CGACACCTGT TACTCCTCAG ATGGACVACG GGACCCACAA CGTCCGTGTA 660  
 TACTTGGGTG CAAAAAATGA TGTGATCGAT GCCAGGATCG ACTATCGTTT CTTCGGTTCT 720  
 ATTCCTATC TGGGTACCGA TCCGATGAAG GCTCTCACAG AACATACGCC TGAACCTGAAC 780  
 GTGACGATGA GTAATGAGTT GTCCGATGAT ATTAAGCTCG GTGTCGAAGT TCGTACGGGA 840  
 40 GGATTGTTTT TTGCCAAAAA CAGCGAAATG ATTCAAACGG GCGTTCTGTC CGAAACCGAC 900  
 CGCAACCTGT ATTATGTGGA GGGCGCGCCC ACAATCGSAT TTGTCGGAGA CTCGAGCAAT 960  
 ATGCAATGGA ACATACAGGC CGGAGTAGGG ATTTCTTCCC ATTTCCGAGC CAAAGGGAGG 1020  
 TTGTTTTTCT GGCCTAAACT GGATGCTTCG CTAGTATCT TCCCTTCATG GCGTGTGTAT 1080  
 GCGAAAGCCT TGGCGGTGT GATTGGAAT GGTCTCGCCG ATGTTATGCA AGAGGAGATG 1140  
 45 CCTACCTGA TGCCCAATAC GATTGTACTC CCTTCGCGCA ATGCTTTGAC CGCCCAATTA 1200  
 GGGGTGAAGG GGAATATAGC CGATGTGTA CGTATGGAGG TTTATGGCGA CTTCCTCAAG 1260  
 CTGACAGGTG TGCCTTTCTA TACTCUGACT CTACCTTAT ATAATCCATC CGACTTGTAT 1320  
 CAGTATATG TGAGTTTCTT GCCGATATAT GCCGAGGGA GCGGCTGGCG CGCAGGTGGT 1380  
 AAGCTGGAAT ACTCTTATCG CGATATGCTC CGCTTTCTGG TAGACGCATC CTATGGCAAG 1440  
 50 TGGATTTTGG ATGGAGGACT TGTCCGCTCC ATGCAGCCCG ATCTTATATT GAAGGCAGAA 1500  
 GTAGTGTTC ATCCCATTCG CCCATTGGAT GTCAGACTCC GGTATACACA GCTGAACGGA 1560  
 CGGTATCGGT ATCTTTTCGG CTCGGCTGGC TCGGAAGCCT TGGGTATCGG TAATGTACAT 1620  
 CTCTTAGTG CGGATGTTT ATACAAGCTG AAAAAAAGT TGAGCCTTTA TCTCAAAATC 1680  
 GATAATATGC TGGCGGAAAC GACAGAGCTT ATCGGTTATT ATCTATGCA GCCGTTCCAT 1740  
 55 TGTTCGCCG GTTTTAGCTG GACTTTC 1767

## (2) INFORMATION FOR SEQ ID NO:208

- 60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1038 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 65 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 70 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature
- 75

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(B) LOCATION 1...1038

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:208

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5  ATGATGGAAT AATGTATCTT TGCTCACTAT CCACATAACC TTGTGTTTAT GATTCGCAAG      60
   CATTTCGGTA TCATTTTGGG ATTTCTTTCT CTGTGTTTTC CGGCAGGTGC TCAACAAGAG      120
   AAGCAGGTGT TTCATTTTCT GAACCTTCGG GCTACTGCAC AGGCTTTGGC TGCCGGAGGC      180
   AAAGCTATCA CCATCGTAGA CGACAATCCC GGACTGGCTT TTGAGAATCC GGCTCTGCTC      240
10  GGATATGAAT CCGGTGGCCG CGCCTTTCTT TCCTATTTAT ATTATATGAG TGGTTCGCAT      300
   ATGGGCAATG CCGTGTATGC CTCGTCCGTC GGAGAGCGTG GCATGTGGGG TGTGGCATG      360
   CGTTTCCTGA ACTACGGGTC TATGCAAGGA TACGATCAGA ATGCGATTGC CACCGGCTCT      420
   TTTAGTGCTT CGGATATAGC TGTACAAGGA TTTTACAGCC ATGAAGTATG CAACCACTTC      480
   CGCGGTGGAG TCAGCCTAAA AGCATTGTAT TCTTCTATCG AGACGTATAG TTCCTTTGGC      540
   CTGTGTGGG ATGTCCGGTAT CAGTTATTAC GACGATGACA AAGGATATTC CGCTTCGCT      600
15  CTGTTCAAGA ACGTAGGGGC GCAACTGAAA GGCTATAATG AAGAACGGGA ACCGCTCGAT      660
   TGGGATTTCC AGCTCGGCTT TTCCCGCAGT TTTATCAATG CTCGTTTCG CTTCACATC      720
   ACCTTGTTC AATCTGAATC GCACTATTTC AAGCGTCTTG TACCACGGCA TCTGTCCAAG      780
   ATGCAAAAGT TCCTCCGACA CTCTCCGATA GGAGCAGAAT TTAATCTTC CGAGAGGTTT      840
   TGGGTCGGGC TGGGATATAC GCCACAGATT GCACAGGATT TCGAGGTGGA AGGCGGCAAC      900
20  AAATGGGGAG GTCTTTCCGC CGGCGTCGGT TTCACTTCAG GTGTAGTACG TGTAGGCGTA      960
   TCTGCTGCCA CCTATCATCC TGCAGCTCTT TCGTTCATGT GTTCGGTAGG TATCCGTTTG      1020
   GACGATAAGA GCATCTTC                                     1038

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(2) INFORMATION FOR SEQ ID NO:209

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   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 1035 base pairs
       (B) TYPE: nucleic acid
30  (C) STRANDEDNESS: double
       (D) TOPOLOGY: circular

   (ii) MOLECULE TYPE: DNA (genomic)

35  (iii) HYPOTHETICAL: NO

   (iv) ANTI-SENSE: NO

   (v) ORIGINAL SOURCE:
40  (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

   (ix) FEATURE:
       (A) NAME/KEY: misc_feature
       (B) LOCATION 1...1035
45

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(x1) SEQUENCE DESCRIPTION: SEQ ID NO:209

```

   ATGGAATAAT GTATCTTTCG TCACTATCCA CATAACCTTG TGTTTCATGAT TCGCAAGCAT      60
   TTCGGTATCA TTTTGGGATT TCTTTCTCTT GTGTTTTCGG CAGGTGCTCA ACAAGAGAAG      120
   CAGGTGTTTC ATTTCTGAA CCTTCGGCT ACTCCACAGG CTTTGGCTGC CGGAGGCRAA      180
   GCTATACCA TCGTAGACGA CAAATCCCGA CTGGCTTTTG AGAATCCGGC TCTGCTCGGA      240
   TATGAATCCG GTGGCCGGCG CTCTCTTTC TATTATATAT ATATAGTGG TTGCGATATG      300
   GGCAATGCCT GTTATGCCTC GTCCGTCGGA GAGCGTGGCA TGTGGGTTGT TGGCATGCGT      360
   TTCTGAATC ACGGGTCTAT GCAAGGATAC GATCAGAATG CGATTGCCAC CGGCTCTTTT      420
55  AGTGCTTCGG ATATAGCTGT ACAAGGATT TACAGCCATG AACTGAGCAA CCACTTCCGC      480
   GGTGGAGTCA GCCTAAAGC ATTGTATTCT TCTATCGAGA CGTATAGTTC CTTTGGCCTT      540
   GGTGTGGATG TCGGTATCAG TTATTACGAC GATGACAAAG GATATTCGCG TTCCGCTCTG      600
   TTCAAGAACG TAGGGGCGCA ACTGAAAGGC TATAATGAAG AACGGGAACC GCTCGATTG      660
   GATTTCACG TCGGCTTTTC CGCAGTITT ATCAATGCTC CGTTTCGCTT GCACATCACG      720
60  TTGTTCAATC TGAATCGCA CTATTTCAAG CGTCTGTAC CACGCGATCT GTCCAAGATG      780
   CAAAGTTC TCGACACTT CTCGATAGGA GCAGAAATTA CTCCTCCGA GAGTTTGG      840
   GTCGGCTGG GATAATCGCC ACAGATTGCA CAGGATTTG AGGTGGAAGG CGGCAACAAA      900
   TGGGGAGGTC TTTCCGGCGG CGTCGGTTTC ACTTCAGGTG TAGTACGTGT AGGCGTATCT      960
   GCTGCCACCT ATCATCCTGC AGCTCTTTCG TTCATGTGTT CGGTAGGTAT CCGTTTGGAC      1020
65  GATAAGAGCA TCTTC                                     1035

```

(2) INFORMATION FOR SEQ ID NO:210

```

70  (1) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 990 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: circular
75

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

10 (ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210

15

ATGATTCCGA	AGCATTTCGG	TATCATTTTG	GGATTTCITT	CTCTTGTTT	TTCGGCAGGT	60
GCTCAACAAG	AGAAGCAGGT	GTTTCATTTT	CTGAACCTTC	CGGCTACTGC	ACAGGCTTTG	120
GCTGCCGGAG	GCAAAGCTAT	CACCATCGTA	GACGACATC	CCGGACTGGC	TTTTGAGAAT	180
CCGGCTCTGC	TCCGATATGA	ATCCGGTGGC	CGCGCCTTTC	TTTCCTATT	ATATTATATG	240
AGTGGTTGGC	ATATGGGCAA	TGCCGTGTAT	GCCTCGTCCG	TCCGAGAGCG	TGCCATGTGG	300
GGTGTGGGCA	TGCGTTTCCT	GAACACGGGG	TCTATGCAAG	GATACGATCA	GAATGCGATT	360
GCCACCGGCT	CTTTTACTGC	TTCCGATATA	GCTGTACAAG	GATTTTACAG	CCATGAACCTG	420
AGCAACCACT	TCCGCGGTGG	AGTCAGCCCTA	AAAGCATGT	ATTCTTCTAT	CGAGACGTAT	480
AGTTCCCTTG	GCCTTGGTGT	GGATGTGGGT	ATCAGTTATT	ACGACGATGA	CAAAAGATAT	540
TCCGCTTCGG	CTCTGTTCAA	GAAOGTAGGG	GCGCACTGA	AAGGCTATAA	TGAAGAACGG	600
GAACCGCTCG	ATTGGGATTT	CCAGCTCGGC	TTTTCCCGCA	GTTTTATCAA	TGCTCCSTTT	660
CGCTTGCACT	TCACGTTGTT	CAATCTGAAT	CCGCACTATT	TCAAGCGTCT	TGTACCAAGC	720
GATCTGTCCA	AGATGCAAAA	GTTCTTCCGA	CACCTTCTGA	TAGGAGCAGA	ATTTACTCCT	780
TCCGAGAGGT	TTTGGGTCCG	GCTGGGATAT	ACGCCACAGA	TTGCACAGGA	TTTCGAGGTG	840
GAAGGCGGCA	ACAAATGGGG	AGGTCTTTCC	GCCGGCGTCG	GTTTCACTTC	AGGTGTAGTA	900
CSTGTAGGCG	TATCTGCTGC	CACCTATCAT	CCTGCAGCTC	TTTCGTTTAT	GTGTTCGGTA	960
GGTATCCGTT	TGGACGATAA	GAGCATCTTC				990

35 (2) INFORMATION FOR SEQ ID NO:211

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 972 base pairs

40 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

45 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

50 (ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...972

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211

ATGTGCCTCG	AACCCATAAT	TGCTCCGATT	TCATCCGAGT	TGCTCGAGCA	GGAGCTGACT	60
GCCGATGTTT	TTCTGCGGAT	GACAAACAAA	GCCGGCAATG	AGATCTATGT	TTTACGGGCC	120
GAAGAAGCTC	CGCATTTGCAT	GAAAGAAGTA	GGCCGACTGC	GAGAAGAAGC	CTTTCGGCAT	180
TATGGCCGAG	GTACTGGCAA	GGCGATCGAT	ATAGACGAGT	TCGACACCAT	GCCCGGGAGC	240
TACAAACAGC	TGATCGTATG	GGATCCGCAA	AACAAGGCTA	TACTCGGAGG	CTACCGCTTT	300
ATCTATGGGC	GGGACGTTGC	TTTCGATACC	GATGGCAAGC	CTTTGCTGGC	AACGGCAGAG	360
ATGTTTGGCT	TCAGTGATGC	TTTTTTGCAC	GATTATCTCC	CTTACACAGT	CGAATTGGGA	420
CGTTTGTTCG	TGTCGCTCCA	GTACCAATCG	ACACGGATGG	GCACAAAGGC	CATTTTGTG	480
CTGGACAATC	TTTGGGACGG	TATCGGAGCA	CTCACTGTAG	TCAATCCAGA	GGCACTCTAT	540
TTCTATGGCA	AGGTGACCAT	GTACAAAGAC	TATGATCGGC	GAGCTCGCAA	TCTGATCTG	600
TATTTTCTTC	GCAAGCACTT	CTCCGATCCG	GAAGGCTTGG	TCAAGGCTAT	TCATCCGCTA	660
CCGATAGAGA	TCAGTGGCGA	GGACGAAGCC	TTGTTCTCCT	CATCCGACTT	TGACACCAAT	720
TACAAGACTC	TCAATATAGA	AGTGGGCAAG	CTGGGTATCA	ATATCCCTCC	TCTCGTGAGT	780
GCATATATAG	CTTTGTCTCC	GGAGATGCGT	GTTTTCGGCA	CTGCAGTGAA	TGAGTCTTTT	840
GGAGAGGTGG	AGGAAACCGG	CATATTCTAT	GCTGTGGGTA	AGATCCTGGA	AGAGAAAAAA	900
CAACGGCACA	TAGAGAGCTT	CATCCTCAGC	CGGAACGAAA	AAAAAGGTCT	CGACAGTAGC	960
AATGGCCGAT	CA					972

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## (2) INFORMATION FOR SEQ ID NO:212

5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1641 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

10 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

15 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

20 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212

25	ATGAAAACCA TTGTAAGATA CAGCCGCCCT CGGGTCGCTC TCTTCTTTTG CCTTTGGGA	60
	GCTGTGCACT TGCTGTGCGA GCGGCAGATG CFCAACTACT CTTTCGAGCT GTCGGATCAG	120
	ATCGTCCTGT CTCCCACCGA AAGGCAATAC AGGGAGATTG GTGTGCAAAAC GAAAGAAAAA	180
	AGGGGGGGCG ATCTTTTCCC GTTGAGCGAT AACCTGCGCG ATTCGGCCTA TGTTGCTTTC	240
	GGCTCGGCCT ATGGCGATAT TGGGGGCGAC TATCTTCCGT ACAACGGCAA TAACTACTCC	300
30	TGCTCTCCGC TCGAATCGGG TGGTCGCATC AGTGTCCGTA ACTATGGCAC ATTGCAGGGC	360
	AGTGCTTCTT ACTCAGTGG CATGCACAAA CGCATCGGCT GGAATGCTCT GCGCAACGCC	420
	GAAGCCTACT ATCCCTATT GGTGTCCGAT TCGACCGGCG GAGACTATCA TTTGGAAGAC	480
	TATCGGCTTG CCGGCTACTA TTCTTTTCGC GCCGGCCGCT TGCOCCTCGG TATAGGCTTC	540
35	TCATACAGGG GCGAAGTTGC TTATCGGCTG ACOGATCCCG GTACGACCAA TACGACCGGT	600
	GCATTGGAGC TTTCTTGTGC TACCTCTTTG ACGCTGCCTC GAGAGAACAG GCTATCGCTT	660
	TCGGCTGCGT ATCTCTATCA TAGACAACAC CTCACACAGT ACAACTGGCG TCCCGGGCAG	720
	CAGGACAAAT TCTTCGTGAG CTACGGTTTC GGTCAAGTGG ATGTCAAGCA CAGCCCTATC	780
	TGGTTCGGTA TCTCCAGAAAT GAACACGTC AACGGATGGA AGCTTAGCTC CCGTCTGGAT	840
40	ACCCGTAGGG GCGATGCCAT CGGTCTCGAC TACAGCGGCT ACTTCCTCGA TACCGAAGAG	900
	AGGTCTGCCA TCAATCTCTT TGCTTTGCTT TACAATCGCC TGCGACTCTA TGGTAGCTGG	960
	CATCTGTGCG ACTTCGATTT TTCATTTTCA GCCGACTATG CTCTGCGCCA AGGGATAGAG	1020
	CGGATATACG AAGACTACAA GCCGGATGAT AATTATCATA TCTACGACCT CCGTATCTTG	1080
	GCCATTGCGC GCTGGTATAT GCTCAATGAG TTTTCTGCCC AAGCCCAAGC CTCTACCGT	1140
45	ATTGCGACGG ATAGAGTTG TGCCCTGAGA GTGAGTGCCG GTAGTGATT CTACGGCTAT	1200
	GATGAGAGCT ATCGCAAGCA TGGACATCAT ACCATGAGCG GAATGCTACG TCCTTTTGCC	1260
	GGTATAGCCT ATGACCATGC CGGATCCAAA TTGGATTITG GACTTTGCTT TCGGCTGCT	1320
	TATCGAATGG TGCTGACGCA TTCGTATAAG ATTCGTACCA TCCAGAAAGA GCAGCTCGAC	1380
	TATCAGCTGG CCTATTGCCC CTATGCCTAT CGTAATAGAG AAGGCGTGGG GGTGCGTTCC	1440
50	TCTCTGTACG TCTCGATTCC GATGCAGAAT ACCCACCGCC TGATGACAGA GCTGCGGTTG	1500
	TATGGCGACC TGATGAAAAG AAAGGACGGT ATAGCCTATG GCAAAACGCC CGGTGTCATC	1560
	TCACATATCC TGTCCGATCC GCAAGCCGAA CGAACGTCGG GCCATACCAT CGGGGCTATC	1620
	TGCAATATCT CTAACCTCTT C	1641

55 (2) INFORMATION FOR SEQ ID NO:213

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2250 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

60 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

65 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

70 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2250

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(x1) SEQUENCE DESCRIPTION: SEQ ID NO:213

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5  ATGAAAAAAC TTCACATGAT TGCCGCTTGA GCCGTCTGCT CTTTCTGCTT GACGGCACAA      60
   GCACCCGTCT CCAACAGCGA GATAGATAGT CTTAGCAATG TGCAGCTCCA GACCGTACAG      120
   GTCTAGTCTA CTCGCGCCAC GCGGAAAACC CCTGTCGCTT ACACCAACGT TCGCAAGGCC      180
   GAACCTTTCCA AGTCCAATTA TGGTCGTGAC ATCCCTATC TGCTGATGCT GACTCCCTCC      240
   GTGGTAGCCA CCAGCGATGC CGGTACGGGT ATCGGATATT CCGGCTTTCG CGTGGGTGGC      300
   ACCGATGCCA ATCGCATCAA CATAACTACC AATCGAGTAC CCCTCAACGA CTCCGAATCT      360
   CAGTCCGTCT TTTGGGTGAA TATGCCCGAC TTCGCTCTT CCATCGAAGA CCTTCAGGTG      420
10  CAGCGAGGTG TGGGTACTTC CACCAATGGT GCCGGAGCTT TTGGGGCAAG TGTCATATG      480
   CSTACGGATA ATTGGGACT GGCCTCTTAT GGCCTGTGCG ATTTGAGCGG AGGTTCTGTC      540
   GGCACATTCC GCCGATCGGT CAAACTCGGT AGCGGACGCA TCGGTGCGCA TTGGGCAGTG      600
   GATGCCCGCC TGTCAAAAT CGGTTGCGAC GGCTACGTGG ATAGAGGAAG CGTGGATCTG      660
   AAATCCTATT TCGCACAGST GGGCTATTTT GGTAGCAACA CGGCTCTCAG GTTCATCACT      720
15  TTCGGAGGAA AAGAAGTTAC GGGTATCGCA TGGAACGGTC TTTCGAAGGA GGATGAAGCC      780
   AATATATGCC GUCGATACAA CAGTGCCGCT CTTATGTACG TGGACGCGCA AGGAGTACCG      840
   CACTACTACC ACAATACCGA CAATTACGAG CAGCGTCACT ACCATGCCAT CATGACGCAC      900
   AGCTTCTCTC CTTCCGTTAT CCTCAACCTC ACGGCACACT ACACGGCCGG ATATGGCTAT      960
20  ACGGACGAAT ATCGTACCGG ACGTAACTA AAGGAATATG CACTGCAGCC CTATGTGGAA      1020
   AACAGTGTGA CCGTGAAGAA AACGATCTC ATCCGTCAGA AGTATCTGGA CAATGACTTC      1080
   GGAGGACTCA TCGGTTGCGT TAACTGGCAC ACCGGTGCAT GGCATTGCA GTTCGGGGCC      1140
   TCGGGCAATA TCTATAAAGG AGACCACTTC GGCGGTATCA CTTACATCAA AAAGTACAAT      1200
   CAGCCCTTAG CTCCCGACTT CGAATATTAT CGGAACAGGG CAGACAAAAG AGAAGGTGCA      1260
   GCCTTTGCCA AAGCCAACTG GCAGATCACT CCGGAACCTG ACATGTATGC CGACCTCCAG      1320
25  TATCGTACCA TCGGCTACAC GATAAACGGC ATCAGCGAGC AATATGATGA GGTACAGGGA      1380
   AGATGCGAGC ACATCGATT TGGACAAGAC TTCCGCTTCC TCAATCCGAA GGCCGGTCTT      1440
   ACCTATAGTT TCGACGATGC CGAAGCGGGA ATAGGACAGT ATCTACGCC TGAGCGACTG      1500
   CCTAACAGAA CCAATTACAC CGAAGCGGGA ATAGGACAGT ATCTACGCC TGAGCGACTG      1560
   ATCGACTATG AGCTGGGCTA CCGCTATGCT TCGCCCTCT TGTGGCCGG AGTAGGTCTC      1620
30  TATTATATGC AATACAAGGA CCAACTCGTG CTGGATGGCC GTTTGAGCGA TGTGGGACAG      1680
   ATGCTCACAA GCAACGTCCC CGACAGCTAC CGTATGGGAC TGGAGCTGAC TCTCGGTTGG      1740
   CAGATCCCTC CTCGTTTGCT GCGTTGGGAT GCTTCTTTCA CTATGAGTGC CAACAAAATC      1800
   GACCGCTAGC TACAATATAC ATCCGTATAT GATGCGGACT ACAACTGGCT CGAACTCAAG      1860
   GAGGAGACCC TCGAAAGCAC GGATATAGCC TACTCGCCCA ATGTCATTGC CGGCAGCATG      1920
35  CTTACCCCTC CTCATGCCGG TTTCGAAATG GCTTGGACGA GCCGCTTCGT CAGCAAGCAA      1980
   TATCTGGACA ATACACAGCG CAGCGATCGC ATGCTTTCTT CCTATTGGGT GAACGACCTC      2040
   CGCCTCGGCT ATGTGCTGCC GGTTCACCTT GTTAAGAGAG TGGCACTGGG CGTACAGCTC      2100
   AATAATCTCT TCAACCTCAT GTATGCGTCC AATGCCTACA TCTACGATGC CGGTTACGTA      2160
40  CAGGCATCCG GAGAACTAAG TGCAATGCCC GATCTGCGTT ATTATCCTCA GGCCGGATTT      2220
   AATGCATGCG GTAGTCTGAC AATCGATTTC

```

(2) INFORMATION FOR SEQ ID NO:214

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45  (1) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 1482 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: double
50  (D) TOPOLOGY: circular

     (11) MOLECULE TYPE: DNA (genomic)

     (111) HYPOTHETICAL: NO

55  (1iv) ANTI-SENSE: NO

     (vi) ORIGINAL SOURCE:
        (A) ORGANISM: PORPHYROMONAS GINGIVALIS

60  (ix) FEATURE:
     (A) NAME/KEY: misc_feature
     (B) LOCATION 1...1482

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(x1) SEQUENCE DESCRIPTION: SEQ ID NO:214

```

65  ATGAAAAGAA GGTTCTATC GCTGTTACTG CTGTACATAC TCTCTCCAT CAGCCTTCT      60
   GCTCAGCGGT TTCCGATGGT GCAGGGAATC GAGTTGGATA CCGATTGCTT TTTCTCTCTG      120
   CCCAAGCGTC CTTGCCGCGC CATCGGTAAA ACGATAGGCG TCAATCTGGC CGTATGGGGC      180
   TTCGATCATT TCATCATGAA CGAGGACTTT GCAGACATCA GTTGGCAGAC TATCAAGAGC      240
   AATTTCCAAA CAGGCTTTGG CTGGGACAA TACAAGTTTG TCACCAACCT CTTCGCACAT      300
   CCTTATCAGC GATGCTCTA TTTCAATGCA GCGAGGTGCA ACGCTTTGAG CTTCAGGCAC      360
   TCTGCTCCGT TTGCTTCTT TGGCAGTCTC ATGTGGGAGC TGCTTATGGA AAACGAGCCA      420
   CCAGATATCA ACGACCTCTG TGCCACCACC ATAGGCGGTA TAGCTTTGGG GGAGATGGGG      480
   CACAGGCTGT CGGACCTGCT CATCGACAAT CGTACCACAG GGTGGGAACG TATGGGGCGC      540
75  GAGGTGGCTA TCGCTCTGAT CAATCCGATG CGCTTCTCA ACCGCTGAC ACCAGGAGAG      600

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5 GTGACTTCTG TCGGGAGTCG CAGCGGACAG ATATTTCACT CTGTCCCCAT AAACATAGTC 660  
 GTCGATGCCG GCTTTGCTT TTTGGCAGAC AAGCGGCATG CCGGAACCGG TGCCACGGCT 720  
 CTGACCCCTGA ATCTGAGATT CGACTACGGC GATCCATTCC GAAGCGAGAC TTTCTCTCCA 780  
 TACGATTCTT TCCAATTCAA AGCCGGATTG AGTTTCTCCG AATCGCAACC TCTGCTGAGC 840  
 CAGATCAATC TGATCGGAAT CCTAAGCGGA TGCCAACTGC TCGCACACGA ACGAACGGTT 900  
 TTGTTGGGAG GTCTCTTTCA GCACTTCGAC TACTACAATT CGGAAAAACG AATAAGCAAA 960  
 AATTCGGAGG AGGTACTCGT CACCCCATAC CGTATCTCGC AAGTGGCAGC TCTGGGAGGC 1020  
 GGTCTTATCT TCCAGCACCA CGGAAAATTT CGACGACGTC CTCTGGAGCT ATATGCCGAG 1080  
 10 ACCTACCTGA ATGTCGTCCC GATGGGAGCC AGTCTGTCGG ATCACTACAA CGTGGACAAT 1140  
 CGGGACTATA ACCTCGGCAG CGGATTGAGC GGCAAGCTAT ACCTTGGTGC TACGTACAAT 1200  
 GATCTGTGGA GCTGGCTCTT GGGAGTCGAA AGCTATCGGC TCTACACATG GATCGGGTAT 1260  
 GAAGAGCCGC ACCAGAAAAA TACCGATGTC AGCTCTTTTA TGGTGCAGGG GGACGAAAGC 1320  
 AAGGCGCGCC TACTGGTGAC GAGTTCGGAG TTCGCATTTC ATCCTGGCCC CTGGCATGTA 1380  
 15 GCCATCGTCG CTCGCCGTTT CATCCGCAAA ACAGCCTATC AATTCTACCC TAACGTATCA 1440  
 TTCGATACCG GCGACATACA GCTGCGTGTC GGATTTCAC T 1482

## (2) INFORMATION FOR SEQ ID NO:215

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 882 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 30 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 35 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...882  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215

40 ATGAACGAC TGATTCTTTT TCTGGCAATG GGTGGCTTGC TGTTCACCTT TGCGAACGCA 60  
 CAAGAAGCAA AACTGTCATC TGACACTCCC AAAAAGGACT GGACTATAAA AGGTGTGACC 120  
 GGACTAAATG CCTCTCAGAC TTCTCTGACC AACTGGGCTG CCGTGGGAGA AAACACGGTG 180  
 45 GCAGGTAACC TCTATTGAA CATAGATGCC AACTACCTGA AAGATAAATG GAGTTGGGAC 240  
 AACGGTTTGC GTACAGACTT CGGTCTGACC TACACAACAG CCAACAAATG GAACAAAAGT 300  
 GTAGACAAGA TCGAACTCTT CACGAAGGOC GGCTATGAGA TCGGCAAAACA TTGGTACGGA 360  
 AGTGCGCTTT TCACTTTCTT CTACAGTAT GCCAAAGGAT ATGAGAAGCC CTCGGATCAC 420  
 TTGACAGGAG TCAAGCATAT CTCTAATTTT TTGCTCTCTG CATATCTCAC TCTCGGTATT 480  
 50 GGTGCGGACT ATAAGCCCAA TGAGAAGTTC TCTCTTACC TCTCTCTAC AACGGGCAAG 540  
 CTGACTGTAG TAGCAGACGA CTACCTCTCA AGTTTGGGAG CCTTCGGGGT GAAAGTTGGT 600  
 GAAAGACAA TGTTGGAAT TGGTGCTTTG GTAGTGGGTT CGGCCAATAT AAATCTGATG 660  
 GAGAATGTCA ATTTGATAAC CAAGGCTTCA TTCTTCTCGG CTATACGCA CGAATTGGG 720  
 AACATTGACA TCAATTGGGA GGCTATGCTG GCCATGAAGA TCAACAAGTT CCTCAGGGCT 780  
 55 ACGATAGCCA CCAATCTTAT CTACGAGCAT GATGTGAAGA TCAACGATGG CCCGAAAATC 840  
 CAGTTCAAAG AAGTTGTGGG CGTGGGTGTT CGGTACACTT TC 882

## (2) INFORMATION FOR SEQ ID NO:216

- 60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 612 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 65 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 70 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 75 (ix) FEATURE:

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(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...612

5 (x1) SEQUENCE DESCRIPTION: SEQ ID NO:216

ATGAAGAAAA	TGATTTTGGC	AGCTACTATG	CTGCTCGCAA	CAATCGGTTT	TGCAAAATGCT	60
CAGAGTCGTC	CTGCTCTTAG	ACTGGATGCT	AACCTTGTG	GTAGTAACTT	AATGCAAAAA	120
GTCSGAAACA	CGAGCGTGAA	CAATAAGATG	ATCGTAGGCT	TACGTGTTGG	TGCTGCTGCT	180
GAGTTCGGCT	TTAGCAATGA	TGGATTCTAT	CTCGCCXCU	GATTGGCCTA	TACGATGAGA	240
GGTGCTAAGA	TGGAATCACT	AAGTGAAACG	ACAACTCGCT	TGCATTATCT	GCAAATACCG	300
GTGAATGCCG	GTATGAGATT	TAGCTTTGCT	GACAACATGG	CTATTTCACT	GGAAGCAGGT	360
CCCTATTTCS	CATATGGTGT	CGCCGGAACG	ATTAAGACTA	AAGTTGCAGG	CGTTACGGCT	420
TCTGTAGATG	CCTTTGGTGA	TAACGGATAT	AACCGTTTCG	ACTTGGGCTT	GGGCTTGTCT	480
GCTGCCCTGA	GCTACGACCG	TTATTACGTA	CAAATTGGAT	ATGAGCATGG	ATTGCTTAAT	540
ATGTTGAASG	ATGCTCCGGA	TAAGACTTCT	TTGCGTAATC	ATGACTTCTT	TGTGGGTCTC	600
GGTGTTCGCT	TC					612

20 (2) INFORMATION FOR SEQ ID NO:217

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 729 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...729

40 (x1) SEQUENCE DESCRIPTION: SEQ ID NO:217

ATGAAAAGGA	TTTTTACTGT	AGCCCTTGTG	CTACTTGCTT	CGGTCACTAT	GGCCATCGGA	60
CAAAGCCGCC	CGGCACTTCG	CGTAGATGCC	AACCTCGTAG	GCAGCAATCA	GAGCATGAAA	120
AGAGACGGAT	ATGTGTGGGA	CACCAAAATG	AATGTGGGCC	TGCGGGTCGG	TGCCGCTGCC	180
GAATTCATGA	TCGGATCAAG	AGGATTCTAC	TTGGCTCCGG	GTCTGAACTA	TACGATGAAG	240
GGCTCCAAAA	CCGAATGGGA	TATACCCGAA	ATGGTTCCTG	GTACCTATAT	TACGATGGTT	300
TCCACTCGCT	TGCACTATCT	GCAACTGCCG	ATCAATGCCG	GCATGCGGTT	CGACCTGATG	360
AATGACATGG	CGGTTTCGAT	CGAAGCGGGT	CCTTTCCTTG	CATACGGTAT	ATATGGTACA	420
TATCGGCAGA	AGTTGGAAGG	ATGGAAGCCG	AACAACATA	GCACAGAGTT	TTTTGGCCCCA	480
ACGCTTGGTG	GCCCAACAAA	TATCCGCTGG	GACATCGGGG	CAACATAAT	AGCCGCATTC	540
CACTATAAGC	GTATATATAT	ACAGATAGGC	TATGAACATG	GATTGTGGA	TATTGTGTCA	600
GGTGGAGGTT	CTGATATTCC	CCGACTGAAC	GACAATAGGC	AATCCTCTTC	GACGACCGCT	660
CTAAGAGAAA	AGGGAAATAA	CGAATACGCT	TATAATCGTG	ACTTCTTCGT	GGGCATAGGT	720
TACCGCTTT						729

60 (2) INFORMATION FOR SEQ ID NO:218

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 621 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature

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(B) LOCATION 1...621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218

5	ATGAAAAGAA	TGCTGCTGCT	TCFCGTTGTA	TTATTATATG	GAATTGCAGG	CCGATTGGCT	60
	GUACAAGACG	TTATCAGACC	ATGGTCATTG	CAGGTCGGAG	CGGGATACTC	CGATACGGAG	120
	AACATCCCGG	GAGGATTAC	CTATGGTTTC	TATTTGGGAA	AGCGTATGGG	GAGCTTTCTG	180
	GAAGTGGGGG	TGTCCATGTA	CAACTCCACA	CGTCAACAG	CCAACAATGC	AGACTCCTTT	240
	GCATCGAAGC	AAGGAGACGG	ATCTTTTCAG	GTAAATATGT	CTTCTCGGAA	TGAGAAGTGG	300
10	TCATTCTTCG	ATGCAGGCAG	TGCCAACTGC	TATATGATCG	TCGTGCGAGT	CAATCCTCTC	360
	CATCTGTTTT	GGCAGAATAG	CCGGCACAAT	TTGTTTCTGG	CAGTACAAGC	CGGCCTGTCC	420
	AATAAGCACA	ATATTCATTT	CATCTATGGA	GACAAGGGAG	CCAAAGTCAG	TATCTACACC	480
	AATTCGAATA	CCTACATCGG	TTACGGAGCA	CGTGTAGCCT	ACGAATATCA	AATTCATAAA	540
15	AACGTGGGGG	CGGGTGCCGC	TGTAATGTAC	GACCACGGCA	ATAAGATGCT	TACGGCCATG	600
	GCCACGCTCT	CCACTCATTT	T				621

(2) INFORMATION FOR SEQ ID NO:219

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2853 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219

40	ATGAGAGTAT	CCGATCTCTG	TTCCAGACTT	TCATGGTTAT	TACCCGTAAT	CCTTGTGCGA	60
	TTGCTCTGTG	CTACTTTGGT	CGCTGCGGAA	CGTCCTATGG	CCGGAGCAGT	CGGATTGCAC	120
	CACCGTCGGC	ATGCTGCGCT	GTCTGATTCT	ACAGCGAAAG	ACACGGTGCC	TCTCGCAAAA	180
	CCTATTCTCT	ACAGTGCTTT	TGAGATTCC	CTTCTGCGG	ATTCCACCGG	ATCGATGCGG	240
45	CAAGATAGCG	TGTATGACGA	TGAATTCGAA	TTGGAAGATA	TAGTGGAGTA	CGAAGCTGCC	300
	GATTCCATCG	TTTTGCTCGG	ACAGAATCGT	GCCTATCTTT	TGGGCAAGAG	CTATGTGAGC	360
	TATCAAAAAG	GTGCTTTGGA	GGCAAACCTC	ATGTATCTCA	ATACCGACAG	CAGTACGGTT	420
	TATACTCGCT	ATGTCTCTGA	TACGGCGGGT	TATCCGATGG	CCTTTCCTGT	TTTCAAGGAT	480
	GGAGAGCAGT	CGTTCGAAGC	CAAGAACTTT	ACCTACAAC	TCCGACCGGA	GAAGGGGATT	540
50	ATCAGCGGAG	TGATCACGCA	GCAGGGCGAA	GGCTATCTGA	CTGCCGGTAA	GACCAAGAAG	600
	ATGCCCGACA	ATATCATGTT	TATGCAAGGA	GGGCGTTATA	CGACCTGCGA	CAATCACGAT	660
	CATCCTCACT	TCTATATCAA	TCTTTCCAAG	GCAAAGGTGC	ATCCGGAGAA	AGACATCGTC	720
	ACAGGTCCGG	TCAATCTGGT	TATCGCCGAT	ATGCCGCTGC	CGATAGGTCT	TCCTTTGGGC	780
	TATTTTCCCT	TTTCCAACAA	ATACTCTTCC	GGTATATTGA	TGCCCACTGA	CGGAGAGGAG	840
55	AATCGCTATG	GATTTTATTT	GAGGAATGGT	GGATATTATT	TTGCCCTCAG	CGACTATATC	900
	GATTTGGCAT	TGCGTGGGGA	GATCTTTTCC	AAAGGGTCAT	GGGGCATTTT	AGCCCAATTC	960
	AAATATAAGA	AGAGGTATAA	GTACAACGGC	TCGTTGGAAG	CCAATTATCT	GGTATCGAAG	1020
	TCCGGCGACA	AATACGTGCC	CGGAGACTAC	AGCAAGACCA	CCAGTCTGAA	TATCCGATGG	1080
	ACACACAGTC	AGGATCCGAA	GGCCAATCCT	TTGCAAACTG	TGTGGGCCAA	TGTCAATTTT	1140
60	GCAACCGGGA	GCTATTTCCA	GAATTCGCTG	AATACCACCT	ATGATGTCAA	TGCCCGTACT	1200
	GCTACGACAC	GAAGTTCGGC	CGTGAGCTAT	TCGGCGAAGT	TTCCGGGTAC	TCCTTTTTCG	1260
	ATTACGGGTA	GCATGGATAT	CAGCCAGAAC	ATGCCGATA	CGACGGTGAG	CCTTACCTTG	1320
	CCGAATCTTT	CGATTAATAT	GTCCACGCGT	TATCCTTTCA	AGCCGAAGAC	CCGTGTAGGA	1380
	CCGAGCGGAT	GGTACGAGAA	STTGAGTGTG	GGCTATTCCG	GTCAGCTTCG	CAATAGTATC	1440
65	TTGACAAAG	AGAAAGATTT	GCTCCAGAGC	AATCTCGTGC	GCGATTGGAA	GAATGGTATG	1500
	CGTCATTCCG	TACGATCAG	TTTGACTGTC	CCTTTGTTGG	ATTATATCAA	TCTGACTATG	1560
	GGGGTTAACT	ACAATGAGTG	GTGGTACACG	AAAGGCATAC	GGAAAGTCGT	GAATGAGGAT	1620
	AAGAAAACAT	TCCTGCCTTC	GGACACGACC	TATAAATTCC	GCAGACTGTA	CGATTACAGT	1680
	CTGTGCGCAG	GCTTATCTAC	CACATTGTAC	GGTATGTTCA	AGCCTTGGAA	ACCTTTTTC	1740
70	TTGCGAGGCA	ATCTCATTAT	GATCCGTGAT	CGCTTCACGC	CCACTGTGAG	TTTCTCCTAT	1800
	ATGCCGGACT	TCAAGAAACG	CCGATATGGC	TTTTGGGAGC	TTCTTGAGCA	TACGGATCAG	1860
	AACGGCAAGC	TGCATACGCT	GCTCTACTCT	CCTTATTTTC	AGCAGATATT	CGGTGCTCCC	1920
	TCCATGGGCA	ATGCAAGATC	TGTCAATTTT	TCTTTTGACA	ACAACCTAGA	GGCCAAGATC	1980
	AAATCCAAAT	CGGATTTCGAC	AGGGATCAAG	AAGATCAGCC	TGATAGATCA	GTTACATGG	2040
75	TCTACATCCT	ATAATATGTT	TGCCGATTTC	ATCCGATGGA	GCAATATCTC	GGCTTCGCTG	2100

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5 GCACTTCGCC TCTCCAAGAG CTTTACCTTG CGCTTGTCCG GTCTGTTCGA TCCCTATTG 2160  
 ACSAAGTATT ATCAGGGGAGA AGATGGGAAG ATCATTCCCT ATAAGAGCAA CGACCTGCGC 2220  
 ATTTTAAACG GCAAGGGGATT GGCACGGCTG ATCAGTACGG GTACITCTTT CAGCTATACG 2280  
 CTCAACAAAG AGTCGCTCAG CGGATTGATA GCTCTTTTCA GTGGCAAAAA GGAGCGGAGA 2340  
 10 GATGAAAAA AAAACACAGG GGCTACTCCT CATGAAGGAG ACGATGCTGC CGATATACTT 2400  
 GAGGGAGGAA GACCGCAAAA TGAAAGTGGG GGGTCGCTCC TCGAGCGCAA CCGTCAGGGC 2460  
 GGAGCAGTGG ATCAGGATGG TTAATTGCGA TATTCGATCC CATGGAGCCT GTCCTTCGAC 2520  
 TATACTTGGG ATATTGCTAC CGACTACAAT AGGTACAATG TCAATAAGAT GGAGCACTAC 2580  
 15 TACCGGGTAA CGCAGAACTCT GAGCTTTCGG GGGCAATATCC AGCCTACACC GAACTGGAGC 2640  
 TTCCGATTCA ATGCGAACTA CAATTTTCGAC TTGAAGAAAA TAACATCGCT TACCTGCAAC 2700  
 GTCACTCGCG ACATGCACTG CTGGGCTATC TCGGCCAGTT TCATCCCTAT AGGAGCATAC 2760  
 AAGTCCCTATA ATTCGTCAT ATCGGTGAAG AGTTCACCT TGCAGGATCT GAAGTATCAG 2820  
 CAGAGCAATC GTCCCATCAC GAATACTTGG TAT 2853

## (2) INFORMATION FOR SEQ ID NO:220

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3678 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature  
 (B) LOCATION 1...3678

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220

40 ATGATGAAAC GATATACAAT AATTCTTGCA GTTTTCTTT TATTCTGCAC GGTATTACC 60  
 TTTCAAAATAA AAGCTCGCCC TTATGAAAGA TTTGCAGATG TAGAGAAGCC TTGGATTACG 120  
 AAACATTCAA TGGATTCTAA ATTGGTGCCCT GCAAATAAGG GTAACTTAAT TCAAGCTGAA 180  
 ATTGTATACC AATCTGTTTC TGAACATAGT GACTTAGTTA TTTCACCTGT GAACGAAATA 240  
 AGGCCTGCMA ATCGTTTCCC TTCCGATAGG AAGTCTTTT TTGCAGAAAA TCTACGGGCA 300  
 45 TCTCCCCCGG TAGTTCCCGT TGCCGTCGAC AAGTATCGCG TACCGGTTGC CAATCCAATG 360  
 SATCCTGAAA ATCCCAATGC CTGGGATGTG ACGCTAAAAA TCACTACTAA AGCGGTAACA 420  
 GTACCTGTGG ATGTGGTGAT GGTATCGAC CAGTCTTCGT CAATGGGAGG GCAAAACATT 480  
 GCCAGATTAA AGTCTGCCAT TGCATCGGGA CAGCGTTTTG TGAATAAAAT GTTGCTTAAG 540  
 GGGACGGCTA CAGAAGGGGT GCSTATCGCT CTGTGAGATT ATGACCATGA GCCTCATCGC 600  
 50 TTATCTGATT TTACCAAGA CACTGCTTTT CTCTGTCAAA AAATCCGGGC TTGACTCCT 660  
 ATTTGGGGAA CACATACCCA GGGGGGGCTT AAAATGGCGA GAAACATTAT GGCCACTTCT 720  
 ACTGCTGTGG ATAAGCATAT CATATTGATG TCTGACGGGT TAGCGACGGA GCAGTATCCT 780  
 GTTAAAAATG TAACTACTGC AGACTTCATT GGCAAACTG GAAATGCGAA TGATCCCATT 840  
 GATTGTGTTA TACAAGGAGC AATTAAITTC CCTACAAAT ATGTTTCCAA CAATCCATCT 900  
 55 ACACCTCTTA CCCCAATTA TCCAACTCAT TCTTCTAAAG TTGGACGGAG AAATCTGCGG 960  
 GAATCCAAAT TCGATTATAG TAATCTGAGT GCAAGGATTA CTTTGTATGG TGTGTGTCG 1020  
 GCATTGGTCT ATGAACCGAG GTTTCCTCAT CCCTATTATT ATTATTCCC TTGTAACGCT 1080  
 GCTATCAATG AGGCTCAGTT TCGCAAAAAAC TCTGGTTATA CAATCCATAC TATTGGCTAT 1140  
 GACCTGGGAG ATTTTGCCTT GGCCAACAAT TCGTTGAAC TAACCGCTAC AGACGAGAAT 1200  
 60 CACTTCTTTA CGGCGACACC GGCCAATTTA GCTGCAGCGT TTGATAATAT TGCCCAAACT 1260  
 ATTAATATAG GTATACAGAG GGGGGAGGTG ACGGACTTTG TAGCTCCTGG TTTATCGTT 1320  
 AAAAATCTGA CGCAATCGGG AGATGTTACT CATTTGCTAA ATGTTTCAA TGGAACGGTG 1380  
 CACTATGATG TCTCTACTAA AAAACTGACA TGGACTACTG GTACTATCCT GAGCTCATCA 1440  
 GAAGCTACCA TAACCTATCG TATTTATGCC GATTTGGATT ATATACAGAA CAATGATATT 1500  
 65 CCGGTAATA CTACTTCTGC TATCGGCCCG GATCTTGGTG GATTGCATAC CATACCGAG 1560  
 GCAAAATGA CCTATACCAA TTCCAATGGC GAACCGAATC AGCAGTTAAT TTCCCACT 1620  
 CCGACGGTTA AGTTAGGTTA TGGTGTATT AAGCGGCACT ATGTATTGGT AAATAAGAC 1680  
 GGTCACCCCA TACAGGCAAA TGGAACAGTT GTCAGTTCCC TAAGCGAGGC TCATGTTCTA 1740  
 CAGTCACAAG ATTTCTTTT GCCCTCAGGT GGAGGTACATA TTGTTCCCAA ATGGATAAAG 1800  
 70 TTGGACAAAA CGACCGAAGC ATTACAGTAC TATTCCGTAC CGCGACTAA CACGGTCATC 1860  
 ACTACTGCCG ATGGTAAACG TTATCGTTT GTCGAAGTCC CAGGCTCCAC GCCGAATCCG 1920  
 GGCCAAATCG GTATCAGTTG GAAAAACCG GCAGGAAACG CTTACTTGGC TTACAAGCTC 1980  
 CTCATTATT CGATGGGAGG AACACAGAC CAACAGAGTG AATGGGATGT GACGTCCAAT 2040  
 TGGACAGGAG CCCAAGTACC GCTCACAGGA GAAGATGTAG AGTTTGAAC GACAGAAAAT 2100  
 75 TCGGTTCTC CGCGGTAGC CGATTGCAAT GTCCCGACAA CCAACCCAA AATTATCGGT 2160  
 AACCTTATCA ATAATCCGA CAAGGATTTA GTTGTACCA CAAGCAGTCA ATTGACGATC 2220

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	AACGGCGTGG	TTGAGGATAA	CAATCCGAAT	GTCGGTACGA	TCGTGCTGAA	GTCGTCGAAA	2280
	GACAATCCTA	CGGGGACATT	GCITTTTGCC	AATCCGGGCT	ATAATCAAAA	TGTAGGGGGG	2340
	ACCGTCGAGT	TTTACAAATCA	GGGATATGAT	TGTGCCGATT	GTGGTATGTA	TCGCAGGAGC	2400
	TGGCAGTATT	TCGGTATCCC	TGTCAATGAA	TCAGGTTTTC	CAATTAATGA	TGTGGGCGGA	2460
5	AACGAGACCG	TCAACCAATG	GGTTGAGCCT	TTCAATGGCG	ATAAGTGGCG	GCCAGCACCT	2520
	TATGCACCTG	ATACAGAGCT	TCAAAAATTC	AAGGGCTACC	AGATCAGGAA	TGACGTGCAG	2580
	GCACAGCCTA	CGGGAGTTTA	CAGCTTCAAG	GGTATGATTT	GTGTGTGCGA	TGCCTTCTCG	2640
	AATCTGACAC	GCACGTCCGG	TGTCAACTAC	TCGGGCGCCA	ACTTGATCGG	CAACTCATAC	2700
	ACTGGAGCCA	TCGACATCAA	GCAGGGTATT	GTCTTCCGCG	CGGAAGTCGA	GCAGACGGTG	2760
10	TATCTGTTCA	ACACGGGAAC	ACGCGACCCG	TGGCGTAAGC	TTAATGGAAG	CACGGTTTCA	2820
	GGCTATCGAG	CCGGTCAGTA	CCTCTCTGTA	CCTAAGAATA	CAGCGGGTCA	GGACAATCTT	2880
	CCGGATCGTA	TTCCATCGAT	GCATTCCTTC	TTGGTGAAGA	TGCAGAACGG	AGCGTCTTGT	2940
	ACGTTGCAHA	TCTTGTAAGA	TAAGCTGCTC	AAGAACACGA	CTGTAAACAA	CGGTAATGGT	3000
	ACGAGATCA	CATGGCGATC	CGGCAACTCC	GGATCGGCGA	ATATGCCGTC	ACTTGTGATG	3060
15	GATGTTCTTG	GTAACGAGTC	GGCCGACCGT	TTGTGGATCT	TTACCGATGG	GGGTCTTTCT	3120
	TTCCGATTCTG	ACAACGGCTG	GGATGGTTCG	AAGCTGACTG	AAAAAGGTTT	GTCACAACCT	3180
	TATGCGATGT	CTGACATCGG	TAATGATAAA	TTCCAGGTTG	CAGGGGTTTC	GGAGTTGAAT	3240
	AACCTGCTGA	TCGGCTTCGA	TGCGGATAAG	GATGGTCAAT	ACACGTTGGA	GTTTGTCTT	3300
	TCGGATCATT	TTGCGAAAGG	GGCTGTTTAC	CTGCACGATC	TTCAAGTCAGG	AGCCAAACAC	3360
20	CGTATTACSA	ATTCTACGTC	GTATTCAATC	GATGCCAAGC	GGGGAGATTC	CGGGGCTCGT	3420
	TTCCGCTTGT	CATATGGATG	TGATGAGAAC	GTAGATGATT	CGCATGTGCT	GAGTACAAAT	3480
	GGCUSTGAAA	TTATAATTCT	GAATCAAGAT	GCTCTTGACT	GCACGTGAAC	CTTATTCACA	3540
	ATAGAAGGTA	AGCTTCTTCTG	CCGCTTGAAA	GTATTAGCTG	GTCATAGAGA	AGTCATGAAA	3600
25	GTGCAGACCG	GAGGGGCCCTA	TATTGTGCAT	CTTCAAAATG	CTTTCACATA	TGATGTGCAT	3660
	AAGGTGCTTG	TTGAGTAT					3678

## (2) INFORMATION FOR SEQ ID NO:221

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3675 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...3675
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221

	ATGAAACGAT	ATACAATAAT	TCTTGCAATT	TTCTTTTAT	TCTGCACGGT	ATTACCTTIT	60
	CAAAATAAAG	CTCGCCCTTA	TGAAAGATTI	GCAGATGTAG	AGAAGCCTTG	GATTTCAGAAA	120
	CATTCAATGG	ATTCTAAATT	GGTGCCTGCA	AATAAGGGTA	ACTTAATTCA	AGCTGAAATT	180
	GTATACCAAT	CTGTTTCTGA	ACATAGTGAC	TTAGTTATTT	CACCTGTGAA	CGAAATAAGG	240
55	CCTGCAAATC	GTTTCCCTTC	GCATAGGAAG	TCTTTTITG	CAGAAAATCT	ACGGGCATCT	300
	CCCCCGTAG	TTCCCGTTGC	CGTCGACAAG	TATGCGGTAC	CGGTTGCCAA	TCCAATGGAT	360
	CCTGAAATTC	CCAATGCCTG	GGATGTGACG	CTAAAAATCA	CTACTAAAGC	GGTAACAGTA	420
	CCTGTGATG	TGGTGATGGT	TATCGACCAG	TCTTGTCTCA	TGGGAGGGCA	AAACATTGCC	480
60	AGATTAAAGT	CTGCCATTGC	ATCGGGACAG	CGTTTGTGTA	AAAAAATGTT	GCCTAAGGGG	540
	ACGGCTACAG	AAGGGGTGCG	TATCGCTCTT	GTGAGTTATG	ACCATGAGCC	TCATCGCTTA	600
	TCTGATTTTA	CCAAAGACAC	TGCTTTTCTC	TGTCAAAAAA	TCGGGCTTTT	GACTCCTATT	660
	TGGGGAACAC	ATACCCAGGG	GGGGCTTAAA	ATGGCGAGAA	ACATTATGGC	CACCTCTACT	720
	GCTGTGATATA	AGCATATCAT	ATTGATGTCT	GACGGGTTAG	CGACGGAGCA	GTATCCTGTT	780
65	AAAAATGTAA	CTACTGCAGA	CTTCATTGGC	AAAACTGGAA	ATGCGAATGA	TCCCATTGAT	840
	TTGGTTATAC	AAGGAGCAAT	TAATTTCCTT	ACAAATTATG	TTTCCAACAA	TCCATCTACA	900
	CCTCTTACCC	CAAATTATCC	AACTCATCTT	TCTAAAGTTC	GACGGAGAAA	TCTGCCGGAA	960
	TCCAAATTCG	ATTATAGTAA	TCTGAGTGCA	AGGATTACTT	TTGATCGTGT	TGCTGGCGCA	1020
	TTGGTCTATG	AACCGAGGTT	TCCTCATCCC	TATTATTATT	ATTTCCCTTG	TAACGCTGCT	1080
	ATCAATGAGG	CTCAGTTTGC	GAATAACTCT	GGTTATACAA	TCCATACTAT	TGGCTATGAC	1140
70	CTGGGAGATT	TTGCCCTTGG	CAACAATTCC	TTGAAACTAA	CCGCTACAGA	CGAGAATCAC	1200
	TTCTTTACGG	CGACACCGGC	CAATTTAGCT	GCAGCGTTTG	ATAATATTGC	CCAAACTATT	1260
	AATATAGGTA	TACAGAGGGG	GGAGGTGACG	GACTTTGTAG	CTCCTGGTTT	CATCGTTAAA	1320
	AATCTGAGCG	AATCGGGAGA	TGTTACTCAT	TTGCTAAATG	TTTCAAAATG	AACGGTGAC	1380
	TATGATGTCT	CTACTAAAAA	ACTGACATGG	ACTACTGGTA	CTATCCTGAG	CTCATCAGAA	1440
75	GCTACCATAA	CTTATCGTAT	TTATGCCGAT	TTGGATTATA	TACAGAACAA	TGATATTCCS	1500

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	GTAAATACIA	CTTCTGCTAT	CGGCCCGGAT	CTTGGTGGAT	TCGATACCAA	TACCGAGGCA	1560
	AAATTGACCT	ATACCAATTC	CAATGGCGAA	CCGAATCAGC	AGTTAATTTT	CCGACGTCGG	1620
	ACGGTTAAGT	TAGGTTATGG	TGTTATTAAG	CGGCACATG	TATTGGTAAA	TAAAGACGGT	1680
	CAACCCATAC	AGGCAAAATG	AACAGTTGTC	AGTTCCCTAA	CGCAGGCTCA	TGTTCTACAG	1740
5	TCACAAAGATT	TCTTTTGGCC	CTCAGGTGGA	GGTCATATTG	TTCCTCAATG	GATAAAGTTG	1800
	GACAAAACGA	CGGAAGCATT	ACAGTACTAT	TCCGTACCCG	CGACTAACAC	GGTCATCACT	1860
	ACTGCCGATG	GTAACGTTA	TCGTTTGTG	GAAGTCCGAG	GCTCCACGCC	GAATCCGGGC	1920
	CAATTCGGTA	TCAGTTGGAA	AAAACCGGCA	GGAAACGCTT	ACTTCGCTTA	CAAGCTCCTC	1980
	AATTAATTGGA	TGGGAGGAAC	AACAGACCAA	CAGAGTGAAT	GGGATGTGAC	GTCCAATTGG	2040
10	ACAGGAGCCC	AAGTACCGCT	CACAGGAGAA	GATGTAGAGT	TGCAACGAC	AGAAAATTTC	2100
	GGTTCTCCGG	CGGTAGCCGA	TTTGCAATGC	CCGACAACCA	ACCCCAAAAT	TATCGGTAAC	2160
	CTTATCAATA	ATTCGACAA	GGATTAGTT	GTTACCACAA	GCACTCAATT	GACGATCAAC	2220
	GGCGTGGTTG	AGGATAACAA	TCCGAATGTC	GGTACGATCG	TCGTGAAGTC	GTGGAAGAC	2280
	AATCCTACGG	GGACATTGCT	TTTTGCCAAT	CCGGGCTATA	ATCAAAATGT	AGGGGGGACC	2340
15	GTGAGATTTT	ACAATCAGGG	ATATGATTGT	GCCGATTGTG	GTATGTATCG	CAGGAGCTGG	2400
	CAGTATTTCG	GTATCCCTGT	CAATGAATCA	GGTTTCCAA	TTATGATGT	GGCGGAAAC	2460
	GAGACCGTCA	ACCAATGGGT	TGAGCCTTTC	AATGGCGATA	AGTGGCGGCC	AGCACCTTAT	2520
	GCACCTGATA	CAGAGCTTCA	AAAATTCAG	GGCTACCAGA	TCACGAATGA	CGTGCAGGCA	2580
20	CAGCCTACGG	GAGTTTACAG	CTTCAAGGGT	ATGATTGTG	TGTGCGATGC	CTTCCTGAAT	2640
	CTGACACGCA	CGTCCGGTGT	CACTACTCG	GGCGCCAAC	TGATCGGCAA	CTCATACACT	2700
	GGAGCCATCG	ACATCAAGCA	GGGTATTGTC	TTCCCGCCGG	AAGTCGAGCA	GACGCTGTAT	2760
	CTGTTCAACA	CGGGAACACG	CGACCACTGG	CGTAAGCTTA	ATGGAAGCAC	GGTTTCAGGC	2820
	TATCGAGCGG	GTCAGTACCT	CTCTGTACCT	AAGAATACAG	CGGGTCAGGA	CAATCTTCCG	2880
25	GATCGTATTC	CATCGATGCA	TTCTTCTTG	GTGAAGATGC	AGAACGGAGC	GTCTGTACG	2940
	TTGCAHATCT	TGTACGATAA	GCTGCTCAAG	AACACGACTG	TAAACAACGG	TAATGGTACG	3000
	CAGATCACAT	GGCGATCCGG	CACTCCGGGA	TCGGCGAATA	TGCGGTCACT	TGTGATGGAT	3060
	CTTCTTGGTA	ACGAGTCCGG	CGACCGTTTG	TGGATCTTTA	CCGATGGGGG	CTTTCTTTTC	3120
	GGATTGACGA	ACGCTGGGGA	TGGTCGCAAG	CTGACTGAAA	AAGGTTTGTG	ACAACTTTAT	3180
30	GCGATGTCTG	ACATCGGTAA	TGATAAATTC	CAGGTTGCAG	GGGTTCCGGA	GTTGAATAAC	3240
	CTGCTGATCG	GCTTCGATGC	GGATAAGGAT	GGTCAATACA	CGTTGGAGTT	TGCTCTTTTC	3300
	GATCATTTTG	CGAAAGGGGG	TGTTTACCTG	CACGATCTTC	AGTCAGGAGC	CAAAACCCGT	3360
	ATTACGAATT	CTACGTCGTA	TTCAATCGAT	GCCAAGCGGG	GAGATTCCGG	GGCTCGTTTC	3420
	CGCTTTGTCAT	ATGGATGTGA	TGAGAACGTA	GATGATTCGC	ATGTCGTGAG	TACAAATGGC	3480
35	CGTGAAATTA	TAATTCTGAA	TCAAGATGCT	CTTGACTGCA	CTGTAACTTT	ATTGACAATA	3540
	GAAGGTAAGC	TTCTTCCCGC	CTTGAAAGTA	TTAGCTGGTC	ATAGAGAAAT	CATGAAAGTG	3600
	CAGACCGGAG	GGGCTATAT	TGTGCATCTT	CAAAATGCTT	TCATTAATGA	TGTGCATAAG	3660
	GTGCTTGTG	AGTAT					3675
40	(2) INFORMATION FOR SEQ ID NO:222						
	(i) SEQUENCE CHARACTERISTICS:						
	(A) LENGTH: 1275 base pairs						
45	(B) TYPE: nucleic acid						
	(C) STRANDEDNESS: double						
	(D) TOPOLOGY: circular						
	(ii) MOLECULE TYPE: DNA (genomic)						
50	(iii) HYPOTHETICAL: NO						
	(iv) ANTI-SENSE: NO						
	(vi) ORIGINAL SOURCE:						
55	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS						
	(ix) FEATURE:						
	(A) NAME/KEY: misc feature						
60	(B) LOCATION 1...1275						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222						
	ATGGAAGTGA	AGAAAAACAC	AGTGGTGCTA	GGCCTTCTGA	TTTGGTTCGT	GGCCATTCTT	60
65	CTCTTCCACT	CCTCAGGCT	GTGGGGACAG	GAAGGGGAGG	GGAGTGCCCG	ATACAGATTG	120
	AAAGGATTTC	TGGATACCTA	CCATGCCGTA	CGCAGCTCTT	CTCCTTTTGA	TTTCATGAGC	180
	TCGCGTACGA	GAGTGAGAGG	TGAGCTGGAG	AGGTGCTTCG	GTAATTCGAA	AGTAGCCGTA	240
	TCGGTCAATG	CCACCTACAA	TGCTCTACTG	AAAGACGAGA	CCGGCTTACG	TTTACGTGAA	300
	GCCTTCTTCG	AGCATCAGGA	AGAGCATTGG	GGGTTGCGCC	TGGGACGACA	GATTGTCAAT	360
70	TGGGGGCGTG	CCGACGGTGT	GCGCATCAGC	GATCTGATCT	CCCGGATGGA	TATGACCGAG	420
	TTTCTGGCAC	AGGATTACGA	TGATATTGCT	ATGCCGCTCA	ATGCATTGGC	TTTCTCTGTC	480
	TTCAACGAAT	CGATGAAAGT	GGAACTCGTG	GTAAGTCTCT	TATTCGAGGG	GTACCGTCTG	540
	CCTGTGGATC	CTCGCAATCC	TTGGAATATC	TTCTCCCTTT	CGCCCATTCG	TCAGGGGATG	600
	AATATCGTCT	GGAAAGAAGA	AGCCGGCAAA	CCGGCCTTCA	AGGTTGCCAA	TATCGAGTAC	660
75	GGTGGCGGAT	GGAGCACTAC	GCTCTCCGGT	ATCGACTTCG	CTTTGGCTGC	ATTGCATACA	720
	TGGAAACAGA	TGCCCGTCAT	CGAAGTACAG	GGCATTGTGC	CGACGGAAAT	CATCGTTAGC	780

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CCTCGCTATT ATCGTATGGG ATTGTGCGGC GGGGACCTCT CCGTACCGGT CGGACAGTTT 840  
 GTTTTCAGGG GAGAGGCTGC GTTCAATATC GACAAACACT TCACCTATAA GAGTCATGCC 900  
 GAGCAAGAGG GTTTCCAAAC AATCAATTGG TTGGCCGGAG CCGATTGGTA TGCTCCCGGT 960  
 5 GAATGGATGA TCTCAGGACA ATTCTCAATG GAAAGCATAT TCAGGTATAG GGATTTCATC 1020  
 TCCCAAAGAC AACATTCTAC CCGTATTACT CTCAATGTTT CCAAGAAATT CTTGGGCAGT 1080  
 ACACTCCAAC TTTCGGACTT CACCTACTAC GACCTTACGG GCAAAGGATG GTTCAGTCCG 1140  
 TTTCAGCTG ACTATGCCCT GAACGATCAG ATACATCTGA TGGCCGGATA TGA CTGGTTC 1200  
 AGTAGTAAGG GCAGCGGTAT ATTCGATCGC TACAAAGACA ATTCGGAAT CTGGTTCAAA 1260  
 10 GCGCGCTACA GCTTC 1275

## (2) INFORMATION FOR SEQ ID NO:223

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1212 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 20 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 25 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 30 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1212

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223

35 ATGTCTCTCT GTGAGGTGGC TTATTTTTC CTAAGCCGA TCGATCTGCA GAACATCCGC 60  
 GAACGGAATC ACTCTCCGA CATCGCGCTT TCCAATTTAT TAGACAATTC GAATCAGCTA 120  
 TTAGTACTA TTCTGATCGG GAATAATGTG ATTAATGTAG CCATCGTTAT CCTTCCAAT 180  
 TATGCCATCG AGCAGACATT CGTTTCTCT TCTCCGATCA TTGGATTCT GATCCAGACG 240  
 ATACTCCTGA CCACTGTTCT TTGCTGTTC GGAGAGATTC TGCCGAAAGT GTATGCCGGG 300  
 40 AAGAATCCGC TGCAATACTC GCGCTTTCT GCTGCAGCTA TGTCGGTTAT CTATAAGATA 360  
 TTGTCAACCGT TTTCAAAATT GCTGGTCAA ACTACCGGCA TCGTTACCAG AGGTATCAGC 420  
 AAGAAGAAAT ACGATATGTC CGTGGATGAG CTCTCGAAAG CGGTAGCCCT CACCACTACG 480  
 GAGGAGAGAGC GAGAGGAGAA AGAAATGATT AACGAAATCA TCAAATCTA TAATAAGACA 540  
 GCCTGCGAAA TCATGGTTCC GCGTATCGAT ATTGTGGATG TGGATCTGAG CTGGCCATTT 600  
 45 CGTAAGATGC TTGACTTCGT TGTTCTGTC GGTATTCCA GACTTCCCGT TTCAGAGGGG 660  
 TCAGAAGACA ATATCAAAGG GGTGATTAC ATCAAAGATC TAATCCACA CATGGATAAA 720  
 GGCATGAAT TCGACTGGCA TCCTCTGATT CGTAAAGCAT ATTTGTCCC CGAAAACAAG 780  
 CGCATAGATC ATTTGCTCGA GGAGTTCAGA GCCAATAAGG TCGATGTCTC CATCGTTGTG 840  
 50 GATGAGTTTC GTGGCACTTG CCGACTGATC ACAATGGAGG ACATATTGGA AGAGATCGTC 900  
 GCGAGATTA CCGACGAGTA CGATGAGGAA GAACTCCCTT TTAAGGTTT GGGGATGGC 960  
 AGTTATCTTT TCGAAGGAAA AACGTCTCTC TCCGATGTT CACACTATCT TGACCTTCCG 1020  
 GAAATGCTT TCGGTGAATT GGGGACGAG GTAGATACGC TAAGTGGGCT CTTCCTGGAA 1080  
 ATCAAGCAGG AACTCCCCCA TGTGGCGGAT ACAGCAGTGT ACGAGCCATT CCGCTTCAA 1140  
 55 GTGACCCAAA TGGACAAGCG CCGAATCATC GAAATCAGA TTTCCCTTT CGAGCGCACT 1200  
 TGGAGGTCG AA 1212

## (2) INFORMATION FOR SEQ ID NO:224

60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 780 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 65 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 70 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 75 (ix) FEATURE:

WO 99/29870

PCT/AU98/01023

154/ 490

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...780

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:224

5  
ATGAACTAT TACTTTATCT CCTATTGGTC TTGTGACTC TATCCCGAT GTATTGCAA 60  
ATGCTCTTCT CAGAGAATCT CACAATGAAT ATAGACAGCA CCAAAACCAT ACAAGGAACG 120  
ATATTGCCCG TACTGGATT TCAAACCGAA AAGGAAATG TGTTCACCTT CAAAAATACT 180  
10 GCCAATCTCA ATCTGCTGAT AAAGCACGGT CAAGTAATCA ACTTAATTAA TAAAGCTTGAG 240  
TTTTCTACCT ATGGCAATAA ACTAACCGTA AGTGGAGGAT ATGTACACAC CGAATACCGC 300  
TAITTTGTTGC ATCATGTTTT TGAGGTTTTAT CCTTATGTCG AGTCGCAATG GGCAGAAAGT 360  
ACAGGAATGA AATATAAGGT TTCTACGGGA TTACAGTCGC GTTATCGGCT GGTAAATAGT 420  
GATAACTGTC TCATGTTTGC AACATTGGGG GTATTTTTCG AATTGAAAAA GTGGGAACAG 480  
15 CCAGCCACTA GCCTCTTTTC AGGAACGTAT GCATACAGCC GAAGTATCAA AAGCCACCTG 540  
TCTATCAGTT TCAGACATCG GTTGGGTGAA CATTGGGAAT TTACAACTAC GGCTATTAC 600  
CAGGAAAGC CTGACAGTTA TTTTAAGAAG GCACGTTTTG GAGGAGCTAT CGACCTCAA 660  
TACCATATCA CACCTACGAT AGGAATACGC GGGCCTATC GGATCATCTA CGATACTGCC 720  
CCTATTGTAC CTGTGCGGAA AGATTACAAC ACCGTTGATG TTGGTATCGA TATTTCGTTT 780

(2) INFORMATION FOR SEQ ID NO:225

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 2502 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:

40 (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...2502

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:225

45 ATGAAACGAA TCGTTTTATC ATCTTTCTCG TTCGTTCTGT CCATACCTTC TTTGATGGCA 60  
CAGAACAATA CCCTCGATGT ACACATATCC GGTACGATCA AGGATGCTC CTCCGGGAG 120  
CCAGTGCCCT ATGCCACTGT AAGCATCCGG CTGACAGGAG CAGATACCAC ACAGGTGTT 180  
CGACAAGTGA CTGACGGCAA CGGCTACTTC GTCATAGGCC TGCCGGCAGC TCCTCTCTAT 240  
CACCTGACAG CTTCGTTTGT AGGTATGAAA ACCCATACCA TGCACATTAG TCGGGGAAAT 300  
50 GGCAGCAGC ACATCAAATC CATCGACATT TCTCTCGAAT CCGAGGACNA ACAACTCTCC 360  
ACCGTCAACG TATCGGCAGC ACGACCACTG GTGAAGATGG AGATAGACCG CCGTCTCTAT 420  
AATATGAAAG ATGACCCCGC AGCCAAGACG AACACCTGCG TCGAAATGCT GCGCAACGTT 480  
CCTTTGGTAA CGGTGGATGG TCAGGGCAAT ATCCAGGTGA AAGGATCTTC CAACTTCAAA 540  
ATCCACCTCA ATGGCAGGCC CTCGACCATG GTGAGCAGCA ACCCGAAGGA GGTCTTTCCG 600  
TCCATTCTCG CCCATACGAT CAAACGGGTG GAGGTCTATC CCGATCCGGG TGTAAAGTAC 660  
55 GATGGGGAAG GCACAAGTGC CATCCTGGAC ATCGTCAACG AAGAAGGTAA GAAGCTGGAA 720  
GGATATTGAG GTTCCATCAC GGCAGTGTGC ACCAACATC CCACAGCCAA CGGTAGTATC 780  
TTTCTGACGG CAAAGTCCGG CAAAGTCGGG CTGACTACCA ACTATACTA CTACGGTGGC 840  
AAAAACAAGG GCTCTCGCTA CTTTACCGAA CGTACTACAT CCATGCTCCA AACGATAGAA 900  
GAAGGCAAGG GGCAGAAGAC CTTTGGCGGA CACTTCGGCA ATGCCCTCCT CTCATTGAG 960  
60 ATAGATTGCG TCAATCTCTT TACGGTGGCC GGCATGTATC GCCTTTGGGA GATGACCACC 1020  
GACCGGAACA GCGTAGAAAA AAGCTTTGCC GGCAGCAACC TCATGTCTA CATAGACAGA 1080  
AAACTCAAAA CACAGATGGA TGCCGGATCA TACGAGCTCA ATGCCACTA TCAGCAGAGC 1140  
ACTGCGCTGC CGGCGCAATT GCTCACCGTT TCCTACCGCT TCACTCACA TCTTAATAAT 1200  
AGCGAGACCT TCATTGACCA ATGGAAGCGC GATCCGCTCA ACACAGCTAA TACGATCCAG 1260  
65 TACGCGGSCC AGCACTCCAA ATCCGATGCG GGCATGGACG AACATACGGC ACAAGTGGAC 1320  
TATACAGTTC CCTTAGGACA AGCACATTCT TTGGAAGCAG GGCTGAGTA CATCTATCGT 1380  
CATGCCACGA GCGATCCTCT CTATGAGATA CGACCATCCG AAGATGCTCC GTGGCAGCCC 1440  
GGCTCTCTAT ATGCACAGAA TCCGTGGAAC GAAAGTTTCC GCCACGATCA ATACATCGGA 1500  
70 GLAGCCTATG CCGGCTACAA CTATCGTAAG GATCAGTATT CTTTGCARAC CGGCTCCGA 1560  
GTGGAAABCA GCAAGGTGAA AGCACTCTT CCGGAAACG CAGCAGCAGA TTTTCCCAAC 1620  
AACTCGTTGG ACTGGGTGCC ACAGCTCAGC CTCGGCTATA CCCCTCGCC CATGAAGCAG 1680  
CTTAAGCTGG CCTATAACTT CCGAATCCAA GTCCTTGCAA TGGGCCAACT GAATCCCTAC 1740  
CGGCTACAGA CCAACGATTA TCAAGTACAG TATGGTAATC CCGACCTAAA GTCGGAGAG 1800  
CGTCACCAAG TCGGTCTCTC CTATAATCAA TACGGAGCCA AGGTATGCT TACAGCATCG 1860  
75 CTGACTACG ACTTCTGCAA CAACGCCATC CAGAATTACA CTTCTCCGA CCGGCCAAT 1920

SUBSTITUTE SHEET (Rule 26) (RO/AU)



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5 CCCAATCTCT TCCACCAGAC CTATGGCAAT ATCGGACGAG AGCATTCTTT CAGCTTGAAT 1980  
 ACCTATGCCA TGTACACGCC GGCCGTATGG GTCAGGATTA TGCTCAACGG AAATATCGAT 2040  
 CGCACATTCC AAAAGAGCGA AGCACTCGGC ATTGATGTCA ATTCATGGTC CGGCATGGTA 2100  
 TACTCAGGCC TGAATGTTTAC CCTGCCGAAG GATTGGACTG TGAATCTCTT CGGAGGTAT 2160  
 TATCATGGGG GAAGAAGCTA CCAGACGAAG TATGATGGCA ATGTATTCAA CAATATCGGT 2220  
 ATAGCCAAAC AGCTTTTCCA CAAAAATTG AGAGTCTGCG TGAGCGCAAA CAACATTCAT 2280  
 GCGAAGTATT CGACATGGA GAGCCGGACC ATCGGCAATG GATTACTAT TTATTCGSA 2340  
 AATGCCGGTA TACAACGGAG TGTTCCTCC AGCCTCACCT ACAGCTTCGG TAAGATGAAT 2400  
 10 ACACAAGTGC GCAAGGTAGA GCGTACGATC GTCAACGACG ACCTCAAGCA AACCTCATCC 2460  
 CAAGGACAGC AGGTGGCGG ACAAGGAAAT CCTACCGCCA AT 2502

## (2) INFORMATION FOR SEQ ID NO:226

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1197 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 25 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 30 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1197

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:226

35 ATGAGACTCT CTGCCATTCT TATCGCTTTG ATTGTGATGC TGCCTGCTGT GCTTAGCGGG 60  
 CAGCATTATT ATTCCATGGC GGGAGAGCGA CTGGAGACGG ACAGCATTCG TCCGAACGAA 120  
 CTCTCGGCAT CGATCCGAAG TCGCTTTTC TTTGGGAACA ATGAATACAA TGCACGTTCTG 180  
 40 GTCAAAGGTT ATACGTTGCC GGTGTCACGG GTTTCGGCTT TTGCTCTTA CTCGCTGCCG 240  
 GCAGCACATG GTGTGAAGCT TTCGCTCGGA GTATCTACCC TGAAGTACTG GGGGGCAAGT 300  
 CGCTATCCGG CCGGTATCGC TTATTCGGAT TTACCTTATT GAGCGGACTA TAACGACTAT 360  
 GTACGCTTGC GTATCCTGCC TTATGTACAG GCCATGCTGA AGCCGACGGC CACGACTGCT 420  
 CTCATGCTGG GCAATATAGC CGGTGGTACG GCTCACGGAC TGATCGAACC GATCTACAAT 480  
 45 CCTGAGTTGG ATTTGACGGC TGATCCTGAA GCCGGTGTGC AATTTCGGGG TGATTGGACA 540  
 CGTTTCCGAA TGGATGTTT GGTCAATTGG ATGAGCATGA TTTTCAAAA TGACAATCAT 600  
 CAGGAGTCGT TTGCTTTGG CTGTCTCACT ACTTCGAAAT TGTATCGGG TGAAGGCAAA 660  
 TGGCGACTCG AACTGCCCTT GCAGGCTATT GCCACGCATC GCGGCGGGGA ATCAACTGG 720  
 GCGCAGCAGS ATACCGTGCA TACATGGGTC AATGAGCTG TCGGACTTAA GCTTTCGTAT 780  
 50 CGCCCTCGTA CCGACAAACU CATGCAGATT TGGGATCTG CTTATGGTGT GGCAGCCTTG 840  
 TCAAGCGGAG GATACTTCCC TTACGAAAGA GGGTGGGGCG GTTATCTTTC TCTCGGAATC 900  
 GACTTGGAGC ACTTCGCTTT TCGTACCGAC TATTGGTACG GCAGGCAITA CGTTTCTCCC 960  
 TTTGCTGCAC ACTTCGCCAA TTCCTGACG TATGACAAAC AGCCTCTTAC GAACGGTTGG 1020  
 GGGGATTATA TTCGTCCTTA TGCCGACTAT TCGTGGCGGA TGGCAGGAAG TGTTTCGTTG 1080  
 55 GCGGCTGTTG CTCGGGTATG GTTCCAGCCT TCGGATCGTT TTGCGATGAG CCAGCGCTTG 1140  
 GAAGTACGA TCGTATCGA TCCCAATTG CCAATAGCTT TTCTGAAAGG CAATCAT 1197

## (2) INFORMATION FOR SEQ ID NO:227

- 60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1146 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 65 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 70 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 75 (ix) FEATURE:

WO 99/29870

PCT/AU98/01023

156/ 490

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1146

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:227

5  
10  
15  
20  
25

ATGAACAAAT	CGCTATTATC	ATTGGCATGC	CTCATCCTGT	GCGGTATGCC	GGCCATCGCC	60
CAACAGACAG	GACCGGCCGA	ACGCAGCGGC	GAGCCTTCTC	TGCCCGAAGC	TGTATTCCGT	120
CTGGAGCAGA	AGCAGAAAAA	GCTGAAGGTG	TACTTAGGCA	TACAGTCGTT	CTACGACCAG	180
CCGCTTGTCC	ATGACGAATC	CCATATCGGA	CACTTCAAGG	TACAGGAGCT	GCGGATGTCT	240
GCTCATGGCG	AACTGAACCG	CCACCTCAGC	TTCGACTGGC	GACAACTCT	CAACCGTGCC	300
GCCGACGGCA	CTTCGTTTGC	CGACAATCTC	TCCAATGCCA	TGCACATCGC	AGGTGTGGAC	360
TGGCACCCGA	ACGACAAGGT	GTCTTTCTTC	TTCGGACGTC	AGTACGCGCG	TTTCGGAGGG	420
ATAGAATACG	ACATGAACCC	CGTAGAGATC	TACCAGTACA	GCGACCTTGT	GGATTACATG	480
ACCTGCTATA	CTTCGGGCGT	GAACCTTCGA	TGGAACTTCC	ACCCCGAACA	GCAGCTGCAG	540
CTACAGGTAC	TCAATGCTTA	CAACAACCGC	TTCGCCGACC	GCTACCAAGT	GACACCCGAT	600
GTCGCTACCG	CCACGAGCTA	CCCGCTCCTC	TACTCGGCAC	AGTGGAAAGG	TACCTCTCTC	660
GGAGGAGCAC	TGCATATGCG	TTACGCCGTG	TGCATGGGTC	ATCAGGCCCA	AGAGCGTAAT	720
ATGTGGTACT	TCACTGCGGG	CAACCTGTTC	AATCCGGGCA	AACGGATCAA	CGGATACCTC	780
GACCTACCT	ACTCGATCGA	GGGATTGGAC	GACAAAGGCA	TTATGACTGC	TCGCTACGGC	840
AAGGGCAAGA	CCCTCACGGA	CGTCAAGTAC	TATGCTCTGG	TATCGAAGTG	GAACCTCGC	900
ATTTTCGATC	AGGTCAATCT	CTTCCTCAAA	GGCATGTACG	AGAACGGCTA	TGGCGCTGCC	960
CAATACGGCG	AGAGCAGCCA	CACGCGCCAC	TCCTACGGCT	ATATGGGAGG	GGTGGAAATAT	1020
TACCTACGG	AGACCAACTT	CCGTCTGTTC	GTACCTTACA	TAGGACGGCA	TTACCGGTAC	1080
AGTGCGACCG	AGACGGAAAG	CACCAATGCT	CTTCGCGCCG	GTCTGATCTA	TCAGATACCT	1140
TTCTTA						1146

## (2) INFORMATION FOR SEQ ID NO:228

30  
35  
40  
45

(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 666 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...666

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:228

50  
55  
60

ATGAACATT	TGTTTAAGTC	GACATTAGTA	CTTCTTTGTG	CTCTTTCTTT	TTCCGGTACC	60
TATACCTTTG	CACAAGAAAA	TAATACAGAA	AAGTCACGAT	TGATTTTTC	TGTTAGGCTG	120
GGACAGGGAT	ATATTGCAGG	TCAACTACC	AACCTGATGT	ATGGGTATAC	ATCTGCTAAC	180
GATAGACTTT	TGCTGGTGC	AATTTATCTG	GGCTTGACAC	CAAGTAAGAA	AGAAAATGCA	240
ACCGGCGTAG	CATTTCGTTT	CTTATGCCCC	TCCTCGGGTT	ATTATGTCGA	TATATCCGGC	300
AAAGAAAATA	CCTTGAATTA	TGCGTTTAC	GTGTCGGAG	CATATAATAG	AATAGCCATT	360
UCTATACGCC	CTATCAAAAA	TTTTAATTTC	ATCTTCTCTA	CAGAACTCGG	AATGGCTTGG	420
ATCAGTCGTC	ATGAGCAAAAT	TTACAATTCT	ACTTCGCAGA	CTTGGGATAA	GCAGCGCAAG	480
TCGAGGTCGG	GACTGGATTT	TGGTCTCGGG	ATGCATCTGC	AATHCCACAT	TAATAAGACC	540
GTTTACTTTA	TGGCAGGAAC	CGATCTTAGG	TCTTGCATGT	TCGGAATAAG	GATCAATGAC	600
TACCAGCAAA	AGGATCGAAC	CTTCATTGCA	CTTATCGACA	ACAGTATTGG	CATAGGATTA	660
AACCTC						666

## (2) INFORMATION FOR SEQ ID NO:229

65  
70  
75

(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1173 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229

ATGATTATCA	AGAAATGCT	GAAAAATAAA	TTGGCCCCCT	TGGCCATACT	GTTCCCTTTT	60
GCTCCAAAGG	CTATGAAGGC	TCAGGAGCAA	CTGAATGTGG	TACACACCTC	TGTGCCATCG	120
CTGAATATCA	GTCCGGATGC	ACGTGCGGCC	GGTATGGGGG	ATATAGGTGT	GGCAACGACG	180
CCGGATCGGT	ATTCACAGTA	TTGGAATCCG	AGTAAATATG	CTTTCATGGA	TACGAAAGCC	240
GGTATTAGCT	TCTCATATAC	ACCTTGGCTG	TCCAAGCTGG	TCAATGATAT	TGCCCTGATG	300
CAGATGACCG	GTTTCTACAA	ATTGGGAACA	GACGAGAATC	AGGCTATTAG	TGCTTCTCTG	360
CGTTATTTC	CATTAGGAAA	GTTGGAGACT	TTGACGAAT	TGGGCGAATC	CATGGGAGAG	420
GCCCATCCCA	ATGAATTTGC	TGTGCGATTG	GGCTATAGCC	GCCAGTTGTC	GGAGAAGTTC	480
TCCATGGCTG	TTGCACTGCG	TTACATCCGC	TCAGACCAAA	GCACCTCACA	CACCGGAGAG	540
AATCAGGCCG	GAAATGCCTT	TGCGGCGGAT	ATAGCUGGTT	ATTTCGAGAA	GTATGTGCTA	600
CTGGGTAATG	CGGAGAGCTT	GTGGTCGTTG	GGTTTCAACG	TAAAGAATAT	CGGAACGAAG	660
ATCTCCTATG	ACGGAGGTGT	CACGAGTTTT	TTGATCCCTA	CTTCGTTGAA	TCTCGGGACG	720
GGGCTGTTGT	ATCCGATCGA	TGACTATAAC	AGCATCAATT	TCAACCTTGA	ACTTAGCAAG	780
CTCTTGTATC	CCACTCCTCC	TATCATGGAT	CAAAACGATC	AGGCGGGGTA	TGAGGCTGCA	840
CTCAAGAAAT	ATCAGGAAAC	TTCTTCGATC	AGCGGTATAT	TCTCTTCTTT	CGGTGATGCG	900
CCGGGAGGAC	TCAAGGAAGA	ATTCCGTGAG	ATTACATGCG	GACTTGGGGC	TGAATATAGC	960
TATGACGATA	AATTTTTTGT	TCGTGCCGGA	TATTCATACC	TGCACCCAC	CAAAGGCAAT	1020
TTGCAGTACT	TCACGGCCGG	TGCCGGCTTC	AAAATGAACA	TATTCCGTAT	CGATGCTTCU	1080
TACCTGTTGT	CTACGATCCA	GAGTAATCCG	TTGGATCAGA	CTCTGCGGTT	TACGCTTGCT	1140
TTGATATG	ATGGATTGCG	CAATTTGTTT	CAC			1173

(2) INFORMATION FOR SEQ ID NO:230

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1338 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230

ATGAAAACAA	CAGTTCAACA	AATTATTCTG	TGCCTGECTT	TAATGATGTC	AGGTGATTG	60
GGCGGAAACG	CACAGAGCTT	TTGGGAAGAA	ATAGCTCCTC	CTTTTATCAG	TAATGAGCCT	120
AACGTCAAGT	ATATAATTCC	CAATATGGGG	ATTGATTCAA	AGGGAACAAAT	CTATGTAACC	180
GTGACAAAAA	GGATTACGCA	GGGAGCAAAAT	TATACTTCTG	AGCAATTGGG	TATGTACTAT	240
CGACCATTAG	GTGATAATGA	ACAGTGGTGG	AAACATGATC	CGTATTTTGA	TGACAAGATA	300
GTTCGGGATA	TTGAGACAGA	TGCATATGGC	AGAGTTTATG	TATGTACGAC	TTCTTCTCGA	360
GATCAAGAGT	ATCAACTTTA	TATAAACGAG	CAGAACGAAT	GGAGGTGAT	ATTCAAAAC	420
TCTGTGTCTA	CATATGAGCA	TGGTATGGCT	GTTTTCGCT	CTTCGACAGG	GGTGACTTAT	480
ATAGGTACCA	GGCATCACAT	CTTCGCATCA	GGTGTAATG	ATTTCGAGTT	CAACACTATC	540
TATGAAGACT	CTACACCTAT	GAGCTGTGCG	TTTGACAGG	CTACGAATAG	TGGCACCATC	600
TATCTGGCAT	TGATGCATGA	AACCACAATG	TCTACGACTA	TCCTTACTTA	TCAAAACGGT	660
GAGTTCGTCG	ATATCTCGGA	AAGTGAATTG	AGTAACTCGA	TATTGTCATC	CATGTGCTCT	720
AATAAAGAAG	GTGATATAAT	AGCTCTGTTT	ACTTCATAAT	CAGGATTAT	GAGTGAAC	780
CTTGCGATCA	GAAAAGCAGA	TGAAGGCAAA	TGGCAACTTG	TTGGCGGAGA	TATACAGAA	840
GCGATCGTTC	AAAATATATG	CATGATGGAC	GACAACAAGA	TTGCTTGTA	AGTCTTCGGG	900
ACTCCTAAGC	GAGTAGATGG	TGGGACAAGG	GTTTGTGTTT	CTGACGCATC	TGTCTTTGAT	960
TTTGAGTGGT	ATGAAGATGA	AATATACGGA	GGCCTGATAT	TTGACACTTT	CTTCTATAGC	1020
CCTTGGGACA	AACTTCTTTA	TGCGAAATTT	GGTGGGATTA	TGCTCAGGAG	TAAAGAGTCT	1080

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TTTATAACCT CTTTCATTTC TCCGACAGTT GTACAAGGAG TGGATGTCTA TACTTTGGCC 1140  
 GGCAGATAAA GGATCGAAAG TGAAACTCCG GTGTCTGAGG TGTTCCTTTT CGACCTGGCT 1200  
 GGCAGGATGG TACTTCGGCA AACCATTGAT AATAAAATCT ATTCGGACAT AGATACTAAC 1260  
 GGAATAAAGC GAAGCGGTAT TTACGTAGTC TCGGTGCGGC TCTCTCCGG ACAGGTATT 1320  
 5 AGTCATAAGG TGCAGGTA 1338

## (2) INFORMATION FOR SEQ ID NO:231

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 924 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...924
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:231

30 ATGATAATCC GGTGTCTTAT CCGTCGTCGG AGAACCSTCC TGTTCGGGTT GATATTCGTG 60  
 GTAGGTCTTT TCTCTGCGAT GCGCAAGAG AAAAAGGATA GTCTCTCTAC GGTCAGCCA 120  
 GTGCCGAATA GCAGCATGGT GGAGCAGACC CCTCTTCTCT CCATTGATCA CCCCCTCCTG 180  
 CCCCCTTCTT TTCAGAATAC CCGTACACTG AAAAGGTTA GAGACAAACA TCTTCCGAT 240  
 35 GCTTTGCTCA ATGGATTGAA GCCTCATCGC TCATCTTTGC AATTGAATGA GGAACCTAAC 300  
 TTCGCGCGAG AGCGTCGGGA TTCTGTTTCT CCCCCTTTCG AAACCTCGCA CGCTGCCGGT 360  
 GTCCTTTTCAT GCGACCGGAC CGATAGGATG CATTTTATA CATCGGGCAA TATCGTCTT 420  
 GGCCATGATT TATTGACCGG TGTGCGCAAG GACTTCGGAT GGAATGCTGG TGCCGACTTC 480  
 40 TTGCTGACTC AAAATCTTAC GGCACATGTC CAAGGC3GTT GGCAGCAGAA TTTCGGCTTT 540  
 ATACCTATGA CCGCTGTCAA TGGCCCACTG CGTTGGCAAG CCACCGAGAG ATTGAGTTT 600  
 ACCACCGTA TCGATTATCG ACAGGTACAG TGGAAATGCTT TCGATAATAG AACGTCTTCG 660  
 CTTAAAGGAA GTGCTCGATA CGAAGTGATG GACAATGTCT TTGTCAATGG ATTTGGCAGC 720  
 TATCCTCTCT ACAGCAGTAC GCGCTCAGGA CTCAATATGG CTGTTCCGAT GCATGGATT 780  
 45 GGCCTCAGT ACGGTGGATC GCTTGAGCTG AAAGTCTCCG AGCGATTCCG CTTTGCCGTC 840  
 GGTATGGAGC GCGAATACAA TATCTGGACT CGTCGGTGGG AAACGCATTA CTTTGTCTAT 900  
 CCTGTATTCT ATGGCGATAA GAAG 924

## (2) INFORMATION FOR SEQ ID NO:232

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 945 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 55 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 60 (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 65 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...945
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:232

ATGAAAACGA ATAGACGATA CGCATTTGTT TTGCCGCTTC TGCTACTCAC CGGATTGTTG 60  
 GCATGGGGGC AGGATTCTTC CCAOGGTAGC AATACAGCGT TTGCAACTGA TTCTTCGAGT 120  
 75 AGAGAGTTGC CCACGGAGCA GTCCGCCTAC CGCATTCATT CTGCCTATAT GGTCGGTGGT 180  
 GCGGAGCA TAACGCGCA CACCTATTG TCACCCCTTC GTTATGGAGC ATGGACACTG 240

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AATTTGTTGG GAGAGAAGAC GTTCCCTCTC AAAGCCTCCG ATTCCCCTTG GATGATCCGT 300  
 ACCGGGCATG AGCTGGATT TGCCTGATG GACAATCCGG CCAATAATGC TCATTCTAT 360  
 TCCCTGCTGT ATAACGGTTC CGCTGCGGCT CTTTACCGCC TTGGCGGTAA GCATCTGCGA 420  
 GCGCGGTGGA TGGACRATCT GCGCTTGCCA TTGGGCCCGG GCTTGGAAAT CGGGCTTGGA 480  
 5 GGAATTTATA GTACACGCAA CGGCAATAAT CCTGCGACAT TGAAGCTCTA CACCAATGCC 540  
 ATCGCCCAAG CCTCGATAGG ATACTACGTC CCCTCCGAAA CTITTCCTCT GTATTTTCGG 600  
 TTGCTCTCCC AGATCAATCT CTTCGGTATA GCCTATGGAA ATGGTTTGG TGAGAGCTAT 660  
 TACGAGAATT TTTTGCTCAA TAACGGCATT GCAGGCTCCC TGCAATTCAC TTATCCGGGC 720  
 10 AAGTTTACTC GGTTCACGAC ACTCATACG GCGGATATTC CCATTGGGAA CTTCGTAGG 780  
 CTTCGTGTCG GTTATCGCTA TTCCCATTTG GGCTCTTCGC TTAACGCATT GGATACTCGA 840  
 ATCCACAGTC ATACGGCTTT TATCGGTTTC GTCACGGAGT TTTACCGATT CCGTGGGCGC 900  
 AAAGCCATGA ATACGGGTCG GAGAACCACT CTITACTATC ATGAT 945

15 (2) INFORMATION FOR SEQ ID NO:233

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 855 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

25 (111) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...855

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:233

ATGGTAGTGA CGCTGCTCGT AATTGTCCGT ATTGTGGTAG TAGTGCGGTA CTCCTTGGCG 60  
 GTCCACGTAC ATAAGACCGG CACTGTTGTA TCGGCGGGCA TATTGGGCTT CATCCTCCTT 120  
 40 GGAAAGACCG TTCCATGCGA TACCGGTAAC TTCTTTTCTT CCGAAAGTGA TGAACCTGAG 180  
 AGCCGTGTIG CTACCGAAAT AGCCACCTG TCGGAAATAG GATTTCAGAT CCACGCTTCC 240  
 TCTATCCACG TAGCCGTCCG AACCGATTTT GGACAGGCGG GCATCCACTG CCCAATGGCG 300  
 ACCGATGCGT CCGCTACCGA GTTTGACCGA TCGGCGGAAAT GTGCGGAACG AACCTCCGCT 360  
 45 CAAATCGACA CGGCCATAAG GAGCCAGTCC CAAATTATCC GTACGCATAT TGACACTTGC 420  
 CCGAAAAGCT CCGGCACCAT TGGTGGAAAT ACCCACACCT CGCTGCACCT GAAGGTCTTC 480  
 GATGGAAGAG CCGAAGTCGG GCATATTCAC CCGAAAGACG GACTGAGATT CGGAGTCGTT 540  
 GAGGGGTACT CCATTGGTAG TTATGTTGAT GCGATTGGCA TCGGTGCCAC GCACGCGAAA 600  
 GCGGGAATAT CCGATACCGG TACCGGCATC GCTGGTGGCT ACCACGGAGG GAGTCAGCAT 660  
 50 CAGCAGATAG GGGATGTCAC GACCATAATT GGAATTGGAA AGTTGGGCTT TCGGAACGTT 720  
 GGTGTAAAGC ACAGGGGTTT TCGCCGTGGC GCGAGTAGCT ACGACCTGTA CCGTCTGGAG 780  
 CTGCACATTG CTAAGACTAT CTATCTCGCT GTTGGAGACG GGTGCTTGTG CCGTCAGGCA 840  
 GAAAGGCAGG ACGGC 855

55 (2) INFORMATION FOR SEQ ID NO:234

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1797 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

65 (111) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...1797

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## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:234

5 ATGGAAGAACT TAAAGAACAT TCAGCCCAAG GAGGATTTC AACTGGGAAGA GTTTGAGGCC 60  
 GGTGGCGTCC ATGCTGCCGT GAGTCGTCAG GAGCAGGAAG CTGCTTATGA CAAAACGCTC 120  
 AATACCATCA AGGAAAAGGA AGTGGTAATG GGTAGGGTAA CTGCTATCAA CAAGCGTGAA 180  
 GTGGTTATCA ATGTAGGGTA CAAATCGGAA GGTGTGGTAC CTGCAACAGA ATTCGGCTAC 240  
 AATCCCGAAC TCAAAGTGGG AGACGAAGTG GAAATTTATA TCGAGAATCA GGAAGATAAG 300  
 AAGGGCCAGC TCGTCTTGT TCACCGCAAG GGTGCTGCCG CTCGCTCTTG GGAGCGCGTG 360  
 10 AACGAGGCTC TCGAAAACA CGAAATCGTA AAGGGCTATG TGAAGTGTG TACCAAGGGT 420  
 GGTATGATCG TCGATGTATT CGGTATCGAG GCTTTCCTCC CGGGATCACA GATCGACGTG 480  
 CGCCCCATTC GCGACTACGA TGCATTCTGT GAGAAGACGA TGGAGTTCAA GATTGTGAAA 540  
 ATCAATCAAG AATATAAGAA TGATGTTGTT TCCCAACAAG TGCTCATCGA AGCAGAGCTC 600  
 GAACAACAGA AGAAGAAGAT CATCGGCAAG CTCGAAAAG GGCAGGTACT CGAAGGTATC 660  
 GTCAAGAATA TTAATTCTTA CGGAGTATTT ATCGACCTCG GTGGAGTGGG TGGTCTTATC 720  
 15 CATATCACTG ACCTTTCATG GGGTCGTGTG GCTCATCCGG AAGAAATCGT ACAGCTGGAT 780  
 CAGAAGATCA ATGTCGTTAT CCTCGACTTT GATGAAGATC GCAAGCGTAT CGCTCTCGGA 840  
 CTCAAACAGC TGATGCCTCA TCCTTGGGAT GCTCTCGACA GCGAGCTTAA GGTAGGCGAT 900  
 AAGGTGAAGC GTAAAGTTGT GGTGATGGCA GATTACGGTG CTITCGTTGA GATTGCACAG 960  
 20 GCGCTTGAGG GTCTTATCCA CGTAAGCGAA ATGTCATGGA CACAGCACTT GCGTCTCTGT 1020  
 CAGGACTTCC TCCATGTAGG CGACGAAGTG GAAGCCGTGA TCCTGACGCT CGACCGCGAA 1080  
 GAACGCAAAA TGTGCTCGG TCTGAAGCAA CTCAGCCGG ATCCTTGGGC TGATATCGAA 1140  
 ACTCGTTTCC CTGTAGGCTC TCGTCACCAT GCTCGTGTTC GCAACTTCAC CAATTTCTGG 1200  
 GTATTCTGTG AGATCGAAGA GGGCGTAGAT GGCCTTATCC ATATTTCGA CTTTCTTGG 1260  
 25 ACGAAGAACA TCAACACCCC CAGCGAGTTT ACGGAAGTAG GTGCTGATAT CGAAGTTCAG 1320  
 GTAATCGASA TCGACAAAGA AAACGTCGT CTCAGCTTG3 GTCACAAACA GTTGAAGAG 1380  
 AATCCTTGGG ATGTATTCGA GACGGTATTC ACTGTAGGAT CTATCCACGA AGGAACGGTA 1440  
 ATCGAAGTGA TGGACAAGGG TGCTGTGCTT TCTCTGCTT AOGGTGTGGA AGGTTTTCGC 1500  
 30 ATCCGGAAGC ACATGCTGAA GGAAGATGCC TCACAGGCTG TACTCGAAGA GAAGTTACCT 1560  
 TTCAAGGTTA TTGAGTTCAA TAAGGATGCC AAGCGAATCA TTGTATCTCA TAGCCGTGTA 1620  
 TTCGAAGATG AGCAGAAAT GGCTCAGCGT GAAGCCAATG CAGAGCGTAA GGCTGAAGCC 1680  
 AAAGCGGCTC AGAAAGAAGC TGCTGCCCAA GCTGCCAATC CTGCACAGSC TGTAGAGAAA 1740  
 GCCACTCTCG GAGACCTCGG CGAGCTGGCC GCTTTGAAAG AAAAGCTTTC AGAAAAC 1797

## 35 (2) INFORMATION FOR SEQ ID NO:235

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1650 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 45 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 50 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 55 (B) LOCATION 1...1650

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235

60 ATGGGTAGGG TAACTGCTAT CAACAAGCGT GAAGTGGTTA TCAATGAGG GTACAAATCG 60  
 GAAGGTGTGG TACCTGCAAC AGAATTCGCG TACAATCCCG AACTCAAAGT GGGAGACGAA 120  
 GTGGAAGTTT ATATCGAGAA TCAGGAAGAT AAGAAGGGCC AGCTCGTCTT GTCTACCCGC 180  
 AAGGTCTGTG CCGCTCGCTC TTGGGAGCGC GTGAACGAGG CTCTCGAAAA AGACGAAATC 240  
 GTAAAGGCGT ATGTGAAGTG TCGTACCAAG GGTGGTATGA TCGTCAATGT ATTCGGTATC 300  
 GAGGCTTTCC TCCCGGGATC ACAGATCGAC GTGCGCCCA TTGCGGACTA CGATGCATTC 360  
 65 GTTGAGAAGA CGATGGAGTT CAAGATTGTG AAAATCAATC AAGAATATAA GAATGTAGTT 420  
 GTTTCCACCA AGGTGCTCAT CGAAGCAGAG CTCGAACAAC AGAAGAAAGA AATCATCGGC 480  
 AAGCTCGAAA AAGGGCAGGT ACTCGAAGGT ATCGTCAAGA ATATTACTT TTACGGAGTA 540  
 TTTATCGACC TCGTGGAGT GGATGCTCTT ATCCATATCA CTGACCTTTC ATGGGGTCTG 600  
 GTGGCTCATC CGGAAGAAAT CGTACAGCTG GATCAGAAGA TCAATGTCTG TATCCTCGAC 660  
 70 TTTGATGAAG ATCGCAAGCG TATCGCTCTC GGACTCAAAC AGCTGATGCC TCATCCTTGG 720  
 GATGCTCTCG ACAGCGAGCT TAAGGTAGGC GATAAGGTGA AGGTTAAAGT TGTGGTATG 780  
 GCAGATTACG GTGCTTCTGT TGACATTGCA CAGGGCGTTG AGGGTCTTAT CCACGTAAAG 840  
 GAATGTCTAT GGACACAGCA CTGCGCTTCT GCTCAGGACT TCCTGCATGT AGGCGACGAA 900  
 GTGGAAGCCG TGATCTGAC GCTCGACCGC GAAGAACGCA AAATGTCTGT CGGTCTGAAG 960  
 75 CAACTCAAGC CGATCCTTG GGCTGATATC GAAACTCGTT TCCCTGTAGG CTCTCGTCAC 1020  
 CATGCTCGTG TTGCAACTT CACCAATTTT GGTGTATTCC TTGAGATCGA AGAGGGCGTA 1080

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5 GATGGCCTTA TCCATATTTC CGACCTTTCT TGGACGAAGA AGATCAAACA CCCAGCGAG 1140  
 TTTACGGAAG TAGGTGCTGA TATCGAAGTT CAGGTAATCG AGATCGACAA GGAAAAACCGT 1200  
 CGTCTCAGCT TGGGTCACAA ACAGTTGGAA GAGAATCCTT GGGATGTATT CGAGACGGTA 1260  
 TTCCTGTAG GATCTATCCA CGAAGGAACG GTAATCGAAG TGATGGACNA GGGTGCTGTC 1320  
 GTTTCTCTGC CTTACGGTGT GGAAGGTTTT GCCACTCCGA AGCACATGGT GAAGGAAGAT 1380  
 GGCTCACAGG CTGTACTCGA AGAGAAGTTA CCTTTCAAGG TTATTGAGTT CAATAAGGAT 1440  
 GCCAAGCGAA TCATTGTATC TCATAGCCGT GTATTGGAAG ATGAGCAGAA AATGGCTCAG 1500  
 CGTGAAGCCA ATGCAGAGCG TAAGGCTGAA GCCAAAGCGG CTCAGAAAGA AGCTGCTGCC 1560  
 10 GAAGCTGCCA ATCCTGCACA GGCTGTAGAG AAAGCCACTC TCGGAGACCT CGGCGAGCTG 1620  
 GCCGCTTTGA AAGAAAAGCT TTCAGAAAAC 1650

## (2) INFORMATION FOR SEQ ID NO:236

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1374 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 20 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 25 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 30 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1374  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:236

35 ATGATCGTCG ATGTATTGCG TATCGAGGCT TTCCTCCCGG GATCACAGAT CGACGTGCGC 60  
 CCCATTCCGG ACTACGATGC ATTCTGTTGAG AAGACGATGG AGTTCAAGAT TGTGAAAATC 120  
 AATCMGAAT ATAAGAATGT AGTTGTTTCC CACAAGGTGC TCATCGAAGC AGAGCTCGAA 180  
 CAACAGAAGA AAGAAATCAT CGGCAAGCTC GAAAAAGGGC AGGTACTCGA AGGTATCGTC 240  
 40 AAGAATATTA CTCTTACGG AGTATTATC GACCTCGGTG GAGTGGATGG TCTTATCCAT 300  
 ATCACTGACC TTTCATGGGG TCGTGTGGCT CATCCGGAAG AAATCGTACA GCTGGATCAG 360  
 AAGATCAATG TCGTTATCCT CGACTTTGAT GAAGATCGCA AGCGTATCGC TCTCGGACTC 420  
 AAACAGCTGA TGCCTCATCC TTGGGATGCT CTCGACAGCG AGCTTAAGGT AGGCGATAAG 480  
 GTGAAGGGTA AAGTTGTGGT GATGGCAGAT TACGGTGCTT TCGTTGAGAT TGCACAGGGC 540  
 45 GTTGAGGGTC TTATCCACGT AAGCGAAATG TCATGGACAC AGCACTTGGC TTCTGCTCAG 600  
 GACTTCCTGC ATGTAGGCGA CGAAGTGGAA GCCGTGATCC TGACGCTCGA CCGCGAAGAA 660  
 CGCAAAATGT CGCTCGGTCT GAAGCAACTC AAGCCGGATC CTTGGGCTGA TATCGAAACT 720  
 CGTTCCCTG TAGGCTCTCG TCACCATGCT CGTGTTCGCA ACTTCACCAA TTTCGGTGTA 780  
 50 TTCGTTGAGA TCGAAGAGGG CGTAGATGGC CTTATCCATA TTTCCGACCT TTCTTGGACG 840  
 AAGAVGATCA AACACCCAG CGAGTTTACG GAAGTAGGTG CTGATATCGA AGTTCAGGTA 900  
 ATCGAGATCG ACAAGGAAAA CCGTCGTCTC AGCTTGGGTC ACAACAGTT GGAAGAGAAT 960  
 CCTTGGGATG TATTGAGAC GGTATTCACT GTAGGATCTA TCCACGAAGG AACGGTAATC 1020  
 GAAGTGATGG ACAAGGGTGC TGTGTTTCT CTGCCTTACG GTGTGGAAGG TTTTGCCACT 1080  
 55 CCGAAGCACA TGGTGAAGGA AGATGGCTCA CAGGCTGTAC TCGAAGAGAA GTTACCTTTC 1140  
 AAGGTTATTG AGTTCAATAA GGATGCCAAG CGAATCATTG TATCTCATAG CCGTGTATTG 1200  
 GAAGATGAGC AGAAATGGC TCAGCGTGAA GCCAATGCAG AGCGTAAGGC TGAAGCCAAA 1260  
 GCGGCTCAGA AAGAAAGCTG TGCCGAAGCT GCCAATCTG CACAGGCTGT AGAGAAAGCC 1320  
 ACTCTCGGAG ACCTCGGCGA GCTGGCCGCT TTGAAAGAAA AGCTTTCAGA AAAC 1374

## (2) INFORMATION FOR SEQ ID NO:237

65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1278 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 70 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 75 (vi) ORIGINAL SOURCE:

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(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- 5 (A) NAME/KEY: misc feature  
(B) LOCATION 1...1278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237

10 ATGGAGTTCA AGATTGTGAA AATCAATCAA GAATATAAGA ATGTAGTTGT TTCCACAAAG 60  
GTGCTCATCG AAGCAGAGCT CGAACAACAG AAGAAAGAAA TCATCGGCAA GCTCGAAAAA 120  
GGGCAGGTAC TCGAAGGTAT CGTCAAGAAAT ATTACTTCTT ACGGAGTATT TATCGACCTC 180  
GGTGGAGTGG ATGGTCTTAT CCATATCACT GACCTTTCAT GGGGTCGTGT GGCTCATCCG 240  
GAAGAAATCG TACAGCTGGA TCAGAAGATC AATGTCGTTA TCCTCGACTT TGATGAAGAT 300  
CGCAAGCGTA TCGCTCTCGG ACTCAAACAG CTGATGCCTC ATCCTTGGGA TGCTCTCGAC 360  
15 AGCGAGCTTA AGGTAGGCGA TAAGGTGAAG GGTAAAGTTG TGGTGATGGC AGATTACGCT 420  
GCTTTCTGTT AGATTGCACA GGGCGTTGAG GGTCTTATCC ACGTAAGCGA AATGTCATGG 480  
ACACAGCACT TCGCTTCTGC TCAGGACTTC CTGCATGTAG GCGACGAAGT GGAAGCCGTG 540  
ATCCTGACGC TCGACCGCGA AGAACGCAAA ATGTCGCTCG GTCTGAAGCA ACTCAAGCCG 600  
GATCCTTGGG CTGATATCGA AACTCGTTTC CCTGTAGGCT CTCGTACCCA TGCTCTGTTT 660  
20 CGCAACTTCA CCAATTTCCG TGTATTCTGT GAGATCGAAG AGGGCGTAGA TGGCCTTATC 720  
CATATTTCCG ACCTTTCTTG GACGAAGTAG ATCAAACACC CCAGCGAGTT TACGGAAGTA 780  
GGTGCTGATA TCGAAGTTCA GGTAAATCGAG ATCGACAAGG AAAACCCGTC TCTCAGCTTG 840  
GGTCAACAAC AGTTGGAAGA GAATCCTTGG GATGTATTCC AGACGGTATT CACTGTAGGA 900  
TCTATCCACG AAGGAACGGT AATCGAAGTG ATGGACAAGG GTGCTGTCTT TTCTCTGCCT 960  
25 TACGCTGTGG AAGGTTTTGC CACTCCGAAG CACATGGTGA AGGAAGATGG CTCACAGGCT 1020  
GTACTCGAAG AGAAGTTACC TTTCAAGGTT ATTGAGTTCA ATAAGGATGC CAAGCGAATC 1080  
ATTGTATCTC ATAGCCGTGT ATTCGAAGAT SAGCAGAAAA TGGCTCAGCG TGAAGCCAAT 1140  
GCAGAGCGTA AGGCTGAAGC CAAAGCGGCT CAGAAAGAAG CTGCTGCCGA AGCTGCCAAT 1200  
CCTGCACAGG CTGTAGAGAA AGCCACTCTC GGAGACCTCG GCGAGCTGGC CGCTTTGAAA 1260  
30 GAAVAGCTTT CAGAAAAC 1278

(2) INFORMATION FOR SEQ ID NO:238

- 35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 720 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular
- 40 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 45 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 50 (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238

55 ATGAAAAAAG CTATTCTTTC CGGAGCGGCC TTGCTCCTCG GCCTATGTGC CAACGCACAA 60  
AACGTGCACT TCGACTACGA TTTCCGGTCAT TCCATCTAAG ACGAACTAGA TGGACGTCCC 120  
AAACTGACTA CCACAGTGGG AAACCTTACA CCGACAAAAT GGGGAAGCAC CTTCTTCTTC 180  
ATCGACATGG ATTACACGGG CAAGGGTATC CAGTCGGCCT ATTGGGAGAT TTCGCGCGAA 240  
CTGAAGTTTT GGCAAGCTCC CGTTTCCATT CATTGGAGT ACAACGGAGG CCTCTCCACA 300  
AGCTTTACTT TCGGACACGA TGCTCTAATC GGTGCCACCT ACACCTACAA CAACCCCTCC 360  
TTTACAGTGG GATTACGAT CACGCCCATG TACAAGCATC TGGGTGCGCA CGACTTCCAC 420  
ACCTATCAGA TCACCGGCAC TTGGTACATG CACTTTCTGG ACGGTCTGCT TACCTTCAAC 480  
GGCTTCTCG ATCTTTGGGG TTTCGCCCAA GAGAACCCAA TCGGGGGGCC TGTGCTCAA 540  
65 GAAGGGGATA AGTTCTGATT CTTGTCCGAA CGCAGTTCT GGATCAACCT CAATGCAATC 600  
AAAGGCATCG ACAAGGATTT CAATCTCAGC ATAGGGACAG AGATGGAAAT CAGCAGGAAC 660  
TTGCTCGCA TGGACAAATT CTCTGCATC CTAATCTTG CGGTCAAAAT GACTTTCAAC 720

(2) INFORMATION FOR SEQ ID NO:239

- 70 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1302 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double
- 75

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(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

5 (111) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...1302

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:239

20	ATGTATAAAG	ACTATAAGGG	TTGTATGCG	TGCTTCGGT	GGTATGCCCT	GATCATTGGG	60
	TTGCTATTTG	CAGCAGACGG	TATACAGGCT	CAGAACAACA	ACTTTACCGA	GTCCGCTTAC	120
	ACTCGCTTCG	GCCCTGGCCG	TCTCGGAGAA	CGGACGACTA	TTAGTGGGCA	TTCCATGGGA	180
	GGACTCGGGG	TCGCTCTGCG	TCAGGGACAA	TACGTCAATG	CCGTCAATCC	TGCTTCATAC	240
	TCGGCTGTGG	ATTCTGATGAC	GTTTATCTTC	GATTTCGGTG	CATCTACCGG	AATTACGTGG	300
	TATGCCGAGA	ACGGGAAAAA	GGACAATAGG	AAAATGGGAA	ACATTGAGTA	TTTCGCCATG	360
	CTTTTTCCTA	TTTCCAAATC	CATTGCTATG	AGTGGCGGGG	TGCTTCCTTA	CTCCGCATCC	420
25	GGGTACCACT	TCGGATCCGT	TGATCAAGTG	GAAGGAGGCA	GCGTCCAGTA	CACCCGTAAA	480
	TACTTGGGGA	CAGGCAATCT	GAACGATCTC	TATGTCGGTA	TAGGTGCAAC	CCCGTTCAAA	540
	AACCTCTCAA	TAGGAGCCAA	TGCTTCATCC	CTTTTGGGCG	GATTACACAC	CAGCAGGCAG	600
	GTAATCTTCT	CCACGGAGGC	TCCTTACAAT	CCCGTACATC	TCTCGACGCT	GTACTTGAAG	660
	GCTGCCAAGT	TGACTTCGG	TATGCAGTAT	CACCTTCTTC	TCAAATCAGA	TCGTTGCTTC	720
30	GTTATCGGTG	CCGCTATATC	TCGCGGGGTG	AAGATGCATA	GCGAGCTGAC	TCAGATAAAG	780
	AATCAGGTTT	AGAACGGTGT	AGTAGTGGAG	AGCGAAACCC	AAGAATATAT	CAAGGGAAATG	840
	GACTATTATA	CCCTGCCTCA	TACATTGGGG	ATAGGTTTTT	CTTATGAAAA	GAAAGATAAA	900
	CTTCTCTTAG	GAGCAGACGT	CCAATATAGT	AAATGGAAAG	GCGAGAAATT	TTTAAATCC	960
	GATTGCAAAAT	TCCAGGACAG	AATACGGGTA	TCTCTCGGCG	GAGAGATCAT	ACCGGATATA	1020
35	AATGCCGTTG	GGATGTGGCC	TAAAGTTGCG	TATCGCTTCG	GTTTACATGG	TGAAAATTCT	1080
	TACCTGAAGA	TGCCGACTAA	AGGCGGTGTA	TATCAAGGAT	ACCATATCGT	AGGTGCTGTA	1140
	TTCCGTATAG	GAATCCCGCT	CAATGACAGA	CGTTGCTTCG	TAAATGCTTC	TCTTGAATAT	1200
	GACCGATTGA	TCCCGAAGGA	GGGTATGATC	AAAGAAAATG	CTCTGAAATT	GACCTTCGGC	1260
40	CTCAGGTTC	ACGAGTCAATG	GTTTAAAAAG	CTGAAACTGA	AC		1302

(2) INFORMATION FOR SEQ ID NO:240

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2778 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

45 (11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

55 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...2778

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:240

65	ATGCGATCGA	TTTATCAATT	ACTGTTGTCA	ATATCCTTGG	CTTCTCTTGG	TTTCGTGCGG	60
	CTGGAAGCCC	AACAAGCCGG	AGTAGCAGGT	AGAGTATTGG	ACGAAGAAGG	CAACCCCATG	120
	ATTCAAGCCA	ACGTACAGCT	TGTACAGAGT	ACCGGCCAAG	TAGCCGTTGC	CGCAGGTGCC	180
	ACTAATGAAA	AAGGTTGTGT	CAGCCTGAAA	ACGTACACAG	AGGGTGACTA	CATTCTGCGC	240
70	TTTTCATATG	TAGGTTACAC	TACCCACGAC	GAAAAATAT	CTCTTAGAAA	CGGGCAAAAC	300
	ATTACGCTCA	AAGATATATC	CATGAACGAA	GATGCCCGTC	TTCTACAGAG	TGTGACGGTG	360
	CAGGCTAAAG	CGGCAGAGGT	CGTGGTACGC	AACGATACGC	TGCAATTCAA	TGCCGGATCC	420
	TATACCGTAG	CACAGGGAGC	TTCTATCGAG	GAAGTATCA	AGAAGCTACC	CGGAGCAGAG	480
	ATCGGATCCG	ATGGGAAGAT	CACCATCAAC	GGCAAGGACA	TTAGCAAGAT	CCTTGTGATG	540
	GGCAAGAGAT	TTTCTCCAA	AGATCCACAG	GTGGCAATAA	AGAATCTTCC	GGCCGATATG	600
75	GTCAATAAAC	TACAGGTACT	GAACAAACTG	AGCGAGCTGT	CGCGGATGAG	CGGTTTCGAT	660

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	GATGGAGAAG	AGGAGACCGT	AATCAACCTG	ACGGTGAAGC	CCGAAAAAAA	GAAAGGCCTC	720
	TTCCGAACGC	TTCCAGGCCG	CTACGGTACC	GACCAACGCT	ATATGGCCGG	AGGGAACGTC	780
	AATCGGTTCC	ATGGAAATAA	GCAATGGACA	TTGATCGGTA	GTGCGAACMA	TACGAACAAT	840
	ATGGGCTTTA	GCGAGATGGA	CAGCGAGATG	GGATCCATGA	CCTTCTTCTC	TCCCAAGGCG	900
5	GGTGGTCCGAC	GCGGCTTCGG	CAATAGTGGA	GGTGTACGTT	CTTCGTGAT	GCTGGGCGGC	960
	AACTTCAGTG	TGGAATTCCT	CTCTGCCCTT	AATACAGGAG	GCGATGCACG	CTACGGATAC	1020
	AACGACAAGG	CCATAGAGAC	GACCAAACGC	GTGAAAAATA	TCCTCGCCGA	AGGGAATACT	1080
	TATATGGACG	AAAATATATT	GGAACGCTCT	TTCTCTCACA	ATGGTCAGGC	GCGATTAGG	1140
	ATGCAATGGA	AAACGTCGGA	ACGTACCGAA	GTGGTATTCG	AGCGGATCT	TTGATATCC	1200
10	AAGATCGATG	GGTCTTTTAA	CGACACATAC	GAGACGAAAG	ATGCCACCGG	AATCTCTATC	1260
	AACAAGGTT	CTATCCACCA	AATACACAA	GGAAACAAC	TCAGACTGAA	CGGAGAATTG	1320
	GATATCAGTC	ACAAGCTCAA	CGACGAAGGC	CGTACGATCA	GTGCGTCCGT	CAGTGGCGGT	1380
	CTGACCGACG	AAGACGGAGA	TGGCATATAT	CAGGCTGTGC	TCCAAAGCGT	GGAGACGAAT	1440
	CAAAAGCAAT	TCAACGACAA	CTCCAACCTG	CAATATCGGC	TTGCGCTCTC	GTATGTGGAA	1500
15	CCGTTGGGTA	AAAACIACIT	CGCACAGCG	ATTCTGAACA	GACGTTTCTC	CCGTCGCAAT	1560
	TGGATCGTTC	AGGTGTACCG	ACTGGGCGAT	GACGGGCAAT	ACTCCATATT	AGACAGTCAG	1620
	TACGGACTCT	CTACAGTAA	CGAGTTCACC	CAGTATCGCA	TCGGACTCAA	CCTCAAGAAG	1680
	ATTGCCAAAA	CGTGGGACTA	CACCGTAGGA	TTCAATGTGG	ATCCCAACAG	AACGTGCAGC	1740
	TATCGGAGCG	TAGCCGGAGT	AGAGCAGGAC	AAACTGGCTT	TCAATCGTGT	CAATCTCTCC	1800
20	CGGATGCTCC	GAATCAACTA	CAAACCGAGC	AGGACTACCA	ACCTCCGAGT	GGACTACCGA	1860
	GGACGCACGA	CACAACCATC	CATCAATCAG	ATCGCTCCCG	TTCAGGACAT	CACGAATCCG	1920
	CTATTCTGTA	CGGAAGGCCAA	TCCCGGTCTG	AAGCCGAGCT	ATTCCAACAA	TGTGATGGCC	1980
	ATGTTCTCGG	ACTTCGATGC	CAAAAGTCAG	CGAGCTTTCA	ACATTGTTTT	CTTCGGCAAC	2040
	TATACATTCC	ACGACATCGT	CCCCAATACG	CACTACGATC	CGTCTACAGG	GATCCGTACC	2100
25	ACTCGTTACG	AAAACGCCCTC	CGGTACGTGG	CAAGCGAATC	TTCATGGGAC	ACTATCGCTT	2160
	CCACTCAAGA	ACAGGGCATT	TTCTTTCAGG	ATGTCCTTGT	TCAACAGGTT	GGCCGAAGGA	2220
	CAAGCTTCCA	TCAATGACGA	TAAGAACAAA	GCTCTCTCTT	TCCGAACGAG	GGAACGCTTG	2280
	ACGCTGACCT	ATCGCAVACA	TGGATTCGAT	ACGAGTATCG	GTGGCAATAT	CGGATTCAT	2340
	ATGGCGAATA	ATAGTCTGAG	CGGACAGAAA	GATTCTCGCA	CATACGATTT	TGGCGGCAAT	2400
30	TATCAAGTTG	CCCTAACGCT	TCCCTATGGA	TTCCGTATCG	ACACGCGATG	TGAATACAA	2460
	ACGAATCCCG	GTTACAGCGG	AGGATTCACT	CTGGACGAAT	GGCTTTGGAA	TGCTTCGCTT	2520
	TCATACAGCT	TCCTCCGTGA	CAAGCCCGGT	ACACTGCGTG	TCAATGGCTA	TGACATCCTC	2580
	GGTCAGCGGT	CAAGTATCAG	CCGTCTGCT	TCGGCCATCA	ATATAGAAGA	GAGCATGTCC	2640
	AATACGATCG	GACGCTACGT	GATGGTGGAC	TTTATCTACC	GATTCAACGC	CTTCAGTGGT	2700
35	GGTGGATCTC	GCAGCGATCA	TCAGCGTGGC	AATATGAATC	GTCCGGGCCC	ACCTTTCGGC	2760
	GGTGGCAGAC	GACCGTCC					2778

- (2) INFORMATION FOR SEQ ID NO:241
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1200
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:241

	ATGGTTATGA	AGCTGATTAA	AAGAAGTTTG	CTCCTGCTTG	GAGCGGTAAT	GCTGATTACG	60
	CTTCTCGGCT	ACTCGCAGAA	TGATGACATC	TTCCGAAGATG	ACATCTATAC	ATCGCGAAAA	120
	GAAATACGTA	AACAAAACCA	AGTTAAAGAC	TGGCAAAACC	AAGAGGACGG	ATACGGCGAC	180
65	GATACGGAAT	ATACAGTGGC	TTCCGATCGG	GACATTGACG	CCTACAAATC	TAGAGATGGC	240
	CAGTCCCTACG	ATGGGAAAAA	GTGTCCAAA	GACAAGAAAA	GAGACTCCAC	TCGTTCTTCT	300
	GTTCGGGCTC	GCTATAGTCG	CCGCTTGGCT	CGATTCTATA	AGCCGAATAC	GATCGTCATT	360
	TCAGGTCGCG	ACAAATGTATA	TGTAACGTAT	GATGGTGAGT	ATTTCGTCTA	TGGAGACGAA	420
	TACTATGATG	ACGCGTCGTC	TGTAACATT	TACATCAACA	GTCTTGGTG	CGATCCGTTT	480
70	CCTTATACGT	CATGGTATCC	ATCTTTCTCC	GGCTGGTACA	ACTATACGTG	GAACTATCCA	540
	TGGTCTTACT	ACGGTAGCCA	TATCCGATGG	GGCGGTATT	ACCCCGGATA	TAATTGGTAT	600
	TGGAGCTACT	ACTATGATCC	TTTCTACAA	CCCTATGGAA	TCGGTATGGG	TTGGGGATAT	660
	CCTTATGACT	GGGGCAGCTA	TTACGGTTGG	GGTGGCTATC	CGGGAGTGAT	ACATCACTAC	720
	CACCACTACC	CCAAGAAGAC	CTATTCCAAT	GGTCAGCATT	CCGGAGCTTA	CTATTCTTAT	780
75	GGCCGACCGA	ATCGTATCAA	AGGTGGAACG	TCCGTGCCA	AACTTGGGAC	AGGACGCTAC	840

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5 GATAGAATTC AAAATTCGTC TTCGCAAAAA AATAAGTTCS GATTGCAGTC GAACAAACCC 900  
 AATAAATAATC TGCAAAATGT CAAGTCGGGA CGTACCGGCC GAGCCAATAG AGACCGAAAT 960  
 ATAGAAACGG TAACTCCAAA CAACGGGCAA AAGCAGAATC GTCCCGTATT CCAGCAGAAT 1020  
 CAGTCCGGCA ATGACCGAGC GACCGGACGG AATATCCGCA GCGAGAGACA GGGGGAAAAAT 1080  
 AACGATAGGA CATTTCGAC TCCTTCTCGT AGCAATAGTA ACGGTGGCTT CTCCACGCCT 1140  
 TCTCGCTCTT CTTCGGCTC TATGAGCGGA GGTGGCGGAC GTAGTGGCCG GGGACGCAAT 1200

10 (2) INFORMATION FOR SEQ ID NO:242  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1194 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...1194  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:242

ATGAAGCTGA TAAAAGAAG TTTGCTCCTG CTGGAGCGG TACTGCTGAT TACGCTTCCT 60  
 GCGTACTCGC AGAATGATGA CATCTTCGAA GATGACATCT ATACATCGCG AAAAGAAATA 120  
 CGTAACAACA ACCAAGTTAA AGACTGGCAA AACCAAGAGG ACGGATACGG CGACGATACG 180  
 GAATATACAG TGGCTTCGGA TCGGGACATT GACGCTACA ATCGTAGAGA TGGCCAGTCC 240  
 TACGATGGGA AAAAGTTGTC CAAAGACAAG AAAAGAGACT CCACTCGTTC TTCTGTTCCC 300  
 GGTGCTATA GTCGCGCTT GGCTCGATT TATAAGCCGA ATACGATCGT CATTTCAGGT 360  
 GCGACAATG TATATGTAAC TGATGATGGT GAGTATTTCT TCTATGGAGA CGAATACTAT 420  
 GATGACGGT GGTCTGTAAA CATTACATC AACAGTCCTT GGTGGGATCC GTTCCCTTAT 480  
 ACGTCATGGT ATCCATCTT CTCCGGCTGG TACAACTATA CGTGGAACTA TCCATGGTTC 540  
 TACTACGGTA GCCATATCGG ATGGGGCGGT TATTACCCCG GATATAAATG GTATTGGAGC 600  
 TACTACTATG ATCCTTTCTA CAATCCCTAT GGAATCGGTA TGGGTGGGG ATATCCTTAT 660  
 GGCTGGGGCA GCTATTACGG TTGGGTGGG TATCCGGGAG TGATACATCA CTACCACCAC 720  
 TACCCCAAGA AGACCTATTC CAATGGTCAG CATTCCGGAG CTTACTATTC TTATGGCCGA 780  
 CGGAATCGTA TCAAGGTGG AACGTCCGGT GCCAACTTG GGCAGGAGC CTACGATAGA 840  
 ATTCAAATTT GGTCTTCGCA AAAAAATAAG TTCGATTGC AGTCGAACAA ACCCAATAAT 900  
 AATCTGCAAA ATGTCAAGTC GGGACGTACC GGCCGAGCCA ATAGAGACCG AATATAGAA 960  
 ACGGTAACTC CAAACAACGG GCAAAAGCAG AATCGTCCCG TATTCCAGCA GAATCAGTCC 1020  
 GGCAATGACC GACCGACCGG ACGGAATATC CGCAGCGAGA GACAGGGGGA AAATAACGAT 1080  
 50 AGSACATTTT CGACTCCTTC TCGTAGCAAT AGTAACGGTG GCTTCTCCAC GCCTTCTCGC 1140  
 TCTTCTCCG GCTCTATGAG CGGAGGTGGC GGACGTAGTG GCCGGGACG CAAT 1194

55 (2) INFORMATION FOR SEQ ID NO:243  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1743 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (v) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...1743  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:243

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5 ATGATCCGCA AGTTGATCTT ACTGCTTGCT CTGATGCCGG TAGCCTCTGT GGCTTTTGCG 60  
 GTACCAACGG ACAGCACGGA ATCGAAAGAC AATCGTATCC TTACAAGCAT GCAATCCTCC 120  
 TCTTTGAATA GGGATGATGC TCCGGATAAA TGGCAACCTA TGCATGCCAA TTTCAGTATT 180  
 CAGAGCGATA TGCTGCTTTC TACTGCCCAA AAGTCCAAGA ACACCTGGTT CGGCAACTCC 240  
 TATATCATGG GTATAATCAA GAACAATTAT CTGGAGTTTG GTGCCCGTTT CGAGGATCTC 300  
 TATAAGCCCC TGCCCCGACA TGAACCCGAG ATGGGGCGTG GCGTTCCTCA CATGTATGTG 360  
 AAGGGAAGCT ATCATTGGGC GGAGCTGACT ATGGGAGACT TCTACGATCA GTTCGGTAGC 420  
 10 GGTATGGTAT TCCGCACCTA TGAAGAGCGC AACCTCGGTA TAGACAACGC GGTTCGCGGC 480  
 GGACGTATAG TACTCACTCC TTTTGATGGA GTGGGTGTCA AGGGTATTGC AGGACAGCAG 540  
 CGTAATACT TCGACCGCAC GGGCAAGGTA TTCAAITCCG GCCGAGGCTA CCTACTGGGT 600  
 TCTGATCTGG AGCTGAATGT AGAGCGTTGG AGCAGTGCCA TCGCGACAA TGACTATCAT 660  
 TTGGCTATCG GGGGATCGTT CGTTTCCAAA CACGAAGCAG ACGAAGATAT ATTTGTGGGT 720  
 GTAGGCGAAG ATCGCAAGCG ACTCAACCTG CCGCTCAATG TCCCGATTAT GGGCCTGCGC 780  
 15 ACCAACTTTC AAAAAGGAGG TCTCGCCCTC TACGCGAGAT ATGGATACAA ATACAACGAT 840  
 CCTCGGCGAG ACAATGACTA TATCTACCAC GACGGACAGG CTGCACTCCT CTCTGCCCTCA 900  
 TACTCCAAAA AAGGGATGAG TATCCTGTTG CAGGCCAAAC GTTGTGAGAA CTITGCTTTC 960  
 CGCAGCAAGC GAAGTGCCCA GCTCACACCG CTTATGATCA ACTATATGCC GGCTTTTACC 1020  
 CAAGCTCACA CTTATACGCT GCGCGCCATC TACCCCTATG CTACTCAGCC TCAGGGAGAA 1080  
 20 TGGGCTTTCC AAGGTGAAC TCGTTACAAC TTTGCTCGCC GGACAGCTCT CGGTGGACGC 1140  
 TACGGTACCG GCTTGCCTAT CAACGTTTCG CATGTGCGTG GTCTGGACAA AAGATGCTC 1200  
 AAAGAGATTC CCGACGAAC TATCGGAACG GATGGCTACA CCGTTTCTTT CTTCGCCATG 1260  
 GCGGACCTCT ATTATTCGGA TATAGATGTG GAGATTACTA AAAAGGTAAG CCCAGGATTC 1320  
 AACTTTACGC TCACCTACTT GAATCAGATC TACAATAACA AGGTACTGCA CGGTGCAGCC 1380  
 25 GGAGAGAACC CTGAGAAGAT CTATGCCAAT ATCTTCGTCT ATGATGGTAA GTATAAGCTG 1440  
 AGTAATAAGG TAGCCCTCGG TACCGAATCG CAATATTTCG ACACGAAGCA GGATCAGGCT 1500  
 GACTGGATCT ACGGCATGGC CGAGCTCTCT ATCCTGCCCT CTCTGATGCT TTCCCTCTCG 1560  
 GAGCAGTATA ATATCGGAGA GACCAAGAAA CATTATGTCA TGGGGTCTGT CACCTATACT 1620  
 CACGGAGCAC ATCGAGTAGC TTTCTCTGCA GGCAAAACCC GTGCAGGAT GAAGTCTCTG 1680  
 30 GGAGGTGTAT GTCGTGTGGT CCCTGAGACT CAGGGATTCT ACCTTTCTTA TAGCAACCAAT 1740  
 CTG 1743

## (2) INFORMATION FOR SEQ ID NO:244

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...717

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:244

55 ATGCGTTCTT TATTTTGAG CGCGTTGCGC AGCTCCTCTC TCCATGCTTC AGAGCGACGC 60  
 AGTCGGATAA GTTCTTCTGT AGTCATGTCA ATAAGGCAGA AATAAGGTT ATTCCATCTC 120  
 TCGGTATGCG CCCAACGCA TGATCATCTC ATCGAAATCC ACTTGGTGTG CATCGAATTC 180  
 60 GGGGCCATCG ACACAGACGA ATTTCTGTCTG TCCTCCCAAG CTTATACGAC AAGCCCCACA 240  
 CATACCGGTG CCATCCACCA TAATTGTATT GACAGAAGCT ATGGTCGGTA TCTCGTAACG 300  
 TTTGGTCAGG AGAGAAACGA ACTTCATCAT CACAGCCGCG CCGATCGTAA CGCAGAGGTC 360  
 TACCGTTTCC CGTTTGATAA CGCTTTCCAC TCCATCCGTT ACGAGGCCCT TCGTCCCAT 420  
 65 AGACCCATCG TCTGTATGA TGATCACTTC ATCGCTATTG GCTCGCATTT GTTCTTCAAG 480  
 GATAACCGA TCTTTAGTTC TGGCAGCCAA TACGACAATT ACACGGTTGC CTGCTTTGTG 540  
 GAAAGCCCTCC ACGATCGGGA GCAAAGGAGC CACACCCACA CCGCCTCCGG CACAAACCAC 600  
 TGTGCCGACC TTTTCGATAT GCGTACTCTG TCCAGCGGGA CCTACCATAT CCGTGATATA 660  
 70 GTCGCCGACT TCGAGTTGCG CCAATTTCTT GGAAGATTTG CCGACGGCCT GAACCCAC 717

## (2) INFORMATION FOR SEQ ID NO:245

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs  
 (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245

20	ATGTCATATAA GGCAGAAAAT AAGGTTATTC CATCTCTCGG TATGCGCCCA AACGCATGAT	60
	CATCTCATCG AAATCCACTT GGTGTGCATC GAATTCGGGG CCATCGACAC AGACGAATTT	120
	CGTCTGTCCT CCCACGCTTA TACGACAAGC CCCACACATA CCGGTGCCAT CCACCATAAT	180
	TGTATTGAGA GAAGCTATGG TCGGTATCTC GTAACGTTTG GTCAGGAGAG AAACGAACCT	240
	CATCATCACA GCGGCGCCGA TCGTAACGCA GAGGTCTACC GTTTCGGGTG TGATAACGCT	300
25	TTCCACTCCA TCCGTTACGA GGCCCTTCGT CCCATAAGAC CCATCGTCTG TCATGATGAT	360
	CACTTCATCG CTATTGGCTC GCATTGTTC TTCAAGGATA ACCAGATCTT TAGTCTGGC	420
	AGCCAATACG ACAATACAC GGTTCGCTGC TTGTGGAAA GCCTCCACGA TCGGGAGCAA	480
	AGGAGCCACA CCCACACCGC CTCGCGCACA AACCAGTGTG CCGACCTTTT CGATATGGGT	540
	ACTCTGTCCC AGCGGACCTA CCACATCGT GATATAGTCG CCGACTTCGA GTTCGGCCAA	600
30	TTTCTTGAA GATTTCGCCA CGGCCTGAAC CAC	633

(2) INFORMATION FOR SEQ ID NO:246

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2343 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...2343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246

55	ATGGATCGTC CTAAGCCTTC ATATATTGTT CGAATAGCAG CCATTCTCTG CTGTTTGTG	60
	GGCAGGCTT TGTTCGCGCA GAGCTATGTG GACTACGTG ATCCGCTGAT CGGGACGCTA	120
	AGTTCTTTTG AGCTGAGTGC GGGCAATACC TATCCGGTGA TCGGTTTACC GTGGGGGAATG	180
	AATAGCTGGA CACCGATGAC CGGTGTACCC GGTGACGGCT GGCAATATAC CTAATCGGCA	240
60	CACAAGATTG GCGGATTCAA ACAGACCCAC CAACCCAGTC CTGGATCAA CGACTACGGC	300
	CAATTCTCCC TTCTTCCCCT TACGGCACCG CAGAAGCCAT CATCGAACGA CTCCATAGCT	360
	CTGACTAAAT GGTGCAAGCA ACTCTTTTCG GACGAACAGA CCTCGTGGTT CTCGCACAAA	420
	GCGGAGACGG CGACGCCATA CTATTATAGT GTCTATTGG CCGATTACGA CACACGGGTG	480
	GAGATGGCTC CGACCGAGCG TGCAGCTATC TTTCGCATAC GTTATTCCGG CAATACCGAA	540
	AGTGGCTCCG GTCGATGGCT TCGTCTTGAT GCCTTTACCG GTGGTTCCGA GATTAGCATC	600
65	GTGGATCCTC ACACCGTAGT GGGCATATCT CGCAAGAATA GCGGAGGTGT GCCGGCTAAC	660
	TTGCGCTGTT ATTTCATCCT GCAGTCCGAT ACTCCTATGG CCGATGTCCT GCTTGAGACA	720
	GATACCGGCA AGTCAGACGA AGGCACAAGG GCATGGGCAG CCTGTGCTT CGATTCCGCA	780
	GAAGTTACCG TCCGGGTGGC ATCTTCTTTT ATCAGTGTGC AGCAGGCCGA AAGAAATCTT	840
70	GCGGAAGTCA AAGGGCAGAG TTTCGACCGG ATCAGACTTG CCGGTGCGCA AGCTTGGAAAT	900
	AAGGTGCTCG GACGCATACA TGTGGAGGA GGAACGAAG ATGAGCGCAC TACATTCTAT	960
	TCGCACTCT ATCGCTGTCT GCTTTTCCC CGTCGCTTCT ATGAGGAGGA TGCTTCCGGC	1020
	AATTTTGTGC ATTACAGCCC CTACAATGGA GAGGTACTTC CCGGTATCT CTATACCGAT	1080
	ACCGGATTTT GGGACACTTT TCGAGCCCTT TTCCCTCTGC TCAATCTGCT GTATCCCGAT	1140
75	GAAACATTA AAATTCAGGA AGGTCTGCTG AATGTATATC GCGAGAGTGG CTTTTCGCC	1200
	GAATGGGCA GTCCGGGCA TCGGATTGT ATCATAGGCA ACAACTCTGC TTCTGTTCTG	1260

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GCGGATGCCCT ACCTCAAGGG TGTTCGGGTA GAAGATACCC GTACACTGAT GAACGGACTC 1320  
 TTGCATGCTA CGAAAGCCGT CCATCCGAAA ATCTCCTCCA CGGGTCGCAA AGGTTGGGAG 1380  
 TGGTACAACCT CCTTAGGTTA TGTTCGGGCT GATGCAGGCA TCGACGAAAG TGCTGCCCGT 1440  
 ACGCTCGAAT ATGCTTATAA CGATTGGTGC ATCCTCCGAC TGGGGCGCAC ATTGGGTTGG 1500  
 5 GATAGAGCTG CATTGGACAC GTTGGCTCAT CGTTCGATGA ACTATCGTCA TCTGTTCGAT 1560  
 CCGGAAACCA AACTCATGCG CGGTAGAAAT CAGGATGGTA GTTTCGGGAC ACCTTTTTTC 1620  
 CCTTTCAAAT GGGGAGATGT ATTACGGAG GGCAATGCCT GGCACTACAC TTGGTCGGTC 1680  
 TTTCATGATG TGCAGGGGCT TATCGACCTG ATGGGAGGAG ATGCCCCGTT CGTGTCTATG 1740  
 CTCGATTCCG TATTCAATAC TCCTCTATG TTCGATCAGA GCTATTACGG ATTTGTCTATC 1800  
 10 CACGAAATCA GAGAGATGCA AATAGCGGAT ATGGGCAATT ATGCTCATGG CAATCAAOCC 1860  
 ATACAGCATA TGATATATCT GTATAATCAT GCCGGTCATC CATGGAAAGC TCAGGAGAGA 1920  
 CTACGCGAAG TGATGGGGCG GCTCTATCGT CCTACTCCGG ATGGGTATTG CGGCGATGAA 1980  
 GACAAACGAC AGACTTCGGC TTGGTACGTT TTCTCTGCT TAGGCTTCTA TCCTGTTACA 2040  
 CCCGCTACGG ATCAGTATGT GCTCGGTTCC CCGATTTTTT CCAAGGTAAT ACTCTCTTT 2100  
 15 CCGGACGGAC ACAAACGGT GTTGCATGCT CCGGCCAACA GTGCCGATAC GCCTTACATC 2160  
 GCCTCGATCA GCGTAGAAGG AAAAGAATGG AGCTGCAATT ACCTGACTCA CGAACAGCTT 2220  
 CGCTCTTCTG CATCCATTCA ATGGATGATG GACACGAAAC CCAATTATAA TCGTGGTATG 2280  
 AAGGAAAGTG ACAGACCTTA TTCTTCTCC ACGGAGCAAC AGCGTCGGCG TAATCACAAT 2340  
 AAT 2343

## (2) INFORMATION FOR SEQ ID NO:247

- 25 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 813 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 30 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS  
 40 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...813  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:247

45 ATGATGAAAT CCATGCGCAG CGTGCTGTTG CTACTCTTTC CATGTCTTT GATCACTGCT 60  
 TTGGGCTGTA GCAATAACAA AGCTGCCGAA TCGAAGTCTG TCTCTTTGTA TTCGGCCTAT 120  
 CTCGAACGCT ACATCCCTCT GCGGGCAGAC ATAGATACGC CATCGTGCA TGTGATGATC 180  
 AGCTACGTCT ATCCTTCGGG AGATGATATG CTCACAGAGA TTTTCAACGG TTGCTCTTC 240  
 GGGACAGCC TGATGGATTC CTCTTCGCGG GAGAATGCCA TGGAAGGCTA TGCACAGATG 300  
 50 CTGGGACAAG ACTATCGCTC TAACAATGCC GAAGCCAATC TGCAAGGGCT TCCTTCTGAC 360  
 CTTTGGGACT ATATCTACAA GCAGGAAAAT ACCATCGCTT ATTGCGATAC GGGATTGATC 420  
 TCCACGCGCA TCAATACATA TACTTACGAA GCGGGTGAC ATACGGAGAA TACAGTCCGG 480  
 TTTGCCAACA TCCTTCGCAC CACGGGCAAG GTGCTCGAAG AGCGAGATAT ATTCAAGATC 540  
 GACTATGCGG AAAGGCTGTC CGCACTCATC ATAGGACAAT TGGTGACGA TTTCGGCAAG 600  
 55 ACCACACCTG CCGAATTGGA TGCAATAGGT TTCTTCAACG CAGAAGAAAT ACAGCCCAAT 660  
 GGCAATTTTA TGATCGATGA CAAAGGTCTC ACATACTGTT TCAATGAGTA TCAGATAGCT 720  
 GCTTATGCCA GAGGTGCTGT CTATGTCCGT CTCGGATATG ACGTATTGGC TCCTTTGCTA 780  
 AGGGATGATT CCCCACTAAA GCGTTACTTG CCG 813

## (2) INFORMATION FOR SEQ ID NO:248

- 65 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 810 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 70 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 75 (vi) ORIGINAL SOURCE:

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(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...810

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248

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10 ATGAAATCCA TGCGCAGCGT GCTGTTGCTA CTCTTTCCAT TGCTTTGAT CACTGCTTTG      60
   GGCTGTAGCA ATAACAAAGC TGCCGAATCG AAGTCTGTCT CTTTGGATTC GGCCTATCTC      120
   GAACGCTACA TCCCTCTGCG GGCAGACATA GATACGCCAT CCGTGCATGT GATGATCAGC      180
   TACGTCTATC CTTGCGGAGA TGATATGCTC ACAGAGATT TCAACGGTTT GCTCTTCGCG      240
   GACAGCCTGA TGGATTCTCT TTCGCGGAG AATGCCATGG AAGGCTATGC ACAGATGCTG      300
   GGAGAAGACT ATCGCTCTAA CAATGCCGAA GCCAATCTGC AAGGGCTTCC TTCTGACCTT      360
15 TTGGACTATA TCTACAAGCA GGAATAATACC ATCGCTTATT GCGATACGGG ATTGATCTCC      420
   ACGCGCATCA ATACATATAC TTACGAAGGC GGTGCACATA CGGAGAATAC AGTCCGGTTT      480
   GCCAACATCC TTCGCACCAC CGGCAAGGTG CTCGAAGAGC GAGATATATT CAAGATCGAC      540
   TATGCGGAAA GGCTGTCCGC ACTCATCATA GGACAATTGG TGCACGATTT CGGCAAGACC      600
   ACACCTGCCG AATTGCATGC AATAGGTTTC TTCAACGCAG AAGAAATACA GCCCAATGGC      660
20 AATTTTATGA TCGATGACAA AGGTCTCACA TACTGTTTCA ATGAGTATCA GATAGCTGCT      720
   TATGCCAGAG GTGCTGTCTA TGTCCGTCTC GGATATGACG TATTGGCTCC TTGCTAAGG      780
   GATGATTCCC CACTAAAGCG TTACTTGCCG                                     810

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(2) INFORMATION FOR SEQ ID NO:249

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 801 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

30

(ii) MOLECULE TYPE: DNA (genomic)

35

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

40

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...801

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249

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50 ATGCGCAGCG TGCTGTTGCT ACTCTTTCCA TTGTCTTTGA TCACTGCTTT GGGCTGTAGC      60
   AATAACAAAG CTGCCGAATC GAAGTCTGTC TCTTTGATT CGGCCTATCT CGAACGCTAC      120
   ATCCCTCTGC GGGCAGACAT AGATACGCCA TCGCTGCATG TGATGATCAG CTACGTCTAT      180
   CTTTCGGGAG ATGATATGCT CACAGAGATT TTCAACGGTT TGCTCTTCGG CGACAGCCTG      240
   ATGGATTCTT CTTGCGCGGA GAATGCCATG GAAGGCTATG CACAGATGCT GGGAGAAGAC      300
   TATCGTCTTA ACAATGCCGA AGCCAATCTG CAAGGGCTTC CTTCTGACCT TTTGGACTAT      360
55 ATCTACAAGC AGGAAAATAC CATCGCTTAT TGCGATAACG GATTGATCTC CACGCGCATC      420
   AATACATATA CTTACGAAGG CGGTGCACAT ACGGAGAATA CAGTCCGTTT TGCCAACATC      480
   CTTGCGACCA CCGGCAAGGT GCTCGAAGAG CGAGATATAT TCAAGATCGA CTATGCGGAA      540
   AGGCTGTCCG CACTCATCAT AGGACAATTG GTGCACGATT TOGGCAAGAC CACACCTGCC      600
   GAATTGGATG CAATAGGTTT CTTCAACGCA GAAGAAATAC AGCCCAATGG CAATTTTATG      660
60 ATCGATGACA AAGGTCTCAC ATACTGTTTC AATGAGTATC AGATAGCTGC TTATGCCAGA      720
   GGTGCTGTCT ATGTCGGTCT CGGATATGAC GTATTGGCTC CTTTGCTAAG GGATGATTCC      780
   CCACTAAAGC GTTACTTGCC G                                     801

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(2) INFORMATION FOR SEQ ID NO:250

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 777 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

70

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

75

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250

ATGAAAAA	CTACTTTGAC	AGGATCGATA	TGTGCTTTAC	TCCTGTTTT	GGGTCTCTCG	60
GCCAAATGCC	AATCGAAGTT	AAAGATCAAG	AGCATTGAGG	CAGCTACCCAC	TTTCAGTTCTG	120
GCCACGGCCG	GAAATGGTTT	TGSGTGGCAAT	ATCTTCGGCA	TGGACATGAG	CATACGGATG	180
AGGGTACACC	ACAGCATTCT	GCCCGAAGGG	TTGGATTTT	CGGTAGGAAT	ACATGAAAGA	240
AGAGCACACT	GGGAAGAGGC	CGGAAGTCCG	AAGCTCATGT	ATACGAATGT	CCCAAGTATC	300
ATTGGTATTG	TTGAAAAGGT	AATAGTCTTC	GAAGACGCAG	AAGACTTTT	TGACAAAAA	360
GCTCTCGGCC	GCTTCCTCAT	CAGTTTGGGG	ATATCCTATA	CCAAGCATCT	GGGAGCGTAT	420
TGGGGATGGA	CCAATGACGC	CCATATTCTT	TTCTCACCGA	TACCCAGAG	CAAGGTCCAC	480
TATGACACCT	ACACAAGAGC	TGGCAGTGAC	CTTGTACTTC	AGTCCGAAGA	TGTTGCCACA	540
GTGAGCAATG	GCTTTTCACC	GGGGATCGGA	CTCAAAAGTT	CTATTGGGTG	GAAAATGCC	600
ATCAAGAGCA	AATATGATTT	TCGCCCTCGT	TTGAGCTGG	GCTATGAGTA	TCTGAACCTG	660
CTATATCCGT	ATCGTAATT	CAAGCTGGAT	GGAAATAAGC	CGCTTTCAGC	ACTATCTCCT	720
CGCATGAACC	ACATCGGCCA	TGTGGGCTTC	AACTTTACCG	TGGGTCTTTG	GACTAAT	777

(2) INFORMATION FOR SEQ ID NO:251

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3798 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...3798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251

ATGGGCAAGT	ATAAAGAGC	TAAGTACCGC	TATTGGCTTT	TTCTTTCTG	TTCCGATTAT	60
TATACCTTTG	AGGGAGTTAC	TTTTTTATGC	GCATCTGACG	ATATGACAAC	CAAGAAACCC	120
CAAGCCATTT	TAGACTTAGA	GAAGGCCTAT	AACATTGAAA	TTCTGATCT	CTCCTCACAA	180
GAAGGGATAA	GCTGGTCGGT	AAATAGATAT	TTCAAGCAAG	ATTCTCTCGG	TGCACTCGTT	240
GAGCTTTGCT	TGGGAGATG	TCAGATAGAA	AGCATGACTT	GGCTTATGA	TTTTCTTGCT	300
CTAAAAAGC	TTGATCTATC	GTATAACCAA	ATCAGTAAGC	TAGAGGGTCT	AGAAGCTCTT	360
ACTTCGTTAA	CAAAACTTCG	TCTAAGAACT	AACCAATCC	GTAAGCTAGA	GGGCTCGGAT	420
AGTCTCACCT	CGCTAACAAA	ACTTTCTCTC	TCCGATAACC	AAATCAGTAA	GCTAGAGGGT	480
CTGGAACGTC	TCACCTCGTT	AGCGGAGCTT	TATCTTTTGG	ATAACCAAT	CAGTAAACTA	540
GAGGGCTCTG	AACGTCTCAC	GTCTTAGCA	ACGCTTGAAC	TATCGGGTAA	CCAAATCOGT	600
AAGCTGGAGG	GTCTGGAACG	TCTCACGTCC	TTAGCAACGC	TTGAACATC	GGSTAACCAA	660
ATCCGTAAGC	TAGAGGGTCT	GGAACTCTC	ACTTCGTTAA	CRAAGCTTCG	TCTAAGAACT	720
AACCAATCA	GTAAGCTAGA	GGGTCTGGAA	CGTCTCACGT	CCTTAGCAAC	GCTTGAACCTA	780
TCGGGTAACC	AAATCCGTAA	GCTGGAGGGT	CTGGAACGTC	TCACGTCCTT	AGCAACGCTT	840
GAACCTGTCG	GTAACCAAT	CAGTAAGCTA	GAGGGTCTGG	AACGTCTCTC	TTCTGTTAACA	900
AAGCTTCGTC	TAAGAGTAA	CCAGATCAGT	AACTAGAGG	GCCTGGAACG	TCTCACCTCG	960
CTAACAAAAC	TTTCTCTCTC	CGATAACCAA	ATCAGTAAGC	TAGAGGGTCT	GGAACTCTCTC	1020
ACCTCGTTAG	CGGAGCTTTA	TCTTTTGGAT	AACCAATCC	GTAAGCTGGA	GGGCTGGAA	1080
CGTCTCACCT	CGTTAACAAA	GCTTCGTCTA	AGAAGTAACC	AAATCAGTAA	ACTAGAGGGC	1140
CTGATAGTCT	TCACCTCGCT	AACAAAACCT	TCTCTCTCG	ATAACCAAT	CAGTAAACTA	1200
GAGGGCTG	AACGTCTCAC	GTCTTAGCG	GAGCTTTATC	TTTTGGATAA	CCAAATCCGT	1260
AAGCTGGAGG	GTCTTGATGG	TCTTGCTTCC	TTAACAAGGC	TTAGTCTAAG	GGGCAACCAA	1320
ATCAGTAAGC	TGGAAGGACT	AGACAGACTA	AAGGTTTTGA	GAAAACCTGA	TGTTTCGGGC	1380
AATGATATTC	AATCTATTGA	TGATATTAA	CTATTGGCTC	CGATTCTGGA	GCAAACTTTA	1440
GAAAACTGA	GAATCCATGA	CAATCCATT	GTTCATCAT	CAGGCTTGAT	ACTCTCTCCT	1500
TATGATAATC	ATTGCGCGGA	GATTAAAGCT	CTTCTTGAAA	AAGAAAAAGA	AAAACAGAAA	1560



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	AAGACTTCAG	TTGAATATCA	CCCATTTTGC	AAAGTAATGC	TATTGGGAAA	TCATTCTTCG	1620
	GGTAAACAA	CATTTCTTAG	TCAATACGAT	ACAAATTATA	CGTATCAGAA	AAATACACAT	1680
	GTGTGTGCGA	TACATCGAAG	CAATAACCCT	AATGCCATCT	TTTACGACTT	TGGGGGACAG	1740
5	GACTATTATC	ATGGGATTTA	CCAAGCCTTT	TTTACCACCC	AATCGTTATA	CCTTCTCTTT	1800
	TGGGATGCTA	AGAAAGGATCG	AAACTTTGTG	AGCGTAGATG	ATAAAGAATA	TCAGACTCTT	1860
	AATTTCATC	GCCCTTATTG	GTTAGGACAG	ATAGCCTATG	CCTGCAATCG	TTGTATGTCC	1920
	GTTGGAGGAA	ATCCTGATGG	CAAGGACACA	CCACAGACCA	CAGACGATAC	AATTATCATT	1980
	CAGACTCATG	CCGATGAAAC	GGGCGCTAAG	CAGCAATCCT	TAGGCTGTGC	AGCCGAGAAT	2040
	GGAGTATTGG	AAGAAATCTA	TGTATCCTTA	GAGCCCAAGG	CGAATAGTGC	CGTACATGCG	2100
10	CTCAACTATC	TGAATGAGCG	GGTGCGAGAA	GTTGTGCGAA	GCAGGAGTAA	ATCAATTTCAG	2160
	ATCACAGAAA	AAGATAAGGG	ATTGTACGAA	GCTCTTCCCA	CAATCGCCCG	TGATAATAAA	2220
	CACATCCCTA	TCTCTCTCGA	AGCTCTTGCG	GCTCAATTGA	ATAAGGGAAG	AGCTGAAAT	2280
	GATCTTTACA	CCATAGAGTA	TCTACAGACC	GAATTGAACC	AGCTTAGTCT	GCGAGGGGAG	2340
	GTGCTTACT	ATCGTGAGAA	TGAGAAGCTG	AACAATTATG	TCTGGTTAGA	TCCGGCAGCT	2400
15	TTTGCCAAA	TGATTTCATG	AGAAATCCTC	CAAAAAGACA	ACATCAATAG	AGGAACAGTT	2460
	CCTAAGNCA	TTTTTGAATG	CAAACTGCAT	AATCTAAGTT	CCGGAAGTAT	ATTTGAAGAA	2520
	CATGCGGAAA	ATGGTAATAT	GATCTTGCAAG	CTATTATTGG	AAGAGCTGAT	CGTATATGAA	2580
	GATAAGGACT	GCTATGTGAT	ACCGGGCTAT	CTCCCTTTCG	ATTCCGATGA	CGAAGCCTAT	2640
	AAATGGCTTA	CTTTGGGATT	CGAGAGGCC	AATTTTGTCC	TCAAATTCGA	ACGTTTTATC	2700
20	CCCTTTGGCC	TGATCAACCA	GATTATAGCC	TACTATGGCC	GGGAAGAAGG	TGCTCTAAAG	2760
	CGGTATTGGC	GAGATCAGGT	CATCTTCACA	GCAGGCCGTG	AGATGGATAG	GCAACCGCTT	2820
	GAGCAAGAAA	AAGAGAAAGA	GGGTTTGCCC	AAGACGAATG	CCGAGGATTA	TCAGATCTGG	2880
	ATCAAGCTCG	ACTTTACCGA	CTTGCCATA	TCCGTATTCA	TCAAAGAGCA	GAGAAAGACA	2940
	TCAGCTAAGG	ATATGCAGCG	GAAAGAGGCT	ACTATCCTCA	GTGATATGTT	GGATATGTAT	3000
25	TGGAACAATA	TCCCTCCGAG	GGAGCAAATA	GGAGATAAGG	ATACGGAGCA	AACGAGAAGC	3060
	ACTATTCGTG	AAACAAACAG	AAAGAAGAGA	CCCATCCAGG	ATCTCTACCT	CTCCTGTGCC	3120
	CAAGCGGATA	AAGATTTGAC	GGAGTCTCAT	TATATCCATT	TGGGCACGCT	GGACGATGAA	3180
	AGCAAGACTA	CGGCGAGGAT	TGCAGCCTAT	CCGTTGAAGA	ACGGCGTTAT	CGATAAAGAG	3240
	CGGGTCCGAG	AAGTATCGAC	TGCTCCCTAC	AAACATCTTT	CCGTCAATAA	AAATCTGGCT	3300
30	ACTGCAAAAC	AGATCTTTAT	TTCTATTCC	AAAGAGGATC	AGACTGAACT	GGAGACCTGT	3360
	CTGCAATTTT	TCAAACCCCT	GGAGAAGAA	GGTCAGATCG	AGATCTACTA	TGATAAGTTG	3420
	ACTAAGTTTG	AAACACCTAT	TCACCCGTGA	ATAAGAAAGC	GTATTGTGCA	AGCCGACTGT	3480
	ATAATCGCTT	TGATCAGCCA	ACGCTATCTG	GCCACGGATT	ACATCCTGGA	TCATGAGTTG	3540
	CCTGTATTTC	GGGAGTATTA	CAAGACCATA	GTGCCGATAT	TGATCAAGCC	TTGTACATTC	3600
35	GAGACGATG	AGTTCCCTCG	GGAGAAATAT	TTTGCTCAGA	AAGCTCAAT	AATCAATCTT	3660
	GGAAAAGAGG	GAAAAACCAT	TAAAGCTTAT	GATAGTATTA	CGGCATCAGC	CCATCGTGAT	3720
	GAAAATTGGG	TGGCAGTAGT	CAGAGAGTTC	AAAGAGAAGA	TATTAAGNAT	AACAAAACAG	3780
	GAGGTAAATA	CAGATGAA					3798
40	(2) INFORMATION FOR SEQ ID NO:252						
	(i) SEQUENCE CHARACTERISTICS:						
	(A) LENGTH: 3696 base pairs						
45	(B) TYPE: nucleic acid						
	(C) STRANDEDNESS: double						
	(D) TOPOLOGY: circular						
	(ii) MOLECULE TYPE: DNA (genomic)						
50	(iii) HYPOTHETICAL: NO						
	(iv) ANTI-SENSE: NO						
55	(vi) ORIGINAL SOURCE:						
	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS						
	(ix) FEATURE:						
60	(A) NAME/KEY: misc feature						
	(B) LOCATION: 1...3696						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252						
65	ATGACAAACCA	AGAAACCCCA	AGCCATTTTA	GACTTAGAGA	AGGCCTATAA	CATTGAAATT	60
	CCTGATCTCT	CCTCACAAGA	AGGGATAAGC	TGGTCGGTAA	ATAGATATTT	CAAGCAAGAT	120
	TCTCCGGTG	CAGTCGTTGA	GCTTTGCTTG	CGAGAATGTC	AGATAGAAAG	CATGACTTGG	180
	CTTATTGATT	TTCTGCTCT	AAAAAAGCTT	GATCTATCGT	ATAACCAAT	CAGTAAGCTA	240
	GAGGGTCTAG	AACGTCTTAC	TTGTTAACA	AACTTCGTC	TAAGAAGTAA	CCAAATCCGT	300
70	AACTAGAGG	GCCTGGATAG	TCTCACTCG	CTAACAAAC	TTTCTCTCTC	CGATAACCAA	360
	ATCAGTAAGC	TAGAGGGTCT	GGAACGTCTC	ACCTCGTTAG	CGGAGCTTTA	TCTTTTGGAT	420
	AACCAATCA	GTAACCTAGA	GGGTCTGGAA	CGTCTCACGT	CCTTAGCAAC	GCTTGAACCTA	480
	TGGGTAAACC	AAATCCGTAA	GCTGGAGGGT	CTGGAACGTC	TCACGTCCTT	AGCAACGCTT	540
	GAACTATCGG	GTAACCAAT	CCGTAAGCTA	GAGGGTCTGG	AACGTCTCNC	TTGTTAACA	600
75	AAGCTTCGTC	TAAGAAGTAA	CCAAATCAGT	AAGCTAGAGG	GTCTGGAACG	TCTCACGTCC	660
	TTAGCAACGC	TTGAACATC	GGGTAACCAA	ATCCGTAAGC	TGGAGGGTCT	GGAACGTCTC	720

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5 ACGTCCTTAG CAACGCTTGA ACTGTCGGGT AACCAAATCA GTAAGCTAGA GGGTCTGGAA 780  
 CGTCTCTCTT CGTTAACAAA GCTTCGTCTA AGAAGTAACC AGATCAGTAA ACTAGAGGGC 840  
 CTGGAACGTC TCACCTCGCT AACAAAACCT TCTCTCTCCG ATAACCAAAT CAGTAAGCTA 900  
 GAGGCTGCGG AACGCTCTCAC CTCGTTAGCG GAGCTTTATC TTTTGGATAA CCAAAATCCGT 960  
 AAGCTGGAGG GCCTGGAACG TCTCACCTCG TTAACAAAGC TTCGCTAAG AAGTAACCAA 1020  
 ATCAGTAAC TAGAGGGCCT GGATAGTCTC ACCTCGCTAA CAAAACCTTC TCTCTCCGAT 1080  
 AACCAAATCA GTAAACTAGA GGGCCTGGAA CGTCTCAGT CCTTAGCGGA GCTTTATCTT 1140  
 TTGGATAACC AAATCCGTAA GCTGGAGGGT CTTGATGGTC TTGCTTCCTT AACAAAGGCTT 1200  
 10 AGTCTAAGGC GCAACCAAAT CAGTAAGCTG GAAGGACTAG ACAGACTAAA GGTTTTGAGA 1260  
 AACTTTGATG TTTGCGGCAA TGATATTCAA TCTATTGATG ATATTAAGCT ATTGGCTCCG 1320  
 ATTCGAGGC AAACCTTAGA AAAACGAGA ATCCATGACA ATCCATTTGT TGCAATCATCA 1380  
 GGCTTGATAC TCTCTCCTTA TGATAATCAT TTGCCGAGGA TTAAGCTCT TCTTGAAAAA 1440  
 GAAAAAGAAA AACAGAAAAA GACTTCAGTT GAATATCACC CATTTTGCAA AGTAATGCTA 1500  
 15 TTGGGAAATC ATTCTTGGGG TAAAACAACA TTCTTAGTC AATACGATAC AAATATATAG 1560  
 TATCAGAAAAT ATACACATGT GTTGTCGATA CATCGAAGCA ATAACCTTAA TGCGATCTTT 1620  
 TACGACTTTG GGGGACAGGA CTATTATCAT GGGATTATCC AAGCCTTTT TACCACCCAA 1680  
 TCGTTATACC TTCTCTTTG GGATGCTAAG AAGGATCGAA ACTTTGTGAG CGTAGATGAT 1740  
 AAGAATATC AGACTCTTAA TTCAATCGC CCTATTGGT TAGGACAGAT AGCCTATGCC 1800  
 20 TGCAATCGTT GTATGTCCTG TGGAGGAAAT CCTGATGGCA AGGACACACC ACAGACCACA 1860  
 GACGATACAA TTATCATTC GACTCATGCC GATGAAACGG GCGCTAAGCA GCAAACTTAA 1920  
 GGCTGTGCAG CCGAGAAATG AGTATTGGA GAAATCTATG TATCCTTACA GCCCAAGGCG 1980  
 AATAGTGCCG TACATGCGCT CAACATCTG AATGAGCGGG TCGGAGAAGT TGTCGCAAGC 2040  
 AGGAGTAAT CAATTGAGT CACAGAAAAA GATAAGGGAT TGTACGAAGC TCTTCCACA 2100  
 25 ATCGCCGGTG ATAATAACA CATCCCTATC TCTCTCGAAG CTCTTGGCGC TCAATTGAAT 2160  
 AAGGGAAGAG CTGAAATGA TCTTTACACC ATAGAGTATC TACAGACCGA ATTGAACAG 2220  
 CTTAGTCTGC GAGGGGAGGT GCTTTACTAT CGTGAGATG AGAAGCTGA CAATTATGTC 2280  
 TGCTTAGATC CGGCAGCTTT TGTCCAAATG ATTCATGGAG AAATCCTCCA AAAAGACAC 2340  
 ATCAATAGAG GAACAGTTC TAAAGACATT TTTGAATGCA AACTGCATA TCTAAGTTCC 2400  
 GGAAGTATAT TTGAAGAAGA TGGCCAAAT GGTAAATATGA TCTTGAGCT ATTATTGGAA 2460  
 30 GAGCTGATCG TATATGAAGA TAAGGACTGC TATGTGATAC CGGGCTATCT CCCTTTGCAT 2520  
 TCCGATGACG AAGCCTATAA ATGGCTTACT TTGGGATTG AGAGGCCCAA TTTTGTCTC 2580  
 AAATTCGAAC GTTTTATCCC CTTTGGCCTG ATCAACCAGA TTATAGCCTA CTATGGCCGG 2640  
 GAAGAGGGTG CTCTAAAGCG GTATTGGCGA GATCAGGTCA TCTTCACAGC AGGCCGTGAG 2700  
 35 ATGGATAGGC AAACGCTTGA GCAAGAGAA GAGAAAGAGG GTTTGCCCAA GACCAATGCC 2760  
 GAGGATTATC AGATCTGGAT CAAGCTCGAC TTTACCGACT TGGCCATATC CGTATTATC 2820  
 AAGAGCAGA GAAAGACATC AGCTAAGSAT ATGCAGCGGA AAGAGGCTAC TATCCTCAGT 2880  
 GATATGTTGG ATATGATTG GAACAATATC CCTCCGAGG AGCAAAATAGG AGATAAGGAT 2940  
 ACGGAGCAAA CGAGAAGCAC TATTCGTGAA ACAACAGAA AGAAGAGACC CATCCAGGAT 3000  
 40 CTCTACCTCT CCTGTGCCCA AGCGGATAAA GATTGACGG AGTCTCATT TATCCATTG 3060  
 GGCAGCTGG ACGATGAAAG CAAGACTACG GCGAGGATTG CAGCCTATCC GTTGAAGAAC 3120  
 GGCGTTATCG ATAAAGAGCG GGTGCGAGAA GTATCGACTC GTCCCTACAA ACATCTTCC 3180  
 GTCAATAAAA ATCTGGCTAC TGCAAAACAG ATCTTTATTT CCTATTCCAA AGAGGATCAG 3240  
 ACTGAACCTG AGACCTGTCT GCAATTTTTC AAACCTTGG AGAAGATGG TCAGATCGAG 3300  
 45 ATCTACTATG ATAAGTTGAC TAAGTTTGAA ACACCTATTC ACCCTGAAAT AAGAAAGCGT 3360  
 ATTGTGGAAG CCGACTGTAT AATCGCTTGG ATCAGCCAAC GCTATCTGGC CACGGATTAC 3420  
 ATCTGGATC ATGAGTTGCC TGTATTTOGG GAGTATAACA AGACCATAGT GCCGATATTG 3480  
 ATCAAGCCTT GTACATTGCA AGACGATGAG TTCCTTCGGG AGAAATATTT TGCTCAGAAA 3540  
 GCTCAATAAA TCAATCTTGG AAAAGAGGGA AAAACCATTA AAGCTTATGA TAGTATTAGC 3600  
 50 GCATCAGCCC ATCGTATGA AAATTGGGTG GCAGTAGTCA GAGAGTTCAA AGAGAAGATA 3660  
 TTAAGAATAA CAAACAGGA GGTAAATACA GATCAA 3696

## (2) INFORMATION FOR SEQ ID NO:253

- 55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3525 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRAIDEDNESS: double  
 (D) TOPOLOGY: circular  
 60 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 65 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 70 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...3525  
 75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:253

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	ATGACTTGGC	TTATTGATT	TCCTGCTCTA	AAAAAGCTTG	ATCTATCGTA	TAACCAAAATC	60
	AGTAAGCTAG	AGGGTCTAGA	ACGTCTTACT	TCGTTAACAA	AACCTCGTCT	AAGAAGTAAC	120
	CAAAATCCGTA	AAC TAGAGGG	CCTGGATAGT	CTCACCTCGC	TAACAAAAC	TTCTCTCTCC	180
	GATAACCAAA	TCAGTAAGCT	AGAGGGTCTG	GAACGTCTCA	CCTCGTTAGC	GGAGCTTTAT	240
5	CTTTTGGATA	ACC/AAATCAG	TAAACTAGAG	GGTCTGGAAC	GTCTCACGTC	CTTAGCAACG	300
	CTTGAACAT	CGGGTAACCA	AATCCGTAA	CTGGAGGGTC	TGGAACGCT	CACGTCTCTA	360
	GCAACGCTTG	AACTATCGGG	TAACCAAAATC	CGTAAGCTAG	AGGGTCTGGA	ACCTCTCACT	420
	TCGTTAACAA	AGCTTCGTCT	AAGAAAGTAAC	CAAAATCAGTA	AGCTAGAGGG	TCTGGAACGT	480
	CTCACGTCTCT	TAGCAACGCT	TGAACATACG	GGTAACCAAA	TCCGTAAGCT	GGAGGGTCTG	540
10	GAACGTCTCA	CGTCTTAGC	AACGCTTGAA	CTGTCGGGTA	ACCAATCAG	TAAGCTAGAG	600
	GGTCTGGAAC	GTCTCTCTTC	GTTAACAAAG	CTTCGTCTAA	GAAGTAACCA	GATCAGTAAA	660
	CTAGAGGGCC	TGGAACGCT	CACCTCGCTA	ACAAAACCTT	CTCTCTCCGA	TAACCAAAATC	720
	AGTAAGCTAG	AGGGTCTGCA	ACGTCTCAC	TCGTTAGCGG	AGCTTTATCT	TTTGGATAAC	780
	CAAAATCCGTA	AGCTGGAGGG	CCTGGAACGT	CTCACCTCGT	TAACAAAGCT	TCGTCTAAGA	840
15	AGTAACCAAA	TCAGTAAACT	AGAGGGCCTG	GATAGTCTCA	CCTCGCTAAC	AAAACCTTCT	900
	CTCTCCGAT	ACCAATCAG	TAAACTAGAG	GGCCTGGAAC	GTCTCACGTC	CTTAGCGGAG	960
	CTTTATCTTT	TGGATAACCA	AATCCGTAA	CTGGAGGGTC	TTGATGGTCT	TGCTTCCTTA	1020
	ACAAGGCTTA	GTCTAAGCG	CAACCAAAATC	AGTAAGCTTG	AAGGACTAGA	CAGACTAAAG	1080
	GTCTTGAAG	AACTTGATGT	TTGGGCAAT	GATATTCAAT	CTATTGATGA	TATTAAGCTA	1140
20	TTGGCTCCGA	TTCTGGAGCA	AACCTTAGAA	AACTGAGAA	TCCATGACAA	TCCATTGTGT	1200
	GCATCATCAG	CCTTGATCT	CTCTCTTAT	GATAATCATT	TGCGGAGAT	TAAAGCTCTT	1260
	CTTGAAAGAG	AAAAAGAAA	ACAGAAAAAG	ACTTCAGTTG	AATATCACCC	ATTTTGCAAA	1320
	GTAAATGCTAT	TGGGAATCA	TTCTTCGGGT	AAAAACAAT	TTCTTAGTCA	ATACGATACA	1380
	AAATATACGT	ATCAGAAAA	TACACATGTG	TTGTCGATAC	ATCGAAGCAA	TAACCTTAAT	1440
25	GCGATCTTT	ACGACTTTGG	GGGACAGGAC	TATTATCATG	GGATTACCA	AGCCTTTTTT	1500
	ACCACCCAAT	CGTTATACCT	TCTCTTTGG	GATGCTAAGA	AGGATCGAAA	CTTTGTGAGC	1560
	GTAGATGATA	AAGAATATCA	GACTCTTAAT	TTCAATCGCC	CCTATTGGTT	AGGACAGATA	1620
	GCCTATGCCT	GCAATCGTTG	TATGTCCGTT	GGAGGAAATC	CTGATGGCAA	GGACACACCA	1680
	CAGACCCAG	ACGATACAA	TATCATTGAG	ACTCATGCCG	ATGAAACGGG	CGCTAAGCAG	1740
30	CAAACTTAG	GCTGTGCAGC	CGAGAATGGA	GTATTGGAAG	AAATCTATGT	ATCCTTAGAG	1800
	CCCAAGGCGA	ATAGTGCCGT	ACATGCGCTC	AACTATCTGA	ATGAGCGGGT	CGGAGAAGTT	1860
	GTCCGAAGCA	GGAGTAAATC	AATTCAGATC	ACAGAAAAAG	ATAAGGGATT	GTACGAAGCT	1920
	CTTCCCAAA	TCCCGCGTGA	TAATAAACAC	ATCCCTATCT	CTCTCGAAGC	TCTTGGCGGT	1980
	CAATTGAATA	AGGGAAGAGC	TGAAAATGAT	CTTTACACCA	TAGAGTATCT	ACAGACCGAA	2040
35	TTGAACACCG	TTAGTCTGCG	AGGGGAGGTG	CTTTACTATC	GTGAGAATGA	GAAGCTGAAC	2100
	AATTATGCT	GGTTAGATCC	GGCAGCTTTT	GTCCAAATGA	TTCATGGAGA	AATCCTCCAA	2160
	AAAGACAACA	TCAATAGAGG	AACAGTTCCT	AAAGACATTT	TTGAATGCAA	ACTGCATAAT	2220
	CTAAGTTCGG	GAAGTATATT	TGAAGAAGAT	GGCCAAAATG	GTAATATGAT	CTTGCAAGTA	2280
	TTATTGGAAG	AGCTGATCGT	ATATGAAGAT	AAGGACTGCT	ATGTGATACC	GGGCTATCTC	2340
40	CTTTTGCAAT	CCGATGACGA	AGCCTATAAA	TGGCTTACTT	TGGGATTCGA	GAGGCCCAAT	2400
	TTTGTCTCT	CAATCGAACG	TTTTATCCCT	TTTGGCCTGA	TCAACCAGAT	TATAGCCTAC	2460
	TATGGCCGGG	AAGAAGGTGC	TCTAAAGCGG	TATTGGCGAG	ATCAGGTCAT	CTTCACAGCA	2520
	GGCGGTGAGA	TGGATAGGCA	AACGCTTGAC	CAAGAAGAAG	AGAAAGAGGG	TTTGCCCAAG	2580
45	ACGAATGCCG	AGGATTATCA	GATCTGGATC	AAAGCTCGACT	TTACCGACTT	GGCCATATCC	2640
	GTATTTCATCA	AAGAGCAGAG	AAAGACATCA	GCTAAGGATA	TGCAGCGGAA	AGAGGGCTACT	2700
	ATCCTCAGTG	ATATGTTGGA	TATGTATTTG	AACAATATCC	CTCCGAGGGA	GCAAAATAGGA	2760
	GATAAGGATA	CGGAGCAAA	GAGAAGCACT	ATTCGTGAAA	CAAAACAGAA	GAAGAGACCC	2820
	ATCCAGGATC	TCTACCTCTC	CTGTGCCCAA	GCGATAAAG	ATTTGACGGA	GTCTCATTAT	2880
50	ATCCATTGCG	GCACGCTTGA	CGATGAAAGC	AAGACTACGG	CGAGGATTGC	AGCCTATCCG	2940
	TTGAAAGACG	CGGTTATGGA	TAAAGAGCGG	GTGCGAGAAG	TATCGACTCG	TCCCTACAAA	3000
	CATCTTTCCG	TCAATAAAAA	TCTGGCTACT	GCAAAACAGA	TCTTTATTTC	CTATTCCAAA	3060
	GAGGATCAGA	CTGAACCTGA	GACCTGTCTG	CAATTTTTC	AACCTTTGGA	GAAGAATGGT	3120
	CAGATCGAGA	TCTACTATGA	TAAGTTGACT	AAGTTTGA	CACCTATTCA	CCCTGAAATA	3180
	AGAAGCGGTA	TTGTCGAAGC	CGACTGTATA	ATCGCTTTGA	TCAGCCAAAG	CTATCTGGCC	3240
55	ACGGATTACA	TCCGGAATCA	TGAGTTGCCT	GTATTTCCGG	AGTATAACAA	GACCATAGTG	3300
	CGGATATTGA	TCAAGCCTTG	TACATTGGA	GACGATGAGT	TCCTTCGGGA	GAAATATTTT	3360
	GCTCAGAAAG	CTCAAAATAT	CAATCTTGA	AAAGAGGGAA	AAACCATTAA	AGCTTATGAT	3420
	AGTATTACGG	CATCAGCCCA	TCGTGATGAA	AATTGGGTGG	CAGTAGTCAG	AGAGTTCAAA	3480
60	GAGAAGATAT	TAAGAATAAC	AAAACAGGAG	GTAATACAG	ATGAA		3525

(2) INFORMATION FOR SEQ ID NO:254

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 687 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (11) MOLECULE TYPE: DNA (genomic)
- (111) HYPOTHETICAL: NO
- (117) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

5 (ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254

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10 ATGATGAAAA AAGCATTGTG TTTCTACTA CTGGTTTGCC TATTCTCCTC GTTCAGCAGT      60
   TCCGCCCAAA CAACGACGAA CAGTAGCCGG AGTTATTTTA CAGGACGAAT CGAGAAGGTG      120
   AGTTTGAAC TAGGGGTCCC CCCGTAAGC ACAGAGGTTT GGGGAATGAC CCATGATGCG      180
   AACGGTCTCC CTTTCGAAAT ACCTATCTCT TTCAGTCGTT TCAACAGCCA GGGAGATATA      240
15 GCTACCACTT ATTACATAGC GAATAGCGAG GCAACTTTGA ATGAATGGTG CGACTATGCA      300
   CACCCGGSCG GCATCGTGAG GGTAGAAGGT CGTTTTTGGG AAATGACTTA CAACATACCA      360
   ACCTACAATG CAGTCTGCAC CCGGATTACA TTCGAAAATC AAGAAATAGA AGGAACGATC      420
   GTCTTGATAC CCAAGCCCAA AGTCTCGCTG CCTCATGTGT CGGAATCGGT GCCTTGCAIC      480
   CGAACCGAAG CCGGGAGGGA ATTTATCCTT TCGGAAGAAG ACGACACCTT TGTGTCTCAC      540
20 GATGGTAACG AAGTAACGAT AGGCGGTAAA CCTTCTCTGC TCAATACCAA CGTAAAGATT      600
   GTGGGGGACG TATCTCAAAA GTATGCCGTG GGGGTAGGAG AAATTCGATT CCTGCAGATT      660
   TGTGCCCAAA CAGTATCACA ACAAAAAA                                     687

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(2) INFORMATION FOR SEQ ID NO:255

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 684 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

35 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

40 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...684

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:255

```

ATGAAAAAAG CATTGTITT CGTACTACTG GTTTGCCTAT TCTCCTCGTT CAGCAGTTCC      60
GCCCAAAACA CGACGAACAG TAGCCGGAGT TATTTTACAG GACGAATCGA GAAGGTGAGT      120
TTGAACCTAG GGGTCCCCCC CGTAAGCACA GAGGTTTGGG GAATGACCCA TGATGCGAAC      180
GGTCTCCCTT TCGAAATACC TATCTCTTTC AGTCGTTTCA ACAGCCAGGG AGATATAGCT      240
ACCACTTATT ACATAGCGAA TAGCGAGGCA ACTTTGAATG AATGGTGCGA CTATGCACAC      300
CCGGGCGGCA TCGTAGGGGT AGAAGGTCGT TTTTGAAAAA TGACTTACAA CATACCAACC      360
TACAATGCAG TCTGCACCCG GATTACATTC GAAAATCAAG AAATAGAAGG AACGATCGTC      420
55 TTGATACCCA AGCCCAAAGT CTCGCTGCC TATGTGTGCG AATCGGTGCC TTGCATCCGA      480
ACCGAAGCCG GGAGGGAATT TATCCTTTGC GAAGAAGACG ACACCTTTGT GTCTCAGCAT      540
GGTAACGAAG TAACGATAGG CGGTAACCTT TTCTTGCTCA ATACCAACGT AAAGATTGTG      600
GGGGACGTAT CTCAAAAGTA TGCGTGGGG GTAGGAGAAA TTCGATTCTT GCAGATTGTG      660
GCCCAAACAG TATCACAACA AAAA                                     684

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60 (2) INFORMATION FOR SEQ ID NO:256

65 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1620 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

70 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

75 (vi) ORIGINAL SOURCE:

SUBSTITUTE SHEET (Rule 26) (RO/AU)

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256

10 ATGAAGACAA AAGTTTACG CAAATTCGTG GTGGCGGCTT TCGCCGTCCG AACCTCTGT 60  
CCTCTCGCCC AAGCGCAGAC GATGGGAGGA GATGATGTCA AGGTGGTCCA GTACAATCAG 120  
GAAAAACTGG TACAAACCAG GATGAGTGTG GCGGACAACG GATGGATCTA TGTAAATGACC 180  
CACAGTGGAT ACGACACCGG CAATAGCAAT GTGAAGATCT TCCGCTCCAA AGACCAAGGT 240  
GCCACATACC AAAAGTTGAG GGATTGGGAT CCATCGGATG ATTATCAGTT TCAAGACTTC 300  
GATATCGTGG TAACGGGTAA GAATGAATCC GACATCAAGA TTTGGTGGGT AGAGCTCATG 360  
15 AATAAGCCCG GAGGATATAA GAGTAGAGTT GCGGTCTTCA GTCGCGATGC CAACGCGCAG 420  
AATCGGAAC TCGTGATATA GGAAGACTTC TCCAAATGTGC AGTTGTACGA TGTGGATATA 480  
GCCTCCAAT ATCGTTCCGC TTCTTCTCTT AACAAATGGTG GCAACCCCTT TGCCTTGGCT 540  
TTCGCTTACA CCGGCTTCAA CAATACGCAC AAAATAAGTT TTGTGGACTA TGTGTTCTCT 600  
CTGAATGGAG GGCAAAATTT CAATAAAAC TTACTCTTCA GTCAAGATGG AGAGAAGAAA 660  
20 ATTGACAAGG TGGATCTCTC ATTGGGTAGC ACCTCTGAAT CCATGGGTCA CAATGCCTGG 720  
CCGCTAATGG GTGTGGTATT CGAAATGAAT AAACAAGGGG GAAAAAGCGA TATCGGTTTC 780  
TTGTGGAAT TTGTGCAAA TGATCCCGAA TTTCAGTGGT CAGGCCCTAT AAAAGTGAGT 840  
GAAAGCGACA TCTCGTTTCA CCCCATAATC CAAATGTTGC TGGACGAGGA TAACAAATACG 900  
ATCAATGGGG AGAGTTGCCA CAATTCATG ATTACGTACA GCGATTATGA TTCTGAATAT 960  
25 TCGGATTGGG ACATTCCGTA TGTATATCCC AAGAAATCGT TCAAGTATGA AAAAGGAAAA 1020  
ACTCCGACTA TGGGTATGCT GGTGGAAGCT TTCCTTACAG CTTCGTACCA GAGTGAGACC 1080  
AATCGGSGC TGGGTATGA CAAGAAGGCC AATCACTACC TGATTACATA TGCCAAAAAA 1140  
GAAGAGAACG GTACGAACAC GCTGAAATAC CGCTGGGCCA ATTATGACAA GATTCTAATC 1200  
30 AAAGATTGTG GGAAGCAGAC ATTTACGTAT ACATCATCTG CCAATGCTCT CTACACACCT 1260  
CAAGTAGACA TCAATCCGAC CAAGGGTCTC GTGTGCTGGT CATGGGTGGA ATATCTGCCG 1320  
GGCAAAACGA TCGTTTGGTC TGATACGCGG TGGACCCATG CCAACGGTGT AGAAGACATC 1380  
GTAATGCAAG AAGGCAGCAT GAAGCTCTAC CCGAATCCGG CTCAGGAATA TGCTGTGATT 1440  
AGCTGCGCGA CCGCAGCAAA CTGCAAGGCT GTTGTGTTAG ATATGCAAGG CAGAGTAGTC 1500  
35 GCTGAGGCTT CTTTCTCCGG CAACGAATAC AGGCTGAACG TGCAAGCACT GGCTAAGGGT 1560  
ACGTACATAC TCAAGGTCGT ATCCGATACG GAGCGTTTCG TAGAGAAGCT CATCGTGGA 1620

(2) INFORMATION FOR SEQ ID NO:257

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2313 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular  
45 (ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
50 (iv) ANTI-SENSE: NO  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
55 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...2313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257

60 ATGCTGACGA TCCGAACTT CCTCCTCTTT TGTGTCTGT CGCTGATAGC GTTGTCTGCC 60  
GATGCACAAA GCTCTGTCTC TTCGGGTAGA CGACTGACAG AATATGTCAA TCCCTTTATC 120  
GGAACGGCCA ATTACGGTAC CACGAATCCG GAGCAGTAT TGCCCAATGG GTTGATGAGC 180  
65 GTTACCCCTT TCAATGTGAG CGGATCGACA GAGAATCGCT TCGACAAAGA TTCGCGTTGG 240  
TGGAGTGGCG CTATTTCGGC CGACAATAGT TACTGCAATG GTTTCAGCCA TGTGAATCTG 300  
AGTGGAGTAG CCGTCCCGA ACTGAGTGGG ATACTGCTGA TGGCCACTTC CGGCACATTC 360  
GATCCTGATT ACTGCTGCTA TGGCTCTTCG CTCAGTCCAG AATATGCGCG CCGGGGAGAA 420  
TACAAAGGCTG TATTGGACAA ATACGGTATA GATGCAGCCG TGACCGTAAC CGAGCGGACT 480  
70 GCTTTGACCG AATTGCTTT TCCGGAAGGA GAAGGCCATA TCGTGTGAA CCGGGGACAG 540  
GCCCTAAGCA ATGAATCGGG AGCCTCTGTT CGATTCTTAA ACGACTCCAC AGTCGTGGC 600  
AGCAGGCTGA TGGGACGTT CTGCTACAAT CCGCAAGCAG TTTTTCGTCA GTATTTCGTA 660  
CTTCAGGTGA GTCGGCGACC GATCTCTGCC GGCTATTGGA AGAAGCAGCC TCTATGACA 720  
GTGGAAGCCC AATGGGATTC GACTGCAGGG AATATAAGC AGTACGACGG CTACAAGCGT 780  
GAGATGACCG GTGATGACAT CGGTGTCGGA TTCTGTTCA ACTGCGATCA GGGGGAAAAG 840  
75 ATCTATGTAC SATCGGCCGT TTCATTCTGC AGCGAAGCCA ATGCGCTCTA TAATCTGGAA 900

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5 GCGGAGCAAG AAGAGGTGTT CAAAAGTGTC GGAGGGAATC CGGCCAAGCC TTTCTCCGCT 960  
 ATACGCTCTC GCGCTATAGA GCGTTGGGAG GAAGCCCTCG GTACGGTGGA AGTGAAGGA 1020  
 GGCACACCGG ATGAAAAGAC GATATTCTAT ACCGCACTCT ATCACCTGCT GATACATCCG 1080  
 AATATCTTAC AAGATGCCAA TGGAGAATAT CCTATGATGG GCAGTGGCAA AACGGGTAAT 1140  
 ACGGCTCACC ACCGCTACAC CGTGTCTCTT CTTTGGGACA CGTACCGCAA TGTACACCGG 1200  
 CTGCTCTGCC TCCTCTATCC GGAGAAGCAG TTGGATATGG TACGGACACT GATCGACATG 1260  
 TACCGAGAGA GCGGGTGGCT GCCGAGATGG GAGCTGTACG GACAGGAGAC CCTGACGATG 1320  
 GAGGGCGACC CCTCGCTTAT CGTCATCAAT GACACTTGGC AAAGGGGCGT TCGTGTCTTC 1380  
 GATACGGCAA CGGCCATGA AGCCATGAAA AAAAATGCTT CTTCGGCAGG AGCGACCCAT 1440  
 10 CCGATCCGTC CTGACAACGA CGACTATCTC ACCCTCGGCT TCGTACCGCT TCGCGAACAG 1500  
 TACGACAATT CGTATCGCA TCCGCTGGAA TACTATCTGG CCGACTGGAA TCTGTCCCGG 1560  
 TTTGCCACCG CACTTGGGCA TAAAGAAGAC GCAGCTCTAT TCGGAAAACG CTGTTG3GC 1620  
 TACAGACACT ATTATAATAA GGAGTATGGT ATGCTGTGTC CATTGCTGCC GGATGGATCA 1680  
 TTCTCACTC CTTTCGATCC CAAACAGGGT GAAAACCTCG AGCCTAATCC CGGTTTCCAC 1740  
 15 GAGGGCAGTG CTIATAACTA TGCCCTTTTC GTTCCCGACG ATATACAAGG GCTTGCCCGG 1800  
 CTGATGGGAG GAGCAAAGGT TTTTTCGGAA AGGTTSCAGA AAGTCTTGA TGAAGGATAT 1860  
 TATGATCCGA CCAACGAGCC GGACATCGCC TATCCTTACC TCTTCTCTA TTTCCCAAG 1920  
 GAAGCATGGC GAACGAGAA ATTGACCCCG GAGTTGATAG ACAAACATTT TTGCAATGCT 1980  
 20 CCTAACGGCT TGCCCGGTAA TGACGATGCC GGTACGATGA GTGCTTGGCT TGTCTATTCC 2040  
 ATGCTGGGAT TCTACCCCTGA CTGTCCGGGC AGCCCCACT ATACACTGAC CTGCGCGGTA 2100  
 TTCCCGGAG TTAGGATTGG GCTCAATCCG CAGTATTATC CTCAGGGGGA GTTGATCATT 2160  
 ACGACCAATA CAGAGAATCA ACCGACAGAT TCCATTTACA TCCATACGGT TTCTCTTGGC 2220  
 AATAAAACAC TTCCGATGG AACAAAGGAT ATCAGCCATG CCGATTGGT GCGCTGCGGT 2280  
 25 CACCTCCGTT ACGAACAAAG CAATCGTCCT CGA 2313

## (2) INFORMATION FOR SEQ ID NO:258

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2328 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular  
 35 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 40 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS  
 45 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...2328

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:258

50 ATGTGCAAAA TAAGATTCAG CCTCTTGCAG GCTCTGTGCG TCTGCTTATT GTTCACTCT 60  
 TTTCTCTCC AAGCTCAAGA GGAAGGTATT TCGAATACCC TCTTGGCTAT CCACAAGACG 120  
 GAAAAAGCCG TAGAAACGCC CAAGAAAGTC TTTGCCGTAG CCAACGGAGT ACTTTACTCG 180  
 GTGGGCAAG AAGCTCCCCA TGAGGCAAG ATCTTCGACC GTATCAGCGG ACTCAGCGAT 240  
 ACATCGGTAA GCAGCATAGC CTACTCCGAG CAACTAAAAT CCTTGGTCAT ATACTATGCA 300  
 55 TCAGGCAATA TCGACATCTT GGACGAAGCA GGCCGTGTGA CCAACGTACC TGCATTGAAA 360  
 GACAATATCG ATCTGATAGA CAAAACGCTC AATCGCCTTT TGATCGTAGG CAACAGGGCT 420  
 TATTTGGCAG GAGGATTCGG CCTCTCCGTT CTGATGTGCG CCGAAGCTCG CATACCGGCT 480  
 ACCTACGCCA AGGGAACATA GGTGACCGAT GTGGCTAAGT TGGACAATGA TCGCTTGTCTG 540  
 ATGCTGAAAG AAGGSCAGCT CTTTCATCGGA AAAGAGACCG ATAACCTGCA AGATCCGGCC 600  
 60 GCATGGACAG CCTTGTCTTT GAATTTGCCG ATGGGCTCGG TCACCGGTCT GGGCATTGTC 660  
 GGGGAAGACA TCTGTTTCTT GCTCGCGGAT GGCCGTGTAT ATGTGCGTGC AAACCAATCG 720  
 TTTGAGCCGG AGCTATTGCT CTCTTCTCC GCGATTACAC GACTGTATGT GACGGATCGT 780  
 GGTCTGTTC TCTGTGCCGA GAATCGAATT TATTTCATAG AAAAAGGTG CAAAACGACA 840  
 65 CAATTTCTTA TAGCCGACGT CTTTGGGTGC GGTGCCATGA ACGAAAGCAA TACGGCATAC 900  
 ATAGCATTGG GAGAAGAAGG TTTGGCTTCA CTTCTTCTCG CAGAGGGAAG TACGGCCGAA 960  
 GCCATGCCG TAGCATTCTGA CCGACCGGGG GACAATGATT TCTACGAGAT GCGGTTTAGT 1020  
 CACGGACGTC TGTATGCAGC CAGCGGACTC TGGGGACAAA AACTGATGGG ACATGCCGGT 1080  
 ATGGTGAAGC TATACGACGG CAACCGATGG ACTAACTTGG ACAGAAGAC CGTACAGGAA 1140  
 CAGTTGGGCG GCGGATTCTG TTTCAATGAT GCTATCGATA TAGCTGTTTC CAACGGAGAC 1200  
 70 CCCGATCACT TTTTGTCCG TACATGGGGA AAGGGTCTGT TCGAATTCAA GGATGGCAA 1260  
 GCGATAGCTC GCTATTCCGG AAACGAAACT GCTATCGCAG AATGTAATCC CCGAGATGCC 1320  
 CGTGTGAAGC CGATTGCTT TGACAATAAG GGCAACCTCT GGGGGAACGT CGGTGCCGTA 1380  
 GGCAGAAACA TCTTCATGTA CGATCCGCAG AGTAGCACAT GGCATTCTTT CAGCTATCCG 1440  
 75 GATGTAGCCA ATCTGGCTC CTTCGGCAAT ATGATTATCC TACCAACGG AGACAATGG 1500  
 GTAAATATCC TTAACCGTAG TGGCGGATCC ACGCGCAAG GTGTCTTGAT CTTCAACGAT 1560

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CGGGGTACAC CGGAAACGAC TTCGGACGAC AGCCATCTTT ACGTCGAGCA GTTTGTCAAT 1620  
 CGCCTCGGG CAGCCATAGG ACATAAGACT ATCTATGCAA TGGCGGTGCA TCATAACGGC 1680  
 TCTGTCTGGA TGGGATCGGA TATAGGCATT TTCGGCGTCT ACAATGCAGC CGGAGTATTG 1740  
 TCCTCGACTT CTACCCCTAT CGCTGTTCCG CCGGTCGGAG GAGAAGAACC CAATTTGTAC 1800  
 TATGTGCTGG ACAAGGTGAC GGTGACAGAC ATCGTCTGTT ACAAACCTCA TCACAAATGG 1860  
 GTTGCCACCC AAGGGACAGG ACTCTATCTC CTTTCGGAAG ATTGCAGTAA GATCCTCGCG 1920  
 CAATTTACCG TAGAAAACAG CCCTTTGCTT TCTAACAAAC TACTATCCCT GGCCTTAAT 1980  
 GACGATAACG GACTGCTGTA CATCGGTACG GCGGACGGAC TGATGAGGTT CCAAAACGGT 2040  
 ACCGGGAGTG GATCAGCTTC CGAACTGGAC GCGTCTATG TATACCCCAA TCCGCTAAGG 2100  
 CCGGAATATC CCGATGGCGT CACCAATTGCC GGAAGTCAAG CCGGCTGTAG TGTCAAAATC 2160  
 ACCGATACCA CCGCAGACT GCTATACCAG ACTGAGAGCG TAACCAACGA AGTCAAAATG 2220  
 NATGCTCGAG GTGCCGATGG CAATAGGGTA GCTTCGGGCG TATATGCCGT TGCAGTGTAC 2280  
 GATCCGGTAT CGAAAAAGTC CAACTAATT CGCTTCGCAG TGATTTCG 2328

## (2) INFORMATION FOR SEQ ID NO:259

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3474 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (v) ORIGINAL SOURCE:

- (A) ORGANISM: PORPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...3474

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:259

ATGAACGAA TACTTCCAAT AGTCGCATTC CTTCTCTCT TCCTTGCCCT TGCTTTGCCT 60  
 GCGAAAGCGC AACGAGCTAT GGGGAAGACG GCCGACCGTT CGCTAATGGC TTCGGGACAT 120  
 TGGGTCAAGA TACGTGTGGA TGCAAGTGGG GTGTATCGCC TTACGGACGA ACAGCTCCGT 180  
 GCCAATGGCT TCTCCGATCC GTCCAAGGTA GGTGTGTTGG GTTATGGTGG AGGGGTGCTT 240  
 CCCGAAGATC TGAGCCGGAT CACGACAGAC GATTTCCTC CGGTACCGGT ACTCCGTCAG 300  
 GGCAATGCGC TGTATTCTA TGCCGTGGGC CCGGTGACAT GGTTCACAA TCCGGCCAAA 360  
 ACCACCATGG AGCATAAGGT GAATACATAC AGTACCGATG GCTACTACTT CCGTCCGGAT 420  
 GCTCCCGAG CACCTTTGCA GATGTCCCAA TATACGGTGG GAGGTGCGTC GGCCGAGGCT 480  
 TTGATCGAT ACTACGATGA GCTGATGCTC CATGAACAGG AATTGTATTG GCCCAAAGAA 540  
 TCGGACGAG ATCTGTATGG CGAGTCTTTC AGTGCAGTCA ATACCGGTAC GGTCAAGTTC 600  
 CCTTTGAGGG GCAACACCCG CTGCTCTGGC GAAGTCCGTA CCGTATTCTC ATACATAGCC 660  
 AAGGCCAGAT CGGCCGGTGG CGGCCGTGAG ATGTCCGCTC CGGCGAATGG CATCTGATC 720  
 TTCAGCGATC CTTTTCCAT GACATCGAAT GAAGTCTCCA ATTCTTATTI GGCCGGCAAG 780  
 AAGCGTCGTC TCTATCACAG TACGCCGATG AACAGCTTGG TCAATGAGTT GCGCTTGGAC 840  
 GCGAATATA GCAATGACAGG AGATGCGGTC AATCTGGATT TCATAGAGGT GGCTACACAG 900  
 AACGACCTCC GGTACGATGG CGCACCCATG CATATCAGGC GGTTTTCCAA TTTGCCCGTT 960  
 TTGGGGGGGG AGTCCCTGCC GTTCGTTATC AGTGAGGTGC CGGAGTCTCT GGTGGTTTGG 1020  
 CAGGCCAATT CTTCCCTGAC AGCATCGCTT GTTCCCGTTA AGACTGTCCG GGATAAGACC 1080  
 ATTGAGTTCC TGGCTCCGCC GAAGGGTCAG GATCGTAGGA CTATCAATAC GTTTTATGCC 1140  
 GTGGAATTGT CACAGGCTTC TGCTCCGAG ATCCTCGGAG CGGTACCCAA TCAAAACCTG 1200  
 CATGGAGAGG AATCCCTGA TCTGATCATT GTCTCTACT AGGCGCTCCT CTTGAGGCT 1260  
 GATCGACTGG CCACCTATCG TAGAGAGAAA AACGGGCTGA AGGTTTTGGT CGTGTTCAG 1320  
 GAACAGGTGT TCAACGAGTT TTCGGGTGGA ACTCCCGATG CTACAGCATA CCGCCTCTTT 1380  
 GCCAAATGT TCTACGACAG ATGGAAGGCA AATGCACCTG TGGGAGAGAC CTTCCCGATG 1440  
 CAAATGCTTC TCTTCGTTGA TCGGGCTCAT GACAACAGGA AGGTCTCCGT AGCTTGGCAG 1500  
 AAACCGTATC TCCAACAAAC GGAGTTCTTG CTGACATTCC AAGCGTCAA TTCCAGGAAC 1560  
 GTAAACASTT ATGTGACGGA TGATTACTTC GGCTTGCTCG ATGATCAGCC GGCCTCGGTC 1620  
 AATATCGGTT GCGCAATTA TAATATGGCT GTAGGGCGAT TCCCGTACG TACTCCGGCT 1680  
 GAAGCTCGCA TCGCAGTGGG CAAGACCATC CGATATGAGG AGGATCGAGA GAGTGGTGCC 1740  
 TGGCTTATTC GTCCCTGTTT TCGGGCAGAC AACGGGGACA AGCAACCAAC CGAGACTTCC 1800  
 CGTTTGATCG ATACCGTCAA GCGTTATGCT CCGCCATCA TCGCGGTACG CGCCTTTGAG 1860  
 GACGTATATC CGCATGTCTC CGAGAACGGG TTGCACAGCA TTCGGGTGTC AAAGAAAAAG 1920  
 ATGCTGGAAC CCCTTCAGTC GGGTATTATC CTGCTTAATT ATGCTGGTCA TGGCGGTCTT 1980  
 GCCGGATGTT CGGACGAGCA TTTGCTGAGC CTCACGATA TACACAAATT CAATTATAAG 2040  
 CATATGCCCA TTTGGATTAC TGCCACGTGC GACTTTGCCA ACTATGACAG TCAGACGACC 2100  
 TCGGCGGGG AGGAGGTTTT CTTCCATGAG AAGAGTGGCA CTCGATCAT GTTCTCGACT 2160  
 ACGCGTGTG TTTACAATAC GCAGAATGAG AAGATCAATG GTTTTATGCT TCGGCGTATG 2220

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5	TTGAGAGAAAG	CTAAGGATGG	GCGTTATCGT	ACGATGGGCG	AGATTATCCG	ATCGGCCAAA	2280
	CAGGGGATGC	TCAGTACTGT	TTTCCCGGAT	TCGATCAACC	AGTTGAGTTT	CTTTCTGATG	2340
	GGTGATCCGT	CGGTGCGTAT	GAATCTTCCT	ACCCACAAAG	TGCAATTGAC	CGCAATCAAC	2400
	GGGACGGATC	CCGAAGGGCA	GTATGGAAC	ATTATGCTCA	AGTCTTTGGA	ACGGGTAGCT	2460
	CTGAAGGGTA	AGGTAACCGA	TGAAAAGGGG	ACATTGCGAG	AGACATTGAG	TGGCAAGGTT	2520
	TTCTTGACCG	TCTTCGATGG	CAGAAAGAAA	ATGACAGCTT	TGGAAGAGGA	GGGAAACGAT	2580
	CTCTCTCTTG	TATATTATGA	CTATCCTAAC	GTGATGTATG	CCGGTATTGC	CGAGGTGAAA	2640
	GACGGACTCT	TGAAAACTTC	GTTTATCGTA	CCCAAGGATG	TGAACTATTG	CGAGCAGGAA	2700
10	GGCCGGATCA	ATCTTTATGC	TTATAACGAG	AGCACAAGG	CGGAAGCCAT	GGGGGTAGAC	2760
	TTCTCCATCA	GAGTCCAACC	GGGTATTCC	GATGAGGTAA	CGGAAGATAA	TACACCGCCT	2820
	GAATCATAA	GCTGCTTCCT	CAATGACAGT	ACATTCCGAT	CGGAGATGA	GGTTAATCCT	2880
	ACTCCTCTGT	TTATGGCCGA	AGTATTGAG	TTGAATGGAA	TCATATCAC	GGGTAGCGGA	2940
	GTAGGGCATG	ATATTACGCT	TTGTATCGAT	GGCCGTGCCG	ACCTGACCTA	CAACCTCART	3000
	GCATATTTC	CAAGTTGCGC	TACGGATGCA	GGTGTGGGCA	CTATTCTCTT	CATGATACCG	3060
15	GCTTTGGCCG	AAGGAGATCA	TACTGCCCGA	CTGACGGTTT	GGGACATTTT	CAATAATGCT	3120
	GTCCATCATG	ACTTTTCATT	CAGAGTGGTA	GATGGCATTG	CTCCGGATGT	GGCTGATGTG	3180
	ATTCTATTC	CGAATCCGCT	ACGCGAGAGT	GCTACGTTCC	GAATCTTCCA	CAATCGCCCC	3240
	GGAGCGGATT	TGAACGTGGC	CGTGGAGATC	TATGACTTCA	CCGGTCTGCT	TGTGAACAGT	3300
20	TTGCCAGTCA	AGACCTATTC	GTCTTCTTAC	GGAGAACCTA	TAGAGATCAA	GTGGGATCTG	3360
	ACCTCCAAAT	ACGGAGTGAA	GATCGGAAAC	GGATTCTACC	TCTATCGTTG	TGTGGTGAAC	3420
	TCTCCCGGAG	GACAGACGGC	CTCCATGGCC	AAGAAAATGA	TCGTGGTAGG	ACAA	3474
25	(2) INFORMATION FOR SEQ ID NO:260						
	(i) SEQUENCE CHARACTERISTICS:						
	(A) LENGTH: 2883 base pairs						
	(B) TYPE: nucleic acid						
30	(C) STRANDEDNESS: double						
	(D) TOPOLOGY: circular						
	(ii) MOLECULE TYPE: DNA (genomic)						
35	(iii) HYPOTHETICAL: NO						
	(iv) ANTI-SENSE: NO						
	(vi) ORIGINAL SOURCE:						
40	(A) ORGANISM: PORPHYROMONAS GINGIVALIS						
	(ix) FEATURE:						
	(A) NAME/KEY: misc_feature						
	(B) LOCATION 1...2883						
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260						
	ATGAAGAAAC	TTTTCCCAT	ATTATTACTC	ATATTGTGCA	TTTGTGGTCG	ATGTGGAAAA	60
	AAAGAAAAAC	ACTCTGTAAC	TGAATACGCC	GGAGAGAAAA	AGCGTATTAC	TGCATTGCTG	120
50	TACGAAAAAG	AACTCCCCAC	TGATCTCTGT	AAACAGCTTT	ACGAGAACAG	CGTACAGAAC	180
	AAGAACCTTG	TGGGACAAAT	GTTATTCCGG	ATCGAGGTCG	GCAAACGGAT	CGCTAATATG	240
	TCCCAATACA	CAGATGCGAT	GCTATATCAC	CAAAAAGGGT	TGAACGCTGC	ATTGAATCTA	300
	AGGGACACCA	TCGTAGCCGC	ACAAGCATGG	AATCATCTCG	GAACGGATAG	CCGTCTGATC	360
	GGTGCTTTGG	CAGAAGCTTC	GGATTATCAT	TACAAGGCTC	TTTCCTTGAT	AGAATCTTTT	420
55	AGCGGAAACC	AGAAATAGCC	TGUGATCAAA	GCCAGATCGG	CGGCCCTGAA	CGGCATCGGC	480
	AACATCAATC	TTGAGTTAGG	ATACCATGAT	GAGGCCGAAA	AGAAATTCCT	GAAGCACTG	540
	CAAGGTGAGA	AAGAATCGCA	CAGTCCCTCT	GGGCAAGCTA	TCAACTATGC	GAACCTCGGA	600
	CGTATCTATC	GACAAACGCA	AGAATACGAC	AAGGCTCGTA	CCTACTCTCT	CTTGTCTCTG	660
	GAGCAGAAAC	ATATGGCAGA	GAATCTGATG	GGTATCGGAC	TCTGTAGCAT	CAATCTCGGA	720
60	GAAGTAGACG	AAGAAAAAGG	GGATTATCAA	AAGSCTTTGC	AAGAGTATGC	CACGGCATAC	780
	AAACTGATGG	AACAGTTGTC	CGATCGATGG	CAGTGGCTGA	ATTCTCTGAT	CCCGATGGCA	840
	CGTATCAATC	TCAAACAAGG	TAACGAAAGG	CTCTACCAGC	ATTTCATTTC	TTTGGCCGAA	900
	GGGACTGCGA	AAGAAATTA	TTGCACTTCA	CATCTGATAG	AAATATACAA	TCTTCAATAC	960
	GAGATCTCG	AGCGTAAAA	AGAATACAAA	CAAGCCCTCG	AAGCATTCG	TCTGAGCAAG	1020
65	ACGTTGAGCG	ACAGCATGTC	CATTGCGCAC	AAGGTGAGCA	GCATACAGA	AACGGGATTC	1080
	AACACGAG	GAACAAAGTC	CCAAAAGAG	CTTGAAGAAA	TACAGCAAGT	AAGCAAGGCA	1140
	AAACAGAGA	AATCGAAGTT	TATCCTCTTG	AGCACTCTTT	TTGCCCTTTT	CATCTCGATT	1200
	CTTTTGATTT	CTGTTCTGAC	ATATGCATAC	CGTCAGGGCA	AGAAGCATAA	CAAGCTGATC	1260
	AAAGAGACGG	ATAAACTTCG	CTCCGGCTTT	TTACCCGGTA	TTACACACGA	ATTTCTAGCG	1320
70	CCTATCACCG	TCATACAGG	TTTGAATGAG	AAAATGAGTT	CAAGTCTGTA	TCTCCAAGCA	1380
	TCGGACAGAA	CCGAGCTGCA	CAAGATAATA	GACAGACAGA	GTAGCCATAT	GCTGAATTG	1440
	GTGAACGAGC	TGTTGGATAT	TTGCAAGATC	AGAAGCGGAG	TATCCACGCC	CGAATGGGCG	1500
	AATGGCGACA	TGCTCTCCTT	CGTACAGATT	CTCATCGATT	CGTTTGCACC	ATAGCCACAG	1560
	GCTCAAGACA	TAACCTTGGA	GCTACAAACC	GAGAGCAAAC	CTATTGTCGT	GGACTTCGTC	1620
75	CCCTCCTACT	TGCAAAAAAT	CATATCCAAT	CTTTGTGCTA	ATGCCATCAA	GTATTCTTTA	1680
	GCCGGAGGGA	GAGTGGTCAT	ATCTCTGGCA	AAAACCAAGA	ATGAAAAAAA	TCTGATCATA	1740

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5 CGGGTTGCAG ACAATGGCAT AGGAATAGAT AAAACTGATC AAGCTCATAT CTTGACATC 1800  
 TTCTATCGAG GACAGTCCGC TACCGAAAAG CATGGATCAG GCGTCGGACT CTCGTTTACC 1860  
 AATATACTGG TCGAAAACCT TCGAGGTACG ATCAAAGTGG AAGCCAGCC GGGGAAAGGA 1920  
 AGTGCCTTCA CCATCAGTAT TCCTACACAA AACCAGTCCT CTTGGGCAGA GATTCTTCCT 1980  
 TGGGTACCTT CCTCGATGA CATTGTCTAT CCTGTCCACA TCGCGCCGA TGAATCACCG 2040  
 ACATCTCCGA TGGTAGCAGC TCTGAATCAT CGCTTCGAGG ACGAAGCTCC GACCATACTG 2100  
 CTCGTGAGAG ACAATAAGGA TATCAACCTG CTCGTCAAAC TACTCCTTTG CGATCGCTAC 2160  
 AATGTGCTAT CCGCCGCAAA CGGAAAAGAG GGTATAGCCC TCGCTACOGA GCATATTCCC 2220  
 GACATTATCA TTACGGATAT TATGATGCCG ATAATGGATG GGATAGAAAT GACATCCGG 2280  
 10 ATGAAGCAAT CGCTCTGCT CTGTACATT CCCATTGTCT CTTTGACGGC CAAGAGTACC 2340  
 GAACAGGACA GATTGGAAGG AATCAAAAGC GGTGTAGTCT CTTATCTATG CAAGCCATTG 2400  
 TCTCCGGAGG AGCTTTTGTAT GCGGATCGAG CAGCTTCTGA AAGACCGTGA GTTGCTCAAG 2460  
 AAGTTCTATA TGCAAAACT CATGCTGGAT CGGAAGCCGG AGGAGGAGCC TCAACCGATA 2520  
 15 GATGACAGCA GTATGCAGTT TCTCCTTGCT GCCAAAGATG CAGTGTCCGG TGAATCAAA 2580  
 CAAAATCCGG ATTTTCCCGC TCAAGACTTG GCCGAAAAA TGTGCATGAG TCCATCCCAA 2640  
 CTCAACAGAA AGCTCAGAG TGTCTAGGT TGCTCCACCA TCGGCTACAT ACAGCAGATC 2700  
 AAGATAAAAT TGGCCTGCAA GCTCCTTGCC GATGAGAGCA AAAACATCTC CGACATTAGC 2760  
 ATTGAGGCGA GCTTTTCGGA TCGGCTTAC TTCTCTCGCA CCTTCAAACG CTACATGAAC 2820  
 20 TGCTCTCCCT CCCAATATCG GCAAAAACCT CTGCCATGC GGGGAGCGA CAAGGAGACA 2880  
 GTT 2903

## (2) INFORMATION FOR SEQ ID NO:261

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1668 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- 30 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 35 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS
- 40 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1668
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:261

ATGAAAAAGC TTTTACAGGC TAAAGCCTTG ATTCTGGCAT TGGGACTCTT CCAACTGCCC 60  
 GCAATCGCCC AAACGCAAAAT GCAAGCAGAC CGAACAAACG GTCAATTTGC AACAGAAGAG 120  
 ATGCAACGAG CATTCAGGA AACGAATCCC CCTGCAGGTC CTGTGCGTGC TATCGCTGAG 180  
 TACGAACGCT CTGCAGCCGT TTTGGTACGC TACCGGTTGG GTATCCOGAT GGAATTGATC 240  
 50 AAAGAGCTGG CCAAGAACGA CAAGGTGATT ACCATTGTGG CGAGTGAAG CCAAAAAAAC 300  
 ACCGTTATAA CCGAGTACAC CCAAGCGSGT GTGAATCTCT CTAATTGCGA TTTCATCATT 360  
 GCGAAAACCT ACTCTTACTG GACACGCGAC TATACCGGTT GGTTCGCAAT GTACGATACG 420  
 AACAAAGTAG GTCTGTGGA CTTTATTAT AACCGCCCTC GTCCTAACGA TGATGAATTC 480  
 CCCAAATACG AAGCACAATA TCTGGGCATC GAGATGTTCG GGTATGAAGCT CAAGCAGACC 540  
 55 GGTGGCAACT ACATGACGGA CGGATATGGA TCGCTGTGTC AGTCACATAT CGCATATACG 600  
 GAGAATCCTT CTCTGTCTCA AGCTCAAGTA AATCAAAAGA TGAAGACTA TCTCGGCATC 660  
 ACACATCATG ATGTGGTACA AGATCCGAAC GGCGAATATA TCAACCATGT GGAATGTTGG 720  
 GGCAAGTATT TGGCACCAGAA CAAATCCTC ATCAGGAAG TGCCTGACAA TCACCCTCAG 780  
 60 CACCAAGCCC TGGGAAGATAT GGCAGCCTAC TTCGCAGCAC AGACCTGCGC ATGGGGAACG 840  
 AAGTACGAGG TATATCGCGC TTTGGCCACC AATGAACAA CGTACACGAA CTCTCTGATT 900  
 CTGAACAACA GGGTATTTGT TCCTGTCTAT GGCCCGCCT CCGTGGACAA CGATGCTCTG 960  
 AACGTCTATA AGACGGCAAT GCCCGGTTAC GAAATTATAG GTGTCAAAGG GGCTTCACGA 1020  
 ACACCTTGGT TAGGAACAGA TGCCCTGCAT TGTGCTACTC ACGAGGTAGC GGATAAGGGC 1080  
 65 TATCTCTATA TCAAGCACTA CCCGATCTG GCGGAACAGG CAGGCCCTGA TTATAAGATC 1140  
 GAAGCAGATG TCGTCTCATG CCGCAATGCT ACTATCTGCG CGGTACAATG TTACTATCGT 1200  
 ATCAATGGTT CCGGTAGCTT TAAGGCTGCT GATATGACGA TGGAAATCAAC AGGTCACTAT 1260  
 ACTTATAGCT TTACAGGTCT TAACAAGAA GATAAGGTAG AATACTATAT CTCTGCGCT 1320  
 GACAATAGTG GTGCGAAAGA GACTTATCCC TTTATCGGCG AACCTGATCC TTTCAAGTTT 1380  
 70 ACGTGTATGA ACGAAACCAA TACATGACT GTGACCGGAG CTGCGAAAGC TCTCTGTGCA 1440  
 TGGTTCAACG CCGGTGCTTC AGAAGTGGCT GTTTCGGTAA GTTTGAATAT TGCCGGCACA 1500  
 TATCGGATAA AGCTTTATAA CACCGCAGGA GAAGAAGTCG CTGCAATGAC CAAGGAATTA 1560  
 GTAGCAGGGA CAGTGTCTT CAGTATGGAT GTGTATTCTC AGGCTCCGGC CACATATGTT 1620  
 75 CTGTTTGTG AAGGAAATGG AATCCGTGAG ACAATGAAAA TTCTCAA 1668

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PCT/AU98/01023

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## (2) INFORMATION FOR SEQ ID NO:262

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1284 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1284
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:262

25 ATGAACTTT CATCTAAGAA AATCTTAGCA ATCATTGCAT TGCTGACGAT GGGACATGCT 60  
 GTGCAGGCAC AGTTTGTTC GGCTCCACCC ACAGGGATTC GCATGTCTGT CACTACAACC 120  
 AAGGCCGTAG GCGAAAAAT CGAATTGTTG GTTCATTCCA TAGAGAAGAA AGGCATCTGG 180  
 ATCGATCTCA ATGGGATGTC CACTTACCA CAAGGAGAGG AAATAACCGT ATTCGATGAG 240  
 GCATACCAAG AATACACGAT CGGGACGCAA ACCCTCACTA TCTATGGTAA TACGACCCGA 300  
 TTGGGCTGTC GATCTACCGG TGCAACGGCT GTCSAIGTAA CGAAAAACCC TAATCTGACC 360  
 30 TATCTCGCAT GCCCGAAAAA TATCTGAAA TCATTGGACT TGACGCAAAA CCCAAAGCTG 420  
 CTGCGAGTTT GGTGCGACTC TAACGAATA GAAAGTTGG ACCTGAGTGG CAATCCGGCT 480  
 TTGATCATCC TCGGCTGTGA CAGGAATAAG CTGACTGAGC TGAAGACCGA TAACAACCCC 540  
 AAGTTGGCCT CTCTTTGGTG TTCTGATAAT AACCTGACGG AGTTGGAAC CAGTGCCAAT 600  
 CCTCGTCTCA ATGATCTTTG GTGCTTCGGT AATCGGATCA CGAAACTCGA TCTGAGTGCC 660  
 35 AATCCTCTAT TGGTACACT TTGGTGCACT GACAATGAGC TTTCGACCTT GGATCTTTCC 720  
 AAGAATTGG AGCTTGCTTA CCTTTGGTGT TCATCGAACA AACTTACATC CTGGAATCTG 780  
 TCGGGGGTGA AGGGAATGAG TGTTTGGTTT TGTCATTCCA ATCAGATCGC AGGTGAAGAA 840  
 ATGACGAAAG TGGTGAATGC TTTGCCACA CTATCTCCCG GCGCAGGCGC TCAGAGCAAG 900  
 TTGTCGTTG TAGACCTCAA GGCACTGAT GAGAAGAATA TCTGTACCGT AAAGGATGTG 960  
 40 GAAAAAGCTA AAAGTAAGAA CTGGCGAGTA TTTGACTTCA ACGGTGATTC TGACAATATG 1020  
 CTTCCATACG AAGGAAGTCC GACATCGAAC TTGGCAGTAG ATGCTCCAC TGTCAGGATA 1080  
 TATCCCAATC CGGTAGGAAG ATATGCGCTC GTCGAGATCC CCGAGTCTCT TTTAGGGCAG 1140  
 GAAGCTGCTT TATAGATAT GAATGGGGTA AAAGTCTATA GTTTCGCGGT AGAGTCTCTT 1200  
 45 CGTCAGAAC A TGACCTGAC ACATCTTCCC GACGGCACTT ATTTCTTCCG TCTCGATAAC 1260  
 TATACCACTA AGCTCATCAA ACAG 1284

## (2) INFORMATION FOR SEQ ID NO:263

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 930 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...930
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:263

70 ATGAGAAAA CAATAATTT CTGCTTGTG CTGCGCCTAT TTGGCTGTTT TTGGGCACAA 60  
 GAAAGAGTCG ATGAAGAAT ATTCTCCGCA GGAACAAGTA TTTTAGGGG CATCCTTGAA 120  
 AAGGTGAAAG CACCGCTTAT GTATGGAGAT CGTGAGGTAT GGGGTATGGC TCGTGCGAGC 180  
 75 GAGGATTTCT TTTTATACT TCCCGTTACG GATGACCTCA CTCGGTGTCT TTTCTAATC 240  
 CGTCTTACAA ACGAACCCCTG CTTTGTGTCA GAUCAAGGAA TAACTGAGTA TTTCAAATTC 300

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5 GCTCAAGAAG GTGATTACAT TGAAGTCGAA GGAAGCTCTG TATTCATGGC GAATCTTTTC 360  
 TACTATCGTT TTTTCCCGAC AAGAATTACC TCCTATAATG CTCCCATGTA AGGTGTTGTG 420  
 AGCAAGACGG GAAATCTCAA ACAACCGCAA AGTCTTTCTG ACCAATCAAT TAGGGGTTGT AAACATCACT 480  
 GACGGGATGG AACCTCCGAT TATTGCCGGA GTCTCTGCTT CCTATGGATC TTCCGTCCGG 540  
 GTGTATGGTC ATGTCTCACA GCGGTGGGAC ATCATAGGCC ATTGCTATTT GGATATCTAC 600  
 CCAACCAATT GCTATCCGCT CAGCACGAAA CCGGTTGCAG GAGACGATGA GGTTTTGTG 660  
 AAACAACAAG GCAGGCAAAAT AGAGATCGAT AGCAACAGCC CCATAGTCCA AGTGGTCGTA 720  
 TACGATCTTG AGGGGAAAAG TGTTTTTCGC AAAAGAATGA CCGAAAACGC TTATACCCTA 780  
 10 TCCTTTAGAG CACCCATGCT CGGCTTTATG ACCATCATGA TCGAAACACA AATTCGATT 840  
 ATCAATAAAA AACTTAATGT TACACAGCTA 900  
 930

## (2) INFORMATION FOR SEQ ID NO:264

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1215 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

20

(ii) MOLECULE TYPE: DNA (genomic)

25

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

30

(A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1215

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264

40 ATGAAAAAAA CAACCATAT TTCTTTGATT GTCTTCGGTG CTTTCTTTC AGCCGTGGGC 60  
 CAAACCAAGG ACAATTCTTC TTACAAACCT TTTTCGAAAG AAGATATTGC CGGAGGAGTT 120  
 TACTCTCTCC CGACTCAAAA TCGTGCGCAG AAGGACAATG CCGAGTGGCT TCTTACAGCG 180  
 ACGGTCTCCA CAAACCAAGT TGCAGATACT CACTTTATCT TCGATGAGAA CAACCGCTAT 240  
 ATCGCTGGTG ACATAAAAGC CAATGGGGTA AGAAAATCCA CGGACTCCAT TTAATACGAT 300  
 GCCAACGGGC GAATATCGCA TGTGGATCTT TATATCTCGT TCAGTGGCGG AGAGCCTGCA 360  
 CTCGACACCC GATTCAAGTA CACCTATGAT GACGAGGGAA AGATGACCGT GAGGGAAGTA 420  
 TTCTATGCTGG TAATGGATCC GAATACACCT ATCTCACGCT TGGAAATATCA TTATGATGCA 480  
 45 CAGGGCAGAC TGACCCACTG GATTTCCTTT GCTTTCGGGG CAGAATCCCA AAAGAATACG 540  
 TATCACTATA ATGAAAAAGG TCTGTTGGTC AGCGAAGTGC TGAGCAATGC AATGGGGACA 600  
 ACCTATTTCAG ACACCGGCAA AACGGAATAC AGCTATGACG ATGCAGATAA TATGGTGAAG 660  
 GCOGAGTACT TCGTCGTCCA GCAAGGAAAG GCATGGCAAG TACTCAAAAG AGAGGAATAC 720  
 ACCTATGAGG ACAATATCTG CATAAATAT TTGGCTATTA ACGGTACCGA CACAAGGTYG 780  
 50 TACAAGCGAG ACATCGAGAG CGATAAGTCC ATCTCCGCAA ATGTCATTGA CATTCGGTCA 840  
 ATGCCGGAAC AGACCTGGCC TAATATGTAC GGATTCAACG CAAAGCGACT GAAAGAGACT 900  
 TATTCCTCCT ACGAAGGAGA TGTGGCTACT CCTATATTCT ACTATATCTA TACGTACAG 960  
 GCTCTTACCT CAATGGCAAC ACCTTCGACA GAAGCTCAGG TAGCAGTCTA TCTCAATCCG 1020  
 TCAACGGACC GGTTAGTGAT TCTGGCCAAC GGCATCACAC ATCTGAGCAT GTACGACTTG 1080  
 55 CAGGGTAAAG TTATCCGTGA TTGTGCTTG AGCGGCCATA AGGTGAAAT GGGTGTCCGA 1140  
 TCTTTGACCA AAGGGACATA CCGCTTAAA GTGAATACGG ATCAGGGAGC CTTTGTGAGA 1200  
 AAGTCGTGA TTCA 1215

60

## (2) INFORMATION FOR SEQ ID NO:265

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

65

(ii) MOLECULE TYPE: protein

70

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

75

(A) NAME/KEY: misc\_feature

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(B) LOCATION 1...454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265

5 Phe Cys Val Met Ala Lys Val Ile Lys Thr Lys Lys Gly Leu Ala Leu  
 1 5 10 15  
 Asn Leu Lys Gly Lys Pro Leu Pro Glu Met Leu Ala Glu Pro Ala Gln  
 20 25 30  
 10 Ser Pro Thr Tyr Ala Val Val Pro Asp Asp Phe Glu Gly Val Ile Pro  
 35 40 45  
 Lys Val Thr Ala Arg Pro Gly Asp Lys Val Arg Ala Gly Ser Ala Leu  
 50 55 60  
 Met His His Lys Ala Tyr Pro Glu Met Lys Phe Thr Ser Pro Val Ser  
 65 70 75 80  
 15 Gly Glu Val Ile Ala Val Asn Arg Gly Ala Lys Arg Lys Val Leu Ser  
 85 90 95  
 Ile Glu Val Lys Pro Asp Gly Leu Asn Glu Tyr Glu Ser Phe Pro Val  
 100 105 110  
 20 Gly Asp Pro Ser Ala Leu Ser Ala Glu Gln Ile Lys Glu Leu Leu Leu  
 115 120 125  
 Ser Ser Gly Met Trp Gly Phe Ile Lys Gln Arg Pro Tyr Asp Ile Val  
 130 135 140  
 Ala Thr Pro Asp Ile Ala Pro Arg Asp Ile Tyr Ile Thr Ala Asn Phe  
 145 150 155 160  
 25 Thr Ala Pro Leu Ala Pro Asp Phe Asp Phe Ile Val Arg Gly Glu Glu  
 165 170 175  
 Arg Ala Leu Gln Thr Ala Ile Asp Ala Leu Ala Lys Leu Thr Gly  
 180 185 190  
 30 Lys Val Tyr Val Gly Leu Lys Pro Gly Ser Ser Leu Gly Leu His Asn  
 195 200 205  
 Ala Glu Ile Val Glu Val His Gly Pro His Pro Ala Gly Asn Val Gly  
 210 215 220  
 Val Leu Ile Asn His Thr Lys Pro Ile Asn Arg Gly Glu Thr Val Trp  
 225 230 235 240  
 35 Thr Leu Lys Ala Thr Asp Leu Ile Val Ile Gly Arg Phe Leu Leu Thr  
 245 250 255  
 Gly Lys Ala Asp Phe Thr Arg Met Ile Ala Met Thr Gly Ser Asp Ala  
 260 265 270  
 40 Ala Ala His Gly Tyr Val Arg Ile Met Pro Gly Cys Asn Val Phe Ala  
 275 280 285  
 Ser Phe Pro Gly Arg Leu Thr Ile Lys Glu Ser His Glu Arg Val Ile  
 290 295 300  
 Asp Gly Asn Val Leu Thr Gly Lys Lys Leu Cys Glu Lys Glu Pro Phe  
 305 310 315 320  
 45 Leu Ser Ala Arg Cys Asp Gln Ile Thr Val Ile Pro Glu Gly Asp Asp  
 325 330 335  
 Val Asp Glu Leu Phe Gly Trp Ala Ala Pro Arg Leu Asp Gln Tyr Ser  
 340 345 350  
 50 Met Ser Arg Ala Tyr Phe Ser Trp Leu Gln Gly Lys Asn Lys Glu Tyr  
 355 360 365  
 Val Leu Asp Ala Arg Ile Lys Gly Gly Glu Arg Ala Met Ile Met Ser  
 370 375 380  
 Asn Glu Tyr Asp Arg Val Phe Pro Met Asp Ile Tyr Pro Glu Tyr Leu  
 385 390 395 400  
 55 Leu Lys Ala Ile Ile Ala Phe Asp Ile Asp Lys Met Glu Asp Leu Gly  
 405 410 415  
 Ile Tyr Glu Val Ala Pro Glu Asp Phe Ala Thr Cys Glu Phe Val Asp  
 420 425 430  
 60 Thr Ser Lys Ile Glu Leu Gln Arg Ile Val Arg Glu Gly Leu Asp Met  
 435 440 445  
 Leu Tyr Lys Glu Met Asn  
 450

(2) INFORMATION FOR SEQ ID NO:266

(1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 201 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(111) ORIGINAL SOURCE:

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(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266

5  
 10 Glu Leu Ser Lys Cys Tyr Met Asp Lys Val Ser Tyr Ala Leu Gly Leu  
 1 5 10 15  
 Ser Ile Gly Asn Asn Phe Lys Ser Ser Gly Ile Asp Ser Val Val Met  
 20 25 30  
 Asp Asp Phe Met Gln Gly Leu Ser Asp Val Leu Glu Glu Lys Ala Pro  
 35 40 45  
 15 Gln Leu Ser Tyr Asp Glu Ala Lys Arg Glu Ile Glu Ala Tyr Phe Met  
 50 55 60  
 Asp Leu Gln Gln Lys Ala Val Lys Leu Asn Lys Glu Ala Gly Glu Glu  
 65 70 75 80  
 Phe Leu Lys Ile Asn Ala His Lys Glu Gly Val Thr Thr Leu Pro Ser  
 85 90 95  
 20 Gly Leu Gln Tyr Glu Val Ile Lys Met Gly Glu Gly Pro Lys Pro Thr  
 100 105 110  
 Leu Ser Asp Thr Val Thr Cys His Tyr His Gly Thr Leu Ile Asn Gly  
 115 120 125  
 25 Ile Val Phe Asp Ser Ser Met Asp Arg Gly Glu Pro Ala Ser Phe Pro  
 130 135 140  
 Leu Arg Gly Val Ile Ala Gly Trp Thr Glu Ile Leu Gln Leu Met Pro  
 145 150 155 160  
 30 Val Gly Ser Lys Trp Lys Val Thr Ile Pro Ser Asp Leu Ala Tyr Gly  
 165 170 175  
 Asp Arg Gly Ala Gly Glu His Ile Lys Pro Gly Ser Thr Leu Ile Phe  
 180 185 190  
 Ile Ile Glu Leu Leu Ser Ile Asn Lys  
 195 200

(2) INFORMATION FOR SEQ ID NO:267

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267

55  
 60 Gln Lys Asn Lys Arg Lys Met Lys Lys Ala Leu Leu Ile Gly Ala Ala  
 1 5 10 15  
 Leu Leu Gly Ala Val Ser Phe Ala Ser Ala Gln Ser Leu Ser Thr Ile  
 20 25 30  
 Lys Val Gln Asn Asn Ser Val Gln Gln Pro Arg Glu Glu Ala Thr Ile  
 35 40 45  
 Gln Val Cys Gly Glu Leu Ala Glu Gln Val Asp Cys Ile Gly Thr Gly  
 50 55 60  
 65 Asn Ser Ala Ile Ile Ala Ala Ala Lys Phe Glu Ser Asp Asp Leu  
 65 70 75 80  
 Glu Ser Tyr Val Gly Trp Glu Ile Met Ser Val Asp Phe Phe Pro Gly  
 85 90 95  
 Tyr Lys Ala Cys Lys Tyr Thr Ser Ala Val Trp Ala Asp Asp Met Thr  
 100 105 110  
 70 Ile Leu Gly Gln Ser Glu Asp Ser Asp Pro Glu Met Gln Thr Ile Asn  
 115 120 125  
 Asn Leu Ala Leu Lys Thr Ser Val Lys Ile Glu Ala Gly Lys Asn Tyr  
 130 135 140  
 75 Ile Val Gly Tyr Ile Ala Asn Thr Ala Gly Gly His Pro Ile Gly Cys  
 145 150 155 160

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Asp Gln Gly Pro Ala Val Asp Gly Tyr Gly Asp Leu Val Ser Ile Ser  
 165 170 175  
 Glu Asp Gly Gly Ala Thr Phe Pro Pro Phe Glu Ser Leu His Gln Ala  
 180 185 190  
 5 Val Pro Thr Leu Asn Tyr Asn Ile Tyr Val Val Val His Leu Lys Lys  
 195 200 205  
 Gly Glu Gly Val Glu Ala Val Leu Thr Asn Asp Lys Ala Asn Ala Tyr  
 210 215 220  
 10 Val Gln Asn Gly Val Ile Tyr Val Ala Gly Ala Asn Gly Arg Gln Val  
 225 230 235 240  
 Ser Leu Phe Asp Met Asn Gly Lys Val Val Tyr Thr Gly Val Ser Glu  
 245 250 255  
 Thr Ile Ala Ala Pro Gln Lys Gly Met Tyr Ile Leu Arg Val Gly Ala  
 260 265 270  
 15 Lys Ser Ile Lys Leu Ala Ile  
 275

## (2) INFORMATION FOR SEQ ID NO:268

- 20 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 157 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 25 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...157  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:268

Arg Unk Phe Leu Pro Glu Lys Ala Leu Tyr Ile Gly Cys Arg Val Glu  
 1 5 10 15  
 40 Thr Gln Glu Gly His Ala Val Gly Phe Gly Leu Asp Asp Gly Pro Ala  
 20 25 30  
 Met Lys Gly Lys Gly Asp Leu Val Gly Ser Tyr Leu Pro Gly Ala Ala  
 35 40 45  
 45 Pro Met Pro Phe Val Pro Leu Ser Asp Ile Pro Ala Arg Ser Met Asp  
 50 55 60  
 Ala Asn Phe Tyr Ile Tyr Ser Arg Ile Ser Leu Gly Ser Gly Thr Gln  
 65 70 75 80  
 Asp Val Leu Gln His Arg Met Lys Val Tyr Pro Asn Pro Ala Thr Thr  
 85 90 95  
 50 Glu Leu His Val Glu Ala Leu Ser Ala Trp Val Gly Glu Gln Ala Ala  
 100 105 110  
 Val Tyr Asp Met Arg Gly Arg Arg Val Ser Ala Arg Thr Val Asp Ser  
 115 120 125  
 55 Glu Lys Leu Cys Ile Asp Ile Ala Ser Leu Pro Val Gly Val Tyr Met  
 130 135 140  
 Leu Arg Ile Gly Ser Tyr Ser Ala Lys Phe Glu Lys Arg  
 145 150 155

## (2) INFORMATION FOR SEQ ID NO:269

- 60 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 562 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 65 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 70 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...562  
 75

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269

5 Thr Arg Asn Val Ser Leu Ile Lys Met Pro Arg Ile Met Lys Leu Lys  
 1 5 10 15  
 Ile Ala Leu Arg Leu Leu Leu Ala Thr Phe Ala Ile Val Leu Phe Ser  
 20 25 30  
 Pro Leu Ala Lys Ala Gln Met Asp Ile Gly Gly Asp Asp Val Leu Ile  
 35 40 45  
 10 Glu Thr Met Ser Thr Leu Ser Gly Tyr Ser Glu Asp Phe Tyr Tyr Lys  
 50 55 60  
 Met Ala Val Ala Asp Asn Gly Trp Ile Tyr Val Met Leu Asp Phe Ser  
 65 70 75 80  
 15 Arg Ile Tyr Phe Asp Asp Val Arg Leu Tyr Arg Ser Lys Asp Gly Gly  
 85 90 95  
 Ala Thr Tyr Gln Lys Leu Gly Ser Leu Gly Ser Leu Val Pro Tyr Asp  
 100 105 110  
 Phe Asp Val Ser His Cys Asp Phe Ile Val Thr Gly Lys Asp Glu Asp  
 115 120 125  
 20 Asp Ile Asn Val Trp Thr Val Met Thr Ala Phe Glu Tyr Val Gly Gly  
 130 135 140  
 Thr Ile Gly Asn Gly Val Leu Leu Met His Arg His Asp Ala Asp Ile  
 145 150 155 160  
 25 Asn Asn Thr Glu Cys Val Tyr Lys Lys Asp Phe Pro Asn Asn Arg Leu  
 165 170 175  
 Met Gly Val Ala Ile Ala Ser Asn Tyr Arg Ala Pro Ser Pro Tyr Gly  
 180 185 190  
 Leu Gly Gly Asp Pro Phe Ala Leu Ala Val Ala Val Ser Gly Ser Gly  
 195 200 205  
 30 Ser Asp His Ser Phe Leu Asp Tyr Ile Phe Ser Leu Asp Gly Gly Val  
 210 215 220  
 His Phe Glu Gln Lys Arg Ile Tyr Thr Arg Pro Gln Lys Leu Thr Ile  
 225 230 235 240  
 35 Asn Arg Val Asp Leu Ser Leu Gly Ser Thr Ser Pro Ser Leu Gly Phe  
 245 250 255  
 Asn Thr Trp Pro Leu Met Gly Val Val Phe Glu Met Asn Lys Asn Leu  
 260 265 270  
 Asp Gly Phe Asp Ile Gly Phe Ile Ser Asn Phe Val Asp Tyr Asp Pro  
 275 280 285  
 40 Arg Tyr Ala Trp Ser Glu Pro Ile Ile Ile Glu Glu Asp Cys Gly Trp  
 290 295 300  
 Thr Asp Phe Asn Pro Leu Gly Ala Leu Ser Ile Glu Ile Gln Met Met  
 305 310 315 320  
 45 Leu Asp Asp Asn Ser Asp Asn Thr Val Gly Gly Glu Arg Ser His Asn  
 325 330 335  
 Phe Leu Ile Thr Tyr Pro Gly His Tyr Val Tyr Pro Lys Gln Ser Phe  
 340 345 350  
 Asn Tyr Ser Pro Gly His Thr Pro Thr Lys Lys Asp Leu Val Phe Lys  
 355 360 365  
 50 His Cys Ile Gly Ile Pro Ala Leu Ala Tyr Asp Lys Glu Gly Asp Arg  
 370 375 380  
 Tyr Leu Thr Thr Phe Gln Asp His Asn Leu Met Arg Tyr Arg Trp Ile  
 385 390 395 400  
 55 Lys Tyr Asp Asp Ile Asn Ser Phe Tyr Gly Trp Ser Trp Pro Tyr Val  
 405 410 415  
 Tyr Ala Lys Glu Ala Lys Asp Lys Lys Arg Arg Arg Pro Gln Val Ala  
 420 425 430  
 Leu Asn Pro Thr Asn Gly Lys Ala Cys Trp Val Trp His Thr Arg Lys  
 435 440 445  
 60 Ser Pro Tyr Asp Glu Thr Lys Pro His Pro Thr Pro Val Ile Ile Lys  
 450 455 460  
 His Phe Leu Trp Ser Asp Thr Glu Trp Val His Ala Leu Asp Val Gly  
 465 470 475 480  
 65 Asp Val Leu Gln Lys Glu Gly Ser Met Lys Leu Tyr Pro Asn Pro Ala  
 485 490 495  
 Lys Glu Tyr Val Leu Ile Asn Leu Pro Lys Glu Gly Gly His Glu Ala  
 500 505 510  
 Val Val Tyr Asp Met Gln Gly Arg Ile Val Glu Lys Val Ser Phe Ser  
 515 520 525  
 70 Gly Lys Glu Tyr Lys Leu Asn Val Gln Tyr Leu Ser Lys Gly Thr Tyr  
 530 535 540  
 Met Leu Lys Val Val Ala Asp Thr Glu Tyr Phe Val Glu Lys Ile Ile  
 545 550 555 560  
 75 Val Glu

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## (2) INFORMATION FOR SEQ ID NO:270

5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 391 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

15 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...391

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:270

Gln Met Lys Arg Leu Leu Pro Phe Leu Leu Ala Gly Leu Val Ala  
 1 5 10 15  
 Val Gly Asn Val Ser Ala Gln Ser Pro Arg Ile Pro Gln Val Asp Val  
 20 25 30  
 His Thr Arg Ile Ala Arg Asn Ala Arg Tyr Arg Leu Asp Lys Ile Ser  
 35 40 45  
 Val Pro Asp Ser Arg Gln Ile Phe Asp Tyr Phe Tyr Lys Glu Glu Thr  
 50 55 60  
 Ile Pro Thr Lys Ile Gln Thr Thr Thr Gly Gly Ala Ile Thr Ser Ile  
 65 70 75 80  
 Asp Ser Leu Phe Tyr Glu Asp Asp Arg Leu Val Gln Val Arg Tyr Phe  
 85 90 95  
 Asp Asn Asn Leu Glu Leu Lys Gln Ala Glu Lys Tyr Val Tyr Asp Gly  
 100 105 110  
 Ser Lys Leu Val Leu Arg Glu Ile Arg Lys Ser Pro Thr Asp Glu Thr  
 115 120 125  
 Pro Ile Lys Lys Val Ser Tyr His Tyr Leu Cys Gly Ser Asp Met Pro  
 130 135 140  
 Phe Glu Ile Thr Thr Glu Met Ser Asp Gly Tyr Phe Glu Ser His Thr  
 145 150 155 160  
 Leu Asn Tyr Leu Asn Gly Lys Ile Ala Arg Ile Asp Ile Met Thr Gln  
 165 170 175  
 Gln Asn Pro Ser Ala Glu Leu Ile Glu Thr Gly Arg Met Val Tyr Glu  
 180 185 190  
 Phe Asp Ala Asn Asn Asp Ala Val Leu Leu Arg Asp Ser Val Phe Leu  
 195 200 205  
 Pro Leu Gln Asn Lys Trp Val Glu Met Phe Thr His Arg Tyr Thr Tyr  
 210 215 220  
 Asp Asn Lys His Asn Cys Ile Arg Trp Glu Gln Asp Glu Phe Gly Thr  
 225 230 235 240  
 Leu Thr Leu Ala Asn Asn Phe Glu Tyr Asp Thr Thr Ile Pro Leu Ser  
 245 250 255  
 Ser Val Leu Phe Pro Thr His Glu Glu Phe Phe Arg Pro Leu Leu Pro  
 260 265 270  
 Asn Phe Met Lys His Met Arg Thr Lys Gln Thr Tyr Phe Asn Asn Ser  
 275 280 285  
 Gly Glu Gly Leu Ser Glu Val Cys Asp Tyr Asn Tyr Phe Tyr Thr Asp  
 290 295 300  
 Met Gln Gly Asn Ala Leu Thr Asp Val Ala Val Asn Glu Ser Ile Lys  
 305 310 315 320  
 Ile Tyr Pro Arg Pro Ala Thr Asp Phe Leu Arg Ile Glu Gly Ser Gln  
 325 330 335  
 Leu Leu Arg Leu Ser Leu Phe Asp Met Asn Gly Lys Leu Ile Arg Ala  
 340 345 350  
 Thr Glu Leu Thr Gly Asp Leu Ala Ile Ile Gly Val Ala Ser Leu Pro  
 355 360 365  
 Arg Gly Thr Tyr Ile Ala Glu Ile Thr Ala Ala Asn Ser Lys Thr Ile  
 370 375 380  
 Arg Ala Lys Val Ser Leu Arg  
 385 390

## (2) INFORMATION FOR SEQ ID NO:271

75 (i) SEQUENCE CHARACTERISTICS:



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(A) LENGTH: 428 amino acids  
 (B) TYPE: amino acid  
 (C) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 10 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...428  
 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:271  
 20 Lys Arg Asn Pro Leu Pro Leu Thr Ala Ser Asn Arg Lys Ile Phe Ile  
 1 5 10 15  
 Lys Met Arg Gln His Leu Ser Leu Phe Pro Phe Ile Leu Phe Leu Leu  
 20 25 30  
 Leu Ala Phe Ser Tyr Val Gly Cys Arg Thr Val Arg Gln Thr Pro Lys  
 35 40 45  
 25 Gln Ser Glu Arg Tyr Val Val Leu Ser Leu Asp Gly Phe Arg Pro  
 50 55 60  
 Asp Tyr Thr Asp Arg Ala Arg Thr Pro Ala Leu Asp Arg Met Ala Gln  
 65 70 75 80  
 Glu Gly Leu Ser Gly Ser Leu Gln Pro Cys Phe Pro Ser Leu Thr Phe  
 85 90 95  
 30 Pro Asn His Tyr Ser Met Ala Thr Gly Leu Tyr Pro Asp His Gly  
 100 105 110  
 Ile Val Ala Asn Glu Phe Val Asp Ser Leu Leu Gly Ile Phe Arg Ile  
 115 120 125  
 35 Ser Asp Arg Lys Ala Val Glu Thr Pro Gly Phe Trp Gly Gly Glu Pro  
 130 135 140  
 Val Trp Asn Thr Ala Ala Arg Gln Gly Ile Arg Thr Gly Val Tyr Phe  
 145 150 155 160  
 Trp Val Gly Ser Glu Thr Ala Val Asn Gly Asn Arg Pro Trp Arg Trp  
 165 170 175  
 40 Lys Lys Phe Ser Ser Thr Val Pro Phe Arg Asp Arg Ala Asp Ser Val  
 180 185 190  
 Ile Ala Trp Leu Gly Leu Pro Glu Lys Glu Arg Pro Arg Leu Leu Met  
 195 200 205  
 45 Trp Tyr Ile Glu Glu Pro Asp Met Ile Gly His Ser Gln Thr Pro Glu  
 210 215 220  
 Ser Pro Leu Thr Leu Ala Met Val Glu Arg Leu Asp Ser Val Val Gly  
 225 230 235 240  
 Tyr Phe Arg Lys Arg Leu Asp Ser Leu Pro Ile Ala Ala Gln Thr Asp  
 245 250 255  
 50 Phe Ile Ile Val Ser Asp His Gly Met Ala Thr Tyr Glu Asn Glu Lys  
 260 265 270  
 Cys Val Asn Leu Ser His Tyr Leu Pro Ala Asp Ser Phe Leu Tyr Met  
 275 280 285  
 55 Ala Thr Gly Ala Phe Thr His Leu Tyr Pro Lys Pro Ser Tyr Thr Glu  
 290 295 300  
 Arg Ala Tyr Glu Ile Leu Arg Ala Ile Pro His Ile Ser Val Tyr Arg  
 305 310 315 320  
 Lys Gly Glu Val Pro Lys Arg Leu Arg Cys Gly Thr Asn Pro Arg Leu  
 325 330 335  
 60 Gly Glu Leu Val Val Ile Pro Asp Ile Gly Ser Thr Val Phe Phe Ala  
 340 345 350  
 Ile Asn Glu Asp Val Arg Pro Gly Ala Ala His Gly Tyr Asp Asn Gln  
 355 360 365  
 65 Ala Pro Glu Met Arg Ala Leu Leu Arg Ala Val Gly Pro Asp Phe Arg  
 370 375 380  
 Pro Gly Ser Arg Val Glu Asn Leu Pro Asn Ile Thr Ile Tyr Pro Leu  
 385 390 395 400  
 Ile Cys Arg Leu Leu Gly Ile Glu Pro Ala Pro Asn Asp Ala Asp Glu  
 405 410 415  
 70 Thr Leu Leu Asn Gly Leu Ile Arg Asp Lys Arg Pro  
 420 425

(2) INFORMATION FOR SEQ ID NO:272

75 (1) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 282 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear
- 5 (ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: YES
- 10 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Porphyromonas gingivalis*
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...282
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:272
- Leu Ser Arg Gly Val Phe Pro Leu Met Tyr Gly Arg Arg Gly Ser Ile  
1 5 10 15  
20 Arg Ala Ser Ser Gly His Arg Asp Lys Ile Phe Lys Asn Thr Ile Ile  
20 25 30  
Arg Phe Ile Thr Met Lys Val Gly Leu Phe Ile Pro Cys Tyr Val Asn  
35 40 45  
25 Ala Val Tyr Pro Glu Val Gly Ile Ala Thr Tyr Lys Leu Leu Lys Ser  
50 55 60  
Leu Asp Ile Asp Val Asp Tyr Pro Met Asp Gln Thr Cys Cys Gly Gln  
65 70 75 80  
Pro Met Ala Asn Ala Gly Phe Glu Gln Lys Ala Gln Lys Leu Ala Leu  
85 90 95  
30 Arg Phe Glu Glu Leu Phe Glu Ser Tyr Asp Val Val Val Gly Pro Ser  
100 105 110  
Ala Ser Cys Val Ala Phe Val Lys Glu Asn Tyr Asp His Ile Leu Arg  
115 120 125  
35 Pro Thr Gly His Val Cys Lys Ser Ala Ala Lys Val Arg Asp Ile Cys  
130 135 140  
Glu Phe Leu His Asp Asp Leu Lys Ile Thr Ser Leu Pro Ser Arg Phe  
145 150 155 160  
Ala His Lys Val Ser Leu His Asn Ser Cys His Gly Val Arg Glu Leu  
165 170 175  
40 His Leu Ser Thr Pro Ser Glu Val His Arg Pro Tyr His Asn Lys Val  
180 185 190  
Arg Arg Leu Leu Glu Met Val Gln Gly Ile Glu Val Phe Glu Pro Lys  
195 200 205  
45 Arg Ile Asp Glu Cys Cys Gly Phe Gly Gly Met Tyr Ser Val Glu Glu  
210 215 220  
Pro Glu Val Ser Thr Cys Met Gly His Asp Lys Val Leu Asp His Ile  
225 230 235 240  
Ser Thr Gly Ala Glu Tyr Ile Thr Gly Pro Asp Ser Ser Cys Leu Met  
245 250 255  
50 His Met Gln Gly Val Ile Asp Arg Glu Lys Leu Pro Ile Lys Thr Ile  
260 265 270  
His Ala Val Glu Ile Leu Ala Ala Asn Leu  
275 280
- 55 (2) INFORMATION FOR SEQ ID NO:273
- (1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 251 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear
- 60 (ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: YES
- 65 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Porphyromonas gingivalis*
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...251
- 70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:273
- 75 Pro Leu Lys Lys Arg Met Asp Ile Val Ser Met Ala Asp Lys Ala Leu

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1      5      10      15
Val Val Glu Met Arg Asp Val Thr Leu Cys Gln Glu Glu Asn Val Ile
20      25      30
5  Phe Gln Asn Leu Asn Leu Thr Leu Ser Ala Gly Asp Phe Val Tyr Leu
35      40      45
Ile Gly Ser Val Gly Ser Gly Lys Ser Thr Leu Leu Lys Ala Leu Tyr
50      55      60
Ala Glu Val Pro Ile Ser Ala Gly Tyr Ala Arg Val Ile Asp Tyr Asp
65      70      75      80
10 Leu Ala Lys Leu Lys Arg Lys Gln Leu Pro Tyr Leu Arg Arg Asn Leu
85      90      95
Gly Ile Val Phe Gln Asp Phe Gln Leu Leu Asn Gly Arg Thr Val Ala
100      105      110
15 Glu Asn Leu Asp Phe Val Leu Arg Ala Thr Asp Trp Lys Asn Arg Ala
115      120      125
Asp Arg Glu Gln Arg Ile Glu Glu Val Leu Thr Arg Val Gly Met Ser
130      135      140
Arg Lys Ala Tyr Lys Arg Pro His Glu Leu Ser Gly Gly Glu Gln Gln
145      150      155      160
20 Arg Val Gly Ile Ala Arg Ala Leu Leu Ala Lys Pro Ala Leu Ile Leu
165      170      175
Ala Asp Glu Pro Thr Gly Asn Leu Asp Ser Val Thr Gly Leu Gln Ile
180      185      190
25 Ala Ser Leu Leu Tyr Glu Ile Ser Lys Gln Gly Thr Ala Val Leu Met
195      200      205
Ser Thr His Asn Ser Ser Leu Leu Ser His Leu Pro Ala Arg Thr Leu
210      215      220
Ala Val Arg Lys Asn Gly Asp Ala Ser Ser Leu Val Glu Leu Ser Ala
225      230      235      240
30 Asp Ala Val Ser Arg Lys Asn Thr Glu Ile Asp
245

```

## (2) INFORMATION FOR SEQ ID NO:274

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 238 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 40 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 45 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Porphyromonas gingivalis*
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...238
- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:274

```

Thr Arg His Cys Pro Ala Cys Arg Ser Ser Phe His Leu Ile Lys Thr
1      5      10      15
55 Ser Lys Thr Met Ile Glu Ile Ser Asn Leu Thr Lys Val Phe Arg Thr
20      25      30
Glu Glu Ile Glu Thr Val Ala Leu Asp Gly Val Ser Leu Lys Val Asp
35      40      45
60 Lys Gly Glu Phe Ile Ala Ile Met Gly Pro Ser Gly Cys Gly Lys Ser
50      55      60
Thr Leu Leu Asn Ile Leu Gly Leu Leu Asp Asn Pro Thr Ser Gly Ile
65 Tyr Lys Leu Asp Gly Ala Glu Val Gly Asn Leu Arg Glu Lys Asp Arg
85      90      95
Thr Ala Val Arg Lys Gly Asn Ile Gly Phe Val Phe Gln Ser Phe Asn
100      105      110
Leu Ile Glu Glu Met Thr Val Ser Glu Asn Val Glu Leu Pro Leu Val
115      120      125
70 Tyr Leu Gly Val Lys Ala Ser Glu Arg Lys Glu Arg Val Glu Glu Ala
130      135      140
Leu Arg Lys Met Ser Ile Ser His Arg Ala Gly His Phe Pro Asn Gln
145      150      155      160
Leu Ser Gly Gly Gln Gln Arg Val Ala Ile Ala Arg Ala Val Val
165      170      175
75 Ala Asn Pro Lys Leu Ile Leu Ala Asp Glu Pro Thr Gly Asn Leu Asp

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180 185 190  
 Ser Lys Asn Gly Ala Asp Val Met Glu Leu Leu Arg Gly Leu Asn Arg  
 195 200 205  
 5 Glu Gly Ala Thr Ile Val Met Val Thr His Ser Glu His Asp Ala Arg  
 210 215 220  
 Ser Ala Gly Arg Ile Ile Asn Leu Phe Asp Gly Lys Ile Arg  
 225 230 235

(2) INFORMATION FOR SEQ ID NO:275  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 604 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...604  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:275

30 Ser Thr Glu Thr Asn Ser Lys Ser Glu Met Lys Glu Phe Phe Lys Met  
 1 5 10 15  
 Phe Phe Ala Ser Ile Leu Gly Val Ile Thr Ala Gly Ile Ile Leu Phe  
 20 25 30  
 Cys Ile Phe Leu Phe Ile Phe Phe Gly Ile Val Ala Gly Ile Ala Ser  
 35 35 40 45  
 Lys Ala Thr Gly Gly Thr Ile Pro Lys Ile Glu Ala Asn Ser Ile Leu  
 50 55 60  
 His Ile Unk Asn Ser Ser Phe Pro Glu Ile Val Ser Ala Asn Pro Trp  
 65 70 75 80  
 40 Ser Met Leu Thr Gly Lys Asp Glu Ser Val Ser Leu Ser Gln Ala Val  
 85 90 95  
 Glu Ala Ile Gly Gln Ala Lys Asn Asn Pro Asn Ile Thr Gly Ile Phe  
 100 105 110  
 Leu Asp Leu Asp Asn Leu Ser Val Gly Met Ala Ser Ala Glu Glu Leu  
 115 120 125  
 45 Arg Arg Ala Leu Gln Asp Phe Lys Met Ser Gly Lys Phe Val Val Ser  
 130 135 140  
 Tyr Ala Asp Arg Tyr Thr Gln Lys Gly Tyr Tyr Leu Ser Ser Ile Ala  
 145 150 155 160  
 50 Asp Lys Leu Tyr Leu Asn Pro Lys Gly Met Leu Gly Leu Ile Gly Ile  
 165 170 175  
 Ala Thr Gln Thr Met Phe Tyr Lys Asp Ala Leu Asp Lys Phe Gly Val  
 180 185 190  
 Lys Met Glu Ile Phe Lys Val Gly Thr Tyr Lys Ala Ala Val Glu Pro  
 195 200 205  
 55 Phe Met Leu Asn Arg Met Ser Asp Ala Asn Arg Glu Gln Ile Thr Thr  
 210 215 220  
 Tyr Ile Asn Gly Leu Trp Asp Lys Ile Thr Ser Asp Ile Ala Glu Ser  
 225 230 235 240  
 60 Arg Lys Thr Ala Met Asp Ser Val Lys Met Phe Ala Asp Lys Gly Glu  
 245 250 255  
 Met Phe Gly Leu Ala Glu Lys Ala Val Glu Met Lys Leu Val Asp Glu  
 260 265 270  
 Leu Ala Tyr Arg Thr Asp Val Glu Lys Glu Leu Lys Lys Met Ser Gln  
 275 280 285  
 65 Arg Gly Glu Lys Asp Glu Leu Arg Phe Val Ser Leu Ser Gln Val Leu  
 290 295 300  
 Ala Asn Gly Pro Met Asn Lys Thr Lys Gly Ser Arg Ile Ala Val Leu  
 305 310 315 320  
 70 Phe Ala Glu Gly Glu Ile Thr Glu Glu Ile Ile Lys Lys Pro Phe Asp  
 325 330 335  
 Thr Asp Gly Ser Ser Ile Thr Gln Glu Leu Ala Lys Glu Ile Lys Ala  
 340 345 350  
 Ala Ala Asp Asp Asp Asp Ile Lys Ala Val Val Leu Arg Val Asn Ser  
 355 360 365  
 75 Pro Gly Gly Ser Ala Phe Thr Ser Glu Gln Ile Trp Lys Gln Val Ala

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370 375 380  
 Asp Leu Lys Ala Lys Lys Pro Ile Val Val Ser Met Gly Asp Val Ala  
 385 390 395 400  
 5 Ala Ser Gly Gly Tyr Tyr Ile Ala Cys Ala Ala Asn Ser Ile Val Ala  
 405 410 415  
 Glu His Thr Thr Leu Thr Gly Ser Ile Gly Ile Phe Gly Met Phe Pro  
 420 425 430  
 Asn Phe Ala Gly Val Ala Lys Lys Ile Gly Val Asn Met Asp Val Val  
 435 440 445  
 10 Gln Thr Ser Lys Tyr Ala Asp Leu Gly Asn Thr Phe Ala Pro Met Thr  
 450 455 460  
 Val Glu Asp Arg Ala Leu Ile Gln Arg Tyr Ile Glu Gln Gly Tyr Asp  
 465 470 475 480  
 15 Leu Phe Leu Thr Arg Val Ser Glu Gly Arg Asn Arg Thr Lys Ala Gln  
 485 490 495  
 Ile Asp Ser Ile Ala Gln Gly Arg Val Trp Leu Gly Asp Lys Ala Leu  
 500 505 510  
 Ala Leu Gly Leu Val Asp Glu Leu Gly Gly Leu Asp Thr Ala Ile Lys  
 515 520 525  
 20 Arg Ala Ala Lys Leu Ala Gln Leu Gly Gly Asn Tyr Ser Ile Glu Tyr  
 530 535 540  
 Gly Lys Thr Lys Arg Asn Phe Phe Glu Glu Leu Ser Ser Ser Ala  
 545 550 555 560  
 25 Ala Asp Met Lys Ser Ala Ile Leu Ser Thr Ile Leu Ser Asp Pro Glu  
 565 570 575  
 Ile Glu Val Leu Arg Glu Leu Arg Ser Met Pro Pro Arg Pro Ser Gly  
 580 585 590  
 Ile Gln Ala Arg Leu Pro Tyr Tyr Phe Met Pro Tyr  
 595 600  
 30  
 (2) INFORMATION FOR SEQ ID NO:276  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 324 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 35  
 (ii) MOLECULE TYPE: protein  
 40  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 45  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...324  
 50  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:276  
 Leu Thr Leu Phe Cys Cys Asn Tyr Phe Lys Gln Met Arg Ala Asn Ile  
 1 5 10 15  
 Trp Gln Ile Leu Ser Val Ser Val Leu Phe Phe Phe Gly Thr Ala Ile  
 20 25 30  
 55 Gly Gln Ala Gln Ser Arg Asn Arg Thr Tyr Glu Ala Tyr Val Lys Gln  
 35 40 45  
 Tyr Ala Asp Glu Ala Ile Arg Gln Met Ser Arg Tyr Asn Ile Pro Ala  
 50 55 60  
 60 Ser Ile Thr Ile Ala Gln Ala Leu Val Glu Thr Gly Ala Gly Ala Ser  
 65 70 75 80  
 Thr Leu Ala Ser Val His Asn Asn His Phe Gly Ile Lys Cys His Lys  
 85 90 95  
 Ser Trp Thr Gly Lys Arg Thr Tyr Arg Thr Asp Asp Ala Pro Asn Glu  
 100 105 110  
 65 Cys Phe Arg Ser Tyr Ser Ala Ala Arg Glu Ser Tyr Glu Asp His Ser  
 115 120 125  
 Arg Phe Leu Leu Gln Pro Arg Tyr Arg Pro Leu Phe Lys Leu Asp Arg  
 130 135 140  
 70 Glu Asp Tyr Arg Gly Trp Ala Thr Gly Leu Gln Arg Cys Gly Tyr Ala  
 145 150 155 160  
 Thr Asn Arg Gly Tyr Ala Asn Leu Leu Ile Lys Met Val Glu Leu Tyr  
 165 170 175  
 Glu Leu Tyr Ala Leu Asp Arg Glu Lys Tyr Pro Ser Trp Phe His Lys  
 180 185 190  
 75 Ser Tyr Pro Gly Ser Asn Lys Lys Ser His Gln Thr Thr Lys Gln Lys

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195 200 205  
 Gln Ser Gly Leu Lys His Glu Ala Tyr Phe Ser Tyr Gly Leu Leu Tyr  
 210 215 220  
 Ile Ile Ala Lys Gln Gly Asp Thr Phe Asp Ser Leu Ala Glu Glu Phe  
 225 230 235 240  
 Asp Met Arg Ala Ser Lys Leu Ala Lys Tyr Asn Asp Ala Pro Val Asp  
 245 250 255  
 Phe Pro Ile Glu Lys Gly Asp Val Ile Tyr Leu Glu Lys Lys His Ala  
 260 265 270  
 10 Cys Ser Ile Ser Lys His Thr Gln His Val Val Arg Val Gly Asp Ser  
 275 280 285  
 Met His Ser Ile Ser Gln Arg Tyr Gly Ile Arg Met Lys Asn Leu Tyr  
 290 295 300  
 15 Lys Leu Asn Asp Lys Asp Gly Glu Tyr Ile Pro Gln Glu Gly Asp Ile  
 305 310 315 320  
 Leu Arg Leu Arg

## (2) INFORMATION FOR SEQ ID NO:277

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...533

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:277

40 Arg Ile Pro Asp Glu Gln Thr Gly Arg Ile Met Asp Gly Arg Arg Tyr  
 1 5 10 15  
 Ser Asp Gly Leu His Gln Ala Ile Glu Ala Lys Glu His Val Lys Val  
 20 25 30  
 Glu Ala Ala Thr Gln Thr Phe Ala Thr Ile Thr Leu Gln Asn Tyr Phe  
 35 40 45  
 45 Arg Met Tyr His Lys Leu Ala Gly Met Thr Gly Thr Ala Glu Thr Glu  
 50 55 60  
 Ala Gly Glu Leu Trp Asp Ile Tyr Lys Leu Asp Val Val Val Ile Pro  
 65 70 75 80  
 50 Thr Asn Lys Pro Ile Ala Arg Lys Asp Met Asn Asp Arg Ile Tyr Lys  
 85 90 95  
 Thr Ala Arg Glu Lys Tyr Ala Ala Val Ile Glu Glu Ile Val Arg Leu  
 100 105 110  
 Val Glu Glu Gly Arg Pro Val Leu Val Gly Thr Thr Ser Val Glu Ile  
 115 120 125  
 55 Ser Glu Leu Leu Ser Arg Met Leu Arg Leu Arg Gly Ile Gln His Asn  
 130 135 140  
 Val Leu Asn Ala Lys Leu His Gln Lys Glu Ala Glu Ile Val Ala Gln  
 145 150 155 160  
 60 Ala Gly Gln Lys Gly Thr Val Thr Ile Ala Thr Asn Met Ala Gly Arg  
 165 170 175  
 Gly Thr Asp Ile Lys Leu Ser Ala Glu Val Lys Lys Ala Gly Gly Leu  
 180 185 190  
 Ala Ile Ile Gly Thr Glu Arg His Glu Ser Arg Arg Val Asp Arg Gln  
 195 200 205  
 65 Leu Arg Gly Arg Ser Gly Arg Gln Gly Asp Pro Gly Ser Ser Ile Phe  
 210 215 220  
 Tyr Val Ser Leu Glu Asp His Leu Met Arg Leu Phe Ala Thr Glu Lys  
 225 230 235 240  
 Ile Ala Ser Leu Met Asp Arg Leu Gly Phe Lys Glu Gly Glu Val Leu  
 245 250 255  
 70 Glu Asn Asn Met Leu Ser Lys Ser Val Glu Arg Ala Gln Lys Lys Val  
 260 265 270  
 Glu Glu Asn Asn Phe Gly Ile Arg Lys His Leu Leu Glu Tyr Asp Asp  
 275 280 285  
 75 Val Met Asn Ser Gln Arg Glu Val Ile Tyr Thr Arg Arg Arg His Ala

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290 295 300  
 Leu Met Gly Glu Arg Ile Gly Met Asp Val Leu Asn Thr Ile Tyr Asp  
 305 310 315 320  
 Val Cys Lys Ala Leu Ile Asp Asn Tyr Ala Glu Ala Asn Asp Phe Glu  
 325 330 335  
 5 Gly Phe Lys Glu Asp Leu Met Arg Ala Leu Ala Ile Glu Ser Pro Ile  
 340 345 350  
 Thr Gln Glu Ile Phe Arg Gly Lys Lys Ala Glu Glu Leu Thr Asp Met  
 355 360 365  
 10 Leu Phe Asp Glu Ala Tyr Lys Ser Phe Gln Arg Lys Met Asp Leu Ile  
 370 375 380  
 Ala Glu Val Ala His Pro Val Val His Gln Val Phe Glu Thr Gln Ala  
 385 390 395 400  
 15 Ala Val Tyr Glu Arg Ile Leu Ile Pro Ile Thr Asp Gly Lys Arg Val  
 405 410 415  
 Tyr Asn Ile Gly Cys Asn Leu Arg Glu Ala Asp Glu Thr Gln Gly Lys  
 420 425 430  
 Ser Ile Ile Lys Glu Phe Glu Lys Ala Ile Val Leu His Thr Ile Asp  
 435 440 445  
 20 Glu Ser Trp Lys Glu His Leu Arg Glu Met Asp Glu Leu Arg Asn Ser  
 450 455 460  
 Val Gln Asn Ala Ser Tyr Glu Asn Lys Asp Pro Leu Leu Ile Tyr Lys  
 465 470 475 480  
 25 Leu Glu Ser Tyr Glu Leu Phe Arg Lys Met Val Glu Ala Met Asn Arg  
 485 490 495  
 Lys Thr Val Ala Ile Leu Met Arg Ala Arg Ile Pro Val Pro Glu Ala  
 500 505 510  
 Pro Ser Gln Glu Glu Leu Glu His Arg Arg Gln Ile Glu Ile Arg His  
 515 520 525  
 30 Ala Thr Gln Gln Arg  
 530

(2) INFORMATION FOR SEQ ID NO:278

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 720 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 40 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 45 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...720  
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:278

Lys Ser Cys Arg Val Ile Gly Gln Thr Arg Arg Tyr Gly Cys Cys Pro  
 1 5 10 15  
 55 Val Gly Leu Arg Pro Cys His Gln Ser Leu Ser Gly Val Cys Arg Cys  
 20 25 30  
 Leu Phe Gln Ser Arg Pro Ala Val Ala Phe Ala Arg Lys Gly Gln Arg  
 35 40 45  
 60 Arg His Arg Arg Ser Glu Ser Gly Arg Arg Ile Arg Ala Leu Gln Gly  
 50 55 60  
 Val Gln His His Gln Thr Asn Glu His Glu Val Met Ile Ser Val Asn  
 65 70 75 80  
 Asn Leu Thr Val Asp Phe Gly Thr Arg Leu Leu Phe Asp Gln Val Ser  
 85 90 95  
 65 Phe Val Ile Asn Arg Arg Asp Arg Ile Ala Leu Val Gly Lys Asn Gly  
 100 105 110  
 Ala Gly Lys Ser Thr Leu Leu Lys Leu Ile Ala Gly Met Glu Glu Pro  
 115 120 125  
 70 Thr Ser Gly His Ile Ala Arg Pro Lys Gly Ile Arg Ile Gly Tyr Leu  
 130 135 140  
 Pro Gln Val Met Arg Leu Gln Asp Gly His Thr Val Tyr Glu Glu Val  
 145 150 155 160  
 Glu Gln Ala Phe Asn Asp Ile Arg Gln Ile Glu Glu Glu Ile Arg Arg  
 165 170 175  
 75 Leu Ser Asp Glu Met Ala Gly Arg Thr Asp Tyr Glu Ser Asp Asp Tyr

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180 185 190  
 Ile Arg Leu Ile Glu His Tyr Thr Asn Met Ser Glu Thr Leu Ser Leu  
 195 200 205  
 Met Gln Gln Gly Asn Tyr His Ala Ala Ile Glu Gln Thr Leu Ile Gly  
 210 215 220  
 Leu Gly Phe Gly Arg Glu Asp Phe His Arg Pro Thr Ala Asp Phe Ser  
 225 230 235 240  
 Gly Gly Trp Arg Met Arg Ile Glu Leu Ala Lys Leu Leu Gln Arg  
 245 250 255  
 Pro Glu Val Leu Leu Leu Asp Glu Pro Thr Asn His Leu Asp Ile Glu  
 260 265 270  
 Ser Ile Gly Trp Leu Glu Gln Phe Ile Ala Thr Asn Ala Gly Ala Val  
 275 280 285  
 Ile Leu Val Ser His Asp Arg Ala Phe Ile Asp Asn Thr Thr Thr Arg  
 290 295 300  
 Thr Ile Glu Ile Glu Leu Gly His Ile Tyr Asp Tyr Lys Thr Asn Tyr  
 305 310 315 320  
 Ser His Tyr Val Glu Leu Arg Glu Glu Arg Leu Arg Gln Gln Met Arg  
 325 330 335  
 Ala Tyr Glu Asn Gln Gln Lys Met Ile Arg Asp Thr Glu Asp Phe Ile  
 340 345 350  
 Glu Arg Phe Arg Tyr Lys Ala Thr Lys Ser Val Gln Val Gln Ser Arg  
 355 360 365  
 Ile Lys Gln Leu Glu Lys Val Glu Arg Val Glu Ile Asp Glu Arg Asp  
 370 375 380  
 Arg Ser Ala Phe His Phe Arg Phe Ile Pro Ala Gln Pro Ser Gly Ser  
 385 390 395 400  
 Tyr Pro Leu Ile Val Asp Asp Leu Ala Lys Ala Tyr Gly Asp His Gln  
 405 410 415  
 Val Phe Ser Gly Ala Thr Tyr Thr Ile Glu Arg Gly Glu Lys Val Ala  
 420 425 430  
 Phe Val Gly Lys Asn Gly Ala Gly Lys Ser Thr Met Val Lys Cys Ile  
 435 440 445  
 Met Gly Glu Leu Thr Asp Tyr Thr Gly Lys Leu Glu Leu Gly His Asn  
 450 455 460  
 Val Gln Leu Gly Tyr Phe Ala Gln Asn Glu Ala Gln Glu Leu Arg Gly  
 465 470 475 480  
 Asp Leu Thr Val Phe Asp Thr Ile Asp Arg Glu Ala Val Gly Asp Ile  
 485 490 495  
 Arg Leu Arg Leu Asn Asp Leu Leu Gly Ala Phe Leu Phe Gly Gly Glu  
 500 505 510  
 Ala Ser Glu Lys Lys Val Ser Val Leu Ser Gly Gly Glu Arg Ala Arg  
 515 520 525  
 Leu Ala Ile Ile Arg Leu Leu Leu Gln Pro Ala Asn Phe Leu Ile Leu  
 530 535 540  
 Asp Glu Pro Thr Asn His Leu Asp Met Arg Ser Lys Asp Val Leu Lys  
 545 550 555 560  
 Glu Ala Ile Lys Asn Phe Asp Gly Thr Val Ile Val Val Ser His Asp  
 565 570 575  
 Arg Glu Phe Leu Asp Gly Leu Val Ser Lys Val Tyr Glu Phe Ala Asp  
 580 585 590  
 Gly Gln Val Asn Glu His Leu Gly Gly Ile Tyr Asp Tyr Leu Arg Thr  
 595 600 605  
 Arg Arg Met Gln Thr Leu Thr Glu Leu Glu Arg Thr Thr Thr Ile Glu  
 610 615 620  
 Thr Lys Thr Thr Arg Glu Ala Ile Pro Glu Thr Glu Ala Lys Ala Asp  
 625 630 635 640  
 Tyr Arg Arg Gln Lys Glu Val Ala Lys Gln Leu Arg Thr Leu Glu Arg  
 645 650 655  
 Thr Val Ala Thr Cys Glu Glu Arg Ile Gly Lys Leu Glu Ser Glu Leu  
 660 665 670  
 Gln Ala Ile Glu Met Leu Leu Gln Asp Pro Lys His Ala Thr Asp Ala  
 675 680 685  
 Asn Leu Phe Glu Arg Tyr Ala Gly Met Lys Gln Glu Leu Glu Lys Ala  
 690 695 700  
 Met Glu Asp Trp Glu Gln Ala Ser Glu Ala Leu Ser Glu Ala Gln Gly  
 705 710 715 720

(2) INFORMATION FOR SEQ ID NO:279

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 386 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear



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- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 5 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Porphyromonas gingivalis*
- (ix) FEATURE:  
(A) NAME/KEY: misc feature  
10 (B) LOCATION 1...386
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:279
- 15 Tyr Leu Lys Leu Leu Ile Leu Gln Ile Ala Leu Met Asn Phe Leu Lys  
1 5 10 15  
Lys Glu Pro Phe Lys Ile Phe Ser Met Ile Tyr Leu Leu Asp Thr  
20 25 30  
Ile Thr Asn Arg Ala Gly Thr Glu Arg Ala Val Ile Asn Leu Ala Asn  
35 40 45  
20 Asn Leu His Ala Asn Gly His Arg Val Ser Leu Val Ser Val Cys Thr  
50 55 60  
Lys Glu Gly Glu Pro Ser Phe Gln Val Glu Lys Gly Ile Glu Val His  
65 70 75 80  
25 His Leu Gly Ile Arg Leu Tyr Gly Asn Ala Leu Ala Arg Lys Thr Val  
85 90 95  
Tyr Phe Lys Ala Tyr Arg Arg Ile Lys Ala Leu Tyr Lys Lys Arg Glu  
100 105 110  
30 Pro Val Leu Leu Ile Gly Thr Asn Ile Phe Ile Asn Thr Ile Leu Ser  
115 120 125  
Gln Ile Ser Asn Arg Gly Arg Ile Phe Thr Ile Gly Cys Glu His Ile  
130 135 140  
Ser Tyr Asp Ile Ala Arg Pro Ile Thr Lys Arg Ile Arg Gly Phe Leu  
145 150 155 160  
35 Tyr Ser Gly Leu Asp Ala Val Val Ala Leu Thr Lys Arg Asp Gln Gln  
165 170 175  
Ser Phe Glu Ala Ile Leu Arg Gly Arg Ser Lys Ala Tyr Val Ile Pro  
180 185 190  
Asn Gln Val Ser Phe Thr Thr Val Gln Arg Asp Ala Thr Thr His Lys  
195 200 205  
40 Gln Met Leu Ala Ile Gly Arg Leu Thr Tyr Gln Lys Gly Phe Glu Phe  
210 215 220  
Met Ile Glu Asp Ala Ser Arg Val Leu Arg Glu Arg Pro Asp Trp Lys  
225 230 235 240  
45 Leu Ile Ile Val Gly Asp Gly Glu Asn Glu Ser Met Leu Arg Lys Glu  
245 250 255  
Ile Ala Ser Arg Asn Met Glu Ser Gln Ile Glu Ile His Pro Ser Thr  
260 265 270  
Pro Glu Ile Arg Lys Tyr Tyr Glu Ser Ser Ala Ile Tyr Leu Met Thr  
275 280 285  
50 Ser Arg Phe Glu Gly Leu Pro Met Val Leu Leu Glu Ala Glu Ala Tyr  
290 295 300  
Ala Leu Pro Ile Ile Ser Tyr Asp Cys Pro Thr Gly Pro Arg Glu Leu  
305 310 315 320  
55 Ile Glu Asn Gly Arg Asn Gly Phe Leu Val Pro Met Glu Ala His Glu  
325 330 335  
Asp Phe Ala Asp Lys Leu Arg Leu Leu Met Asp Asp Glu Thr Leu Arg  
340 345 350  
Lys Lys Met Gly Gln Glu Ser Glu Leu Met Val Lys Ser Tyr Ser Pro  
355 360 365  
60 Ala Asn Ile Tyr Glu Cys Trp Lys Lys Leu Phe Val Glu Ile Gly Tyr  
370 375 380  
Met Asn  
385
- 65 (2) INFORMATION FOR SEQ ID NO:280
- (1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 655 amino acids  
70 (B) TYPE: amino acid  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 75

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## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...655

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:280

10 Thr Thr Lys Glu Asn Glu Thr Thr Thr Lys Asn Glu Tyr Arg Ile Met  
 1 5 10 15  
 Gly Lys Ile Ile Gly Ile Asp Leu Gly Thr Thr Asn Ser Cys Val Ser  
 20 25 30  
 15 Val Leu Glu Gly Asn Glu Pro Ile Val Ile Thr Asn Ser Glu Gly Lys  
 35 40 45  
 Arg Thr Thr Pro Ser Val Val Ala Phe Val Asp Gly Gly Glu Arg Lys  
 50 55 60  
 Val Gly Asp Pro Ala Lys Arg Gln Ala Ile Thr Asn Pro Thr Lys Thr  
 65 70 75 80  
 20 Ile Tyr Ser Ile Lys Arg Phe Met Gly Glu Thr Tyr Asp Gln Val Ser  
 85 90 95  
 Arg Glu Val Glu Arg Val Pro Phe Lys Val Val Arg Gly Asp Asn Asn  
 100 105 110  
 25 Thr Pro Arg Val Asp Ile Asp Gly Arg Leu Tyr Thr Pro Gln Glu Ile  
 115 120 125  
 Ser Ala Met Ile Leu Gln Lys Met Lys Lys Thr Ala Glu Asp Tyr Leu  
 130 135 140  
 Gly Gln Glu Val Thr Glu Ala Val Ile Thr Val Pro Ala Tyr Phe Asn  
 145 150 155 160  
 30 Asp Ala Gln Arg Gln Ala Thr Lys Glu Ala Gly Glu Ile Ala Gly Leu  
 165 170 175  
 Lys Val Arg Arg Ile Val Asn Glu Pro Thr Ala Ala Ser Leu Ala Tyr  
 180 185 190  
 35 Gly Leu Asp Lys Ser Asn Lys Asp Met Lys Ile Ala Val Phe Asp Leu  
 195 200 205  
 Gly Gly Gly Thr Phe Asp Ile Ser Ile Leu Glu Leu Gly Asp Gly Val  
 210 215 220  
 Phe Glu Val Lys Ser Thr Asn Gly Asp Thr His Leu Gly Gly Asp Asp  
 225 230 235 240  
 40 Phe Asp His Val Ile Ile Asp Trp Leu Ala Glu Glu Phe Lys Ser Gln  
 245 250 255  
 Glu Gly Val Asp Leu Arg Gln Asp Pro Met Ala Met Gln Arg Leu Lys  
 260 265 270  
 45 Glu Ala Ala Glu Lys Ala Lys Ile Glu Leu Ser Ser Thr Ser Ser Thr  
 275 280 285  
 Glu Ile Asn Leu Pro Tyr Ile Met Pro Val Asn Gly Ile Pro Lys His  
 290 295 300  
 Leu Val Met Thr Leu Thr Arg Ala Lys Phe Glu Gln Leu Ala Asp Arg  
 305 310 315 320  
 50 Leu Ile Gln Ala Cys Val Ala Pro Cys Glu Thr Ala Leu Lys Asp Ala  
 325 330 335  
 Gly Met Ser Arg Gly Asp Ile Asp Glu Val Ile Leu Val Gly Gly Ser  
 340 345 350  
 55 Thr Arg Ile Pro Ala Ile Gln Glu Ile Val Glu Lys Ile Phe Gly Lys  
 355 360 365  
 Ala Pro Ser Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala  
 370 375 380  
 Ala Ile Gln Gly Gly Val Leu Thr Gly Glu Val Lys Asp Val Leu Leu  
 385 390 395 400  
 60 Leu Asp Val Thr Pro Leu Ser Leu Gly Ile Glu Thr Met Gly Gly Val  
 405 410 415  
 Met Thr Arg Leu Ile Asp Ala Asn Thr Thr Ile Pro Thr Lys Lys Ser  
 420 425 430  
 65 Glu Ile Phe Thr Thr Ala Val Asp Asn Gln Pro Ser Val Glu Ile His  
 435 440 445  
 Val Leu Gln Gly Glu Arg Ser Leu Ala Lys Asp Asn Lys Ser Ile Gly  
 450 455 460  
 Arg Phe Asn Leu Asp Gly Ile Ala Pro Ala Pro Arg Gln Thr Pro Gln  
 465 470 475 480  
 70 Ile Glu Val Thr Phe Asp Ile Asp Ala Asn Gly Ile Leu Asn Val Thr  
 485 490 495  
 Ala His Asp Lys Ala Thr Gly Lys Lys Gln Asn Ile Arg Ile Glu Ala  
 500 505 510  
 75 Ser Ser Gly Leu Ser Asp Asp Glu Ile Lys Arg Met Lys Glu Glu Ala  
 515 520 525

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Gln Ala Asn Ala Glu Ala Asp Lys Lys Glu Lys Glu Arg Ile Asp Lys  
 530 535 540  
 Ile Asn Gln Ala Asp Ser Met Ile Phe Gln Thr Glu Lys Gln Leu Lys  
 545 550 555 560  
 5 Glu Leu Gly Asp Lys Phe Pro Ala Asp Lys Lys Ala Pro Ile Asp Thr  
 565 570 575  
 Ala Leu Asp Lys Leu Lys Glu Ala His Lys Ala Gln Asp Val Ala Ala  
 580 585 590  
 10 Ile Asp Thr Ala Met Ala Glu Leu Gln Thr Ala Leu Ser Ala Ala Gly  
 595 600 605  
 Glu Glu Leu Tyr Lys Asn Ala Gly Ala Ala Gln Gly Gly Ala Gln Pro  
 610 615 620  
 Gly Pro Asp Phe Gly Gly Ala Gln Gly Pro Ser Ala Gly Asp Gln Pro  
 625 630 635 640  
 15 Ser Asp Asp Lys Asn Val Thr Asp Val Asp Phe Glu Glu Val Lys  
 645 650 655

(2) INFORMATION FOR SEQ ID NO:281

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 467 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 25 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...467  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:281

Lys Trp Ala Arg Thr Thr Thr Leu Arg Ile Ser Asn Ala Thr Ile Tyr  
 1 5 10 15  
 40 Lys Thr Met Arg Tyr Asp Leu Ala Ile Ile Gly Gly Gly Pro Ala Gly  
 20 25 30  
 Tyr Thr Ala Ala Glu Arg Ala Ala Lys Gly Gly Leu Lys Thr Leu Leu  
 35 40 45  
 45 Ile Glu Lys Asn Ala Leu Gly Gly Val Cys Leu Asn Glu Gly Cys Ile  
 50 55 60  
 Pro Thr Lys Thr Leu Leu Tyr Ser Ala Lys Val Leu His Gln Ile Ala  
 65 70 75 80  
 Thr Ala Ser Lys Tyr Ala Val Ser Gly Thr Ala Asp Gly Leu Asp Leu  
 85 90 95  
 50 Gly Lys Val Ile Ala Arg Lys Gly Lys Ile Ile Arg Lys Leu Thr Ala  
 100 105 110  
 Gly Ile Arg Ser Arg Leu Thr Glu Ala Gly Val Glu Met Val Thr Ala  
 115 120 125  
 55 Glu Ala Thr Val Thr Gly Cys Asp Ala Asp Gly Ile Ile Gly Ile Thr  
 130 135 140  
 Ala Gly Glu Ala Gln Tyr Lys Ala Ala Asn Leu Leu Cys Thr Gly  
 145 150 155 160  
 Ser Glu Thr Phe Ile Pro Pro Ile Pro Gly Val Glu Gln Thr Glu Tyr  
 165 170 175  
 60 Trp Thr Asn Arg Glu Ala Leu Gln Asn Lys Glu Ile Pro Thr Ser Leu  
 180 185 190  
 Val Ile Ile Gly Gly Gly Val Ile Gly Met Glu Phe Ala Ser Phe Phe  
 195 200 205  
 65 Asn Gly Ile Gly Thr Gln Val His Val Val Glu Met Leu Pro Glu Ile  
 210 215 220  
 Leu Asn Gly Ile Asp Pro Glu His Ala Ala Met Leu Arg Ala His Tyr  
 225 230 235 240  
 Glu Lys Glu Gly Ile Lys Phe Tyr Leu Gly His Lys Val Thr Ser Val  
 245 250 255  
 70 Arg Asn Gly Ala Val Thr Val Glu Tyr Glu Gly Glu Ser Lys Glu Ile  
 260 265 270  
 Glu Gly Glu Arg Ile Leu Met Ser Val Gly Arg Arg Pro Val Leu Gln  
 275 280 285  
 75 Gly Phe Glu Ser Leu Gly Leu Val Leu Ala Gly Lys Gly Val Lys Thr  
 290 295 300

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Asn Glu Arg Met Gln Thr Ser Leu Pro Asn Val Tyr Ala Ala Gly Asp  
 305 310 315 320  
 Ile Thr Gly Phe Ser Leu Leu Ala His Thr Ala Val Arg Glu Ala Glu  
 325 330 335  
 5 Val Ala Val Asp Gln Ile Leu Gly Lys Thr Asp Glu Thr Met Ser Tyr  
 340 345 350  
 Arg Ala Val Pro Gly Val Val Tyr Thr Asn Pro Glu Val Ala Gly Val  
 355 360 365  
 10 Gly Glu Thr Glu Glu Ser Leu Arg Lys Ala Gly Arg Ala Tyr Thr Val  
 370 375 380  
 Arg Arg Leu Pro Met Ala Phe Ser Gly Arg Phe Val Ala Glu Asn Glu  
 385 390 395 400  
 Gln Gly Asn Gly Glu Cys Lys Leu Leu Leu Asp Glu Glu Asn Arg Leu  
 405 410 415  
 15 Ile Gly Ala His Leu Ile Gly Asn Pro Ala Gly Glu Leu Ile Val Thr  
 420 425 430  
 Ala Ala Met Ala Ile Glu Thr Gly Met Thr Asp Arg Gln Ile Glu Arg  
 435 440 445  
 20 Ile Ile Phe Pro His Pro Thr Val Gly Glu Ile Leu Lys Glu Thr Leu  
 450 455 460  
 Ala Gly Gly  
 465

(2) INFORMATION FOR SEQ ID NO:282  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 945 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...945  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:282

45 Pro Lys Ile Leu Met Glu Leu Lys Arg Phe Leu Ser Leu Gly Leu Leu  
 1 5 10 15  
 Leu Val Gly Phe Ile Pro Met Lys Leu Ser Ala Gln Gln Ala Gln Pro  
 20 25 30  
 Leu Pro Thr Asp Pro Ala Val Arg Val Gly Lys Leu Asp Asn Gly Leu  
 35 40 45  
 50 Thr Tyr Phe Ile Arg His Asn Glu Asn Pro Lys Asp Arg Ala Asp Phe  
 50 55 60  
 Phe Ile Ala Gln Lys Val Gly Ser Ile Leu Glu Asp Ser Gln Ser  
 65 70 75 80  
 55 Gly Leu Ala His Phe Leu Glu His Met Ala Phe Asn Gly Thr Lys Asn  
 85 90 95  
 Phe Pro Gly Lys Asn Leu Ile Asn Tyr Leu Glu Thr Ile Gly Val Arg  
 100 105 110  
 Phe Gly Gln Asn Leu Asn Ala Ser Thr Gly Phe Asp Lys Thr Glu Tyr  
 115 120 125  
 60 Thr Ile Met Asp Val Pro Thr Thr Arg Gln Gly Ile Ile Asp Ser Cys  
 130 135 140  
 Leu Leu Ile Leu His Asp Trp Ser Asn Asn Ile Thr Leu Asp Gly His  
 145 150 155 160  
 65 Glu Ile Asp Glu Glu Arg Gly Val Ile Gln Glu Glu Trp Arg Ala Arg  
 165 170 175  
 Arg Asp Ala Asn Leu Arg Met Phe Glu Ala Ile Leu Ala Lys Ala Met  
 180 185 190  
 Pro Gly Asn Lys Tyr Ala Glu Arg Met Pro Ile Gly Leu Met Asp Val  
 195 200 205  
 70 Val Leu Asn Phe Lys His Asp Glu Leu Arg Asn Tyr Tyr Lys Lys Trp  
 210 215 220  
 Tyr Arg Pro Asp Leu Gln Gly Leu Val Ile Val Gly Asp Ile Asp Val  
 225 230 235 240  
 75 Asp Tyr Val Glu Asn Lys Ile Lys Glu Leu Phe Lys Asp Val Pro Ala  
 245 250 255

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Pro Val Asn Pro Ala Glu Arg Ile Tyr Thr Pro Val Glu Asp Asn Asp  
 260 265 270  
 Glu Pro Ile Val Ala Ile Ala Thr Asp Ala Glu Ala Thr Thr Thr Gln  
 275 280 285  
 5 Leu Ser Ile Ser Phe Lys Ser Asp Pro Thr Pro Gln Glu Val Arg Gly  
 290 295 300  
 Ser Ile Phe Gly Leu Val Glu Asp Tyr Met Lys Gln Val Ile Thr Thr  
 305 310 315 320  
 10 Ala Val Asn Glu Arg Leu Ser Glu Ile Thr His Lys Pro Asn Ala Pro  
 325 330 335  
 Phe Leu Ser Ala Gly Ala Phe Phe Ser Asn Phe Met Tyr Ile Thr Gln  
 340 345 350  
 Thr Lys Asp Ala Phe Asn Phe Val Ala Thr Val Arg Glu Gly Glu Ala  
 355 360 365  
 15 Glu Lys Ala Met Asn Ala Leu Val Ala Glu Ile Glu Ser Leu Arg Gln  
 370 375 380  
 Phe Gly Ile Thr Lys Gly Glu Tyr Asp Arg Ala Arg Thr Asn Val Leu  
 385 390 395 400  
 20 Lys Arg Tyr Glu Asn Gln Tyr Asn Glu Arg Asp Lys Arg Lys Asn Asn  
 405 410 415  
 Ala Tyr Ala Asn Glu Tyr Ser Thr Tyr Phe Thr Asp Gly Gly Tyr Ile  
 420 425 430  
 Pro Gly Ile Glu Val Glu Tyr Gln Thr Val Asn Ala Phe Ala Pro Gln  
 435 440 445  
 25 Val Pro Leu Glu Ala Phe Asn Gln Ala Ile Ala Gln Met Ile Asp Pro  
 450 455 460  
 Val Lys Asn Ala Val Val Thr Leu Thr Gly Pro Ser Lys Ala Glu Ala  
 465 470 475 480  
 30 Lys Ile Pro Ser Glu Ala Asp Phe Leu Ala Ala Phe Lys Ala Ala Arg  
 485 490 495  
 Gln Gln Lys Val Glu Ala Lys Lys Asp Glu Val Ser Asp Gln Lys Leu  
 500 505 510  
 Met Glu Lys Ala Pro Lys Ala Gly Lys Ile Val Ser Glu Lys Lys Asp  
 515 520 525  
 35 Gln Lys Phe Gly Thr Thr Glu Leu Thr Leu Ser Asn Gly Ile Lys Val  
 530 535 540  
 Tyr Leu Lys Lys Thr Asp Phe Lys Ser Asn Glu Ile Leu Met Ser Ala  
 545 550 555 560  
 40 Leu Ser Pro Gly Gly Ile Leu Ser Gly Lys His Ala Pro Asn Gln Ser  
 565 570 575  
 Val Met Asn Ser Phe Met Asn Val Gly Gly Leu Gly Asn Phe Asp Ala  
 580 585 590  
 Ile Gln Leu Asp Lys Val Leu Thr Gly Arg Ser Ala Ser Val Ser Pro  
 595 600 605  
 45 Ser Leu Ser Leu Leu Ser Glu Gly Leu Ser Gly Lys Thr Thr Val Glu  
 610 615 620  
 Asp Met Glu Thr Phe Phe Gln Leu Ile Tyr Leu Gln Met Thr Ala Asn  
 625 630 635 640  
 50 Arg Lys Asp Pro Glu Ala Phe Lys Ala Thr Gln Glu Lys Leu Tyr Asn  
 645 650 655  
 Asn Leu Lys Asn Gln Glu Ala Asn Pro Met Ala Ala Leu Met Asp Ser  
 660 665 670  
 Ile Arg His Thr Met Tyr Gly Asp Asn Pro Met Met Lys Pro Met Lys  
 675 680 685  
 55 Ala Ala Asp Val Glu Lys Val Asn Tyr Asp Gln Val Met Ala Phe Tyr  
 690 695 700  
 Asn Glu Arg Phe Ala Asp Ala Gly Asp Phe Met Phe Phe Ile Gly  
 705 710 715 720  
 60 Asn Leu Asp Glu Ala Lys Met Lys Pro Leu Ile Glu Thr Tyr Leu Ala  
 725 730 735  
 Ser Leu Pro Asn Leu Lys Arg Gly Asp Lys Met Asn Lys Ala Gln Val  
 740 745 750  
 Pro Ala Ala Arg Ser Gly Lys Ile Asp Cys Lys Phe Glu Lys Glu Met  
 755 760 765  
 65 Asp Thr Pro Ser Thr Thr Ile Phe Asp Val Val Ser Gly Asn Val Glu  
 770 775 780  
 Tyr Thr Leu Lys Asn Ser Leu Leu Leu Glu Val Phe Ser Ala Val Met  
 785 790 795 800  
 70 Asp Gln Val Tyr Thr Ala Thr Val Arg Glu Lys Glu Gly Gly Ala Tyr  
 805 810 815  
 Ser Val Ala Ala Phe Gly Gly Leu Glu Gln Tyr Pro Gln Pro Lys Ala  
 820 825 830  
 Leu Met Gln Ile Tyr Phe Pro Thr Asp Pro Ala Arg Ala Glu Glu Met  
 835 840 845  
 75 Asn Ala Ile Val Phe Ala Glu Leu Glu Lys Leu Ala Lys Glu Gly Pro

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850 855 860  
 Asn Val Glu Tyr Phe Lys Lys Thr Ile Glu Asn Leu Asn Lys Gln His  
 865 870 875 880  
 Lys Glu Ser Leu Arg Glu Asn Arg Phe Trp Leu Glu Ala Met Lys Ala  
 5 885 890 895  
 Ser Phe Phe Glu Gly Asn Asp Phe Ile Thr Asp Tyr Glu Ser Val Leu  
 900 905 910  
 Asn Gly Leu Thr Pro Ala Glu Leu Gln Lys Phe Ala Ala Asp Leu Leu  
 915 920 925  
 10 Lys Gln Gln Asn Arg Val Val Val Met Met Ala Pro Val Ala Lys Ala  
 930 935 940  
 Gln  
 945  
 15 (2) INFORMATION FOR SEQ ID NO:283  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 686 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 20 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 25 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...686  
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:283  
 35 Tyr Thr Met Ser Lys Lys Gly Thr Ile Gly Val Thr Ser Asp Asn Ile  
 1 5 10 15  
 Phe Pro Val Ile Lys Lys Phe Leu Tyr Ser Asp His Glu Ile Phe Leu  
 20 25 30  
 40 Arg Glu Ile Val Ser Asn Ala Val Asp Ala Thr Gln Lys Leu Lys Thr  
 35 40 45  
 Leu Thr Ser Val Gly Glu Phe Lys Gly Glu Thr Gly Asp Leu Arg Val  
 50 55 60  
 Thr Val Ser Val Asp Glu Val Ala Arg Thr Ile Thr Val Ser Asp Arg  
 65 70 75 80  
 45 Gly Val Gly Met Thr Glu Glu Glu Val Glu Lys Tyr Ile Asn Gln Ile  
 85 90 95  
 Ala Phe Ser Ser Ala Glu Glu Phe Leu Glu Lys Tyr Lys Asp Asp Lys  
 100 105 110  
 50 Ala Ala Ile Ile Gly His Phe Gly Leu Gly Phe Tyr Ser Ala Phe Met  
 115 120 125  
 Val Ser Glu Arg Val Asp Val Ile Thr Arg Ser Phe Arg Glu Asp Ala  
 130 135 140  
 Thr Ala Val Lys Trp Ser Cys Asp Gly Ser Pro Glu Tyr Thr Leu Glu  
 145 150 155 160  
 55 Pro Ala Asp Lys Ala Asp Arg Gly Thr Asp Ile Val Met His Ile Asp  
 165 170 175  
 Glu Glu Asn Ser Glu Phe Leu Lys Lys Glu Lys Ile Glu Gly Leu Leu  
 180 185 190  
 Gly Lys Tyr Cys Lys Phe Leu Thr Val Pro Ile Ile Phe Gly Lys Lys  
 195 200 205  
 60 Gln Glu Trp Lys Asp Gly Lys Met Gln Asp Thr Asp Glu Asp Asn Gln  
 210 215 220  
 Ile Asn Asp Thr His Pro Ala Trp Thr Lys Lys Pro Ala Asp Leu Lys  
 225 230 235 240  
 65 Asp Glu Asp Tyr Lys Glu Phe Tyr Arg Ser Leu Tyr Pro Met Ser Glu  
 245 250 255  
 Glu Pro Leu Phe Trp Ile His Leu Asn Val Asp Tyr Pro Phe Asn Leu  
 260 265 270  
 70 Thr Gly Ile Leu Tyr Phe Pro Lys Ile Lys Asn Asn Leu Asp Leu Gln  
 275 280 285  
 Arg Asn Lys Ile Gln Leu Tyr Cys Asn Gln Val Tyr Val Thr Asp Glu  
 290 295 300  
 Val Gln Gly Ile Val Pro Asp Phe Leu Thr Leu Leu His Gly Val Ile  
 305 310 315 320  
 75 Asp Ser Pro Asp Ile Pro Leu Asn Val Ser Arg Ser Tyr Leu Gln Ser

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325 330 335  
 Asp Ala Asn Val Lys Lys Ile Ser Ser His Ile Thr Lys Lys Val Ala  
 340 345 350  
 5 Asp Arg Leu Glu Glu Ile Phe Lys Asn Asp Arg Pro Thr Phe Glu Glu  
 355 360 365  
 Lys Trp Asp Ser Leu Lys Leu Phe Val Glu Tyr Gly Met Leu Thr Asp  
 370 375 380  
 Glu Lys Phe Tyr Glu Arg Ala Ala Lys Phe Phe Leu Phe Thr Asp Met  
 385 390 395 400  
 10 Asp Gly His Lys Tyr Thr Phe Asp Glu Tyr Arg Thr Leu Val Glu Gly  
 405 410 415  
 Val Gln Thr Asp Lys Asp Gly Gln Val Val Tyr Leu Tyr Ala Thr Asp  
 420 425 430  
 15 Lys His Gly Gln Tyr Ser His Val Lys Arg Ala Ser Asp Lys Gly Tyr  
 435 440 445  
 Ser Val Met Leu Leu Asp Gly Gln Leu Asp Pro His Ile Val Ser Leu  
 450 455 460  
 Leu Glu Gln Lys Leu Glu Lys Thr His Phe Val Arg Val Asp Ser Asp  
 465 470 475 480  
 20 Thr Ile Asn Asn Leu Ile Arg Lys Glu Glu Arg Ala Glu Val Lys Leu  
 485 490 495  
 Ser Asp Thr Glu Arg Ala Thr Leu Val Lys Leu Phe Glu Ala Arg Leu  
 500 505 510  
 25 Pro Arg Asp Glu Lys Lys His Phe Asn Val Ala Phe Glu Ser Leu Gly  
 515 520 525  
 Ala Glu Gly Glu Ala Ile Leu Ile Thr Gln Ala Glu Phe Met Arg Arg  
 530 535 540  
 Met Arg Asp Met Ala Gln Leu Gln Pro Gly Met Ser Phe Tyr Gly Glu  
 545 550 555 560  
 30 Leu Pro Asp Ser Tyr Asn Leu Val Leu Asn Thr Asp His Pro Leu Ile  
 565 570 575  
 Asp Arg Val Leu Ser Gly Glu Lys Glu Ser Val Glu Pro Ser Leu Thr  
 580 585 590  
 35 Glu Leu Arg Ala Lys Ile Ala Glu Leu Lys Ala Glu Glu Ala Lys Leu  
 595 600 605  
 Leu Asp Glu Glu Lys Gly Lys Lys Pro Glu Glu Ile Pro Val Ala Thr  
 610 615 620  
 Lys Glu Ala Lys Glu Asn Asn Ala Val Glu Gln Ala Lys Thr Glu Gly  
 625 630 635 640  
 40 Ser Ile Asn Asp Gln Leu Thr Lys Tyr Ala Gln Asp Asn Glu Leu Ile  
 645 650 655  
 Gly Gln Leu Ile Asp Leu Ala Leu Leu Gly Ser Gly Leu Leu Thr Gly  
 660 665 670  
 45 Glu Ala Leu Ala Glu Phe Ile Arg Arg Ser Gln Arg Leu Leu  
 675 680 685

(2) INFORMATION FOR SEQ ID NO:284

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 482 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 55 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 60 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...482  
 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:284

Asp Ile Arg Gln Lys Arg Pro Cys Phe Asn Ala Asn Leu Tyr Phe Tyr  
 1 5 10 15  
 70 Arg Ala Met Glu Lys Leu Ile Asp Ile Leu Val Val Asp Asp Asp Val  
 20 25 30  
 Ala Val Cys Ala Ala Leu Arg Leu Val Leu Lys Arg Ala Gly Tyr Asn  
 35 40 45  
 Pro Val Ile Ala Asn Ser Pro Asp Glu Ala Leu Ser Ile Met Arg Asn  
 50 55 60  
 75 Pro Asp Gly Gly Cys Lys Pro Ala Val Ile Leu Met Asp Met Asn Phe

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65      70      75      80
Ser Leu Ser Thr Ser Gly Arg Glu Gly Leu Glu Leu Leu Glu Lys Met
85
5  Gln Ile Phe Thr Ser Cys Pro Val Ile Leu Met Thr Ala Trp Ala Ser
100
Ile Pro Leu Ala Val Glu Gly Met Arg Leu Gly Ala Phe Asp Phe Ile
115
Gly Lys Pro Trp Asp Asn Asp Arg Leu Leu Arg Thr Ile Asp Thr Ala
130
10 Leu His Leu Ala Ala Pro Ser Ala Val Ala Asn Pro Ser Glu Gln Ser
145
Asp Arg Asp Thr Ala Arg Gln Pro Lys Ala Thr Val Gln Glu Asn Asp
165
15 Pro Cys Ala His Ile Ile Gly Arg Ser Asp Ala Ile Cys Lys Ile Lys
180
Glu Arg Ile Arg Arg Ile Ala Pro Thr His Ala Ser Val Leu Ile Thr
195
Gly Glu Ser Gly Thr Gly Lys Glu Leu Ile Ala Glu Ala Leu His Arg
210
20 Gly Ser Lys Arg Ala Ser Ala Pro Phe Val Lys Val Asn Leu Gly Gly
225
Ile Pro Glu Ser Leu Phe Glu Ser Glu Leu Phe Gly His Lys Lys Gly
245
25 Ala Phe Thr Asn Ala Phe Ser Asp Arg Lys Gly Arg Phe Glu Leu Ala
260
Asp Gly Gly Thr Ile Phe Leu Asp Glu Ile Gly Glu Leu Pro Val Gly
275
Asn Gln Val Lys Leu Leu Arg Val Leu Gln Glu Gln Thr Phe Glu Pro
290
30 Leu Gly Glu Ser Val Ser His Arg Val Asp Ile Arg Val Val Ser Ala
305
Thr Asn Ala Ser Leu Glu Arg Met Val Ala Glu Gly Arg Phe Arg Glu
325
35 Asp Leu Tyr Tyr Arg Ile Asn Leu Ile His Leu His Leu Pro Pro Leu
340
Arg Glu Arg Gln Glu Asp Ile Gln Leu Leu Val Glu Ala Phe Ser Glu
355
Ala Phe Ala Gln Ser Asn Gly Leu Pro His Ala Val Trp Ser Ala Glu
370
40 Ala Met Arg Arg Ile Cys Ala Met Pro Leu Pro Gly Asn Val Arg Glu
385
Leu Lys Asn Val Val Glu Arg Thr Leu Leu Leu Ser Gly Ser Arg Glu
405
45 Ile Ser Ala Arg Asp Val Ala Asp Phe Gly Ser Gln Val Thr Ala Ala
420
Asp His Ser Asp Glu Arg Ala Leu Thr Asp Met Glu Glu Ala Ala Ile
435
Arg Glu Thr Leu Thr Lys Tyr Asn Gly Asn Val Ser Arg Ala Ala Arg
450
50 Ala Leu Gly Leu Ser Arg Ala Ala Leu Tyr Arg Arg Met Glu Lys Tyr
465
Gly Leu
470
475
480

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- 55 (2) INFORMATION FOR SEQ ID NO:285
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- 60 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 65 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Porphyromonas gingivalis*
- (ix) FEATURE:
- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...263
- 70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:285
- 75 Arg Ser Leu Gln Ser Phe Gln Asn Lys Lys His Ser Ser Met Leu Lys



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1 Ile Lys Asn Leu His Ala Thr Val Gln Gly Lys Glu Ile Leu Lys Gly  
 5 20 25 30  
 10 Ile Asn Leu Glu Ile Asn Ala Gly Glu Ile His Ala Ile Met Gly Pro  
 15 35 40 45  
 20 Asn Gly Ser Gly Lys Ser Thr Leu Ser Ser Val Leu Val Gly His Pro  
 50 55 60  
 25 Ser Phe Glu Val Thr Glu Gly Glu Val Thr Phe Asn Gly Ile Asp Leu  
 65 70 75 80  
 30 Leu Glu Leu Glu Pro Glu Glu Arg Ala His Leu Gly Leu Phe Leu Ser  
 85 90 95  
 35 Phe Gln Tyr Pro Val Glu Ile Pro Gly Val Ser Met Val Asn Phe Met  
 100 105 110  
 40 Arg Ala Ala Val Asn Glu His Arg Lys Ala Ile Gly Ala Glu Pro Val  
 115 120 125  
 45 Ser Ala Ser Asp Phe Leu Lys Met Met Arg Glu Lys Arg Ala Ile Val  
 130 135 140  
 50 Glu Leu Asp Asn Lys Leu Ala Ser Arg Ser Val Asn Glu Gly Phe Ser  
 145 150 155 160  
 55 Gly Gly Glu Lys Lys Arg Asn Glu Ile Phe Gln Met Ala Met Leu Glu  
 165 170 175  
 60 Pro Lys Leu Ala Ile Leu Asp Glu Thr Asp Ser Gly Leu Asp Ile Asp  
 180 185 190  
 65 Ala Leu Arg Ile Val Ala Gly Gly Val Asn Arg Leu Arg Ser Pro Glu  
 195 200 205  
 70 Asn Ala Ala Ile Val Ile Thr His Tyr Gln Arg Leu Leu Glu Tyr Ile  
 210 215 220  
 75 Lys Pro Asp Phe Val His Val Leu Tyr Lys Gly Arg Ile Val Lys Ser  
 225 230 235 240  
 80 Gly Gly Ala Glu Leu Ala Leu Thr Leu Glu Glu Lys Gly Tyr Asp Trp  
 245 250 255  
 85 Ile Lys Glu Glu Ile Gly Glu  
 260

35 (2) INFORMATION FOR SEQ ID NO:286

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 462 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286

55 Ser Met Ala Lys Glu Lys Thr Ile Tyr Val Cys Arg Ser Cys Gly Thr  
 1 5 10 15  
 Lys Tyr Ala Lys Trp Gln Gly Asn Cys Asn Ala Cys Gly Glu Trp Asn  
 20 25 30  
 60 Cys Ile Asp Glu Glu Lys Val Pro Ala Pro Ala Ser Gly Lys His Ala  
 35 40 45  
 Ala Lys Ser Phe Met Pro Arg Glu Gln Asp Asn Arg Pro Arg Leu Leu  
 50 55 60  
 Gln Asp Val Glu Ser Gly Asp Glu Glu Arg Ile Arg Leu Gly Asp Glu  
 65 70 75 80  
 65 Glu Phe Asp Arg Val Leu Gly Gly Gly Ile Val Lys Gly Ala Phe Val  
 85 90 95  
 Leu Leu Gly Gly Glu Pro Gly Ile Gly Lys Ser Thr Leu Ile Leu Gln  
 100 105 110  
 70 Thr Val Leu Arg Leu Pro Gln Leu Arg Thr Leu Tyr Val Ser Gly Glu  
 115 120 125  
 Glu Ser Ala Arg Gln Leu Lys Met Arg Ala Glu Arg Leu Gly Gln Ala  
 130 135 140  
 Met Asn Gly Cys Tyr Val Tyr Cys Glu Thr Asn Ile Glu Arg Ile Leu  
 145 150 155 160  
 75 Ser Arg Ala Glu Glu Leu Thr Pro Asp Leu Leu Val Ile Asp Ser Ile

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165 170 175  
 Gln Thr Val Tyr Thr Glu Glu Met Glu Ser Ser Ala Gly Ser Val Gly  
 180 185 190  
 5 Gln Ile Arg Glu Cys Ala Ala Leu Leu Lys Tyr Cys Lys Thr Thr  
 195 200 205  
 Gly Ile Pro Val Ile Val Ile Gly His Ile Thr Lys Glu Gly Ser Ile  
 210 215 220  
 Ala Gly Pro Lys Val Leu Glu His Ile Val Asp Thr Val Leu Leu Phe  
 225 230 235 240  
 10 Asp Gly Asp Lys His His Leu Tyr Arg Ile Leu Arg Gly Gln Lys Asn  
 245 250 255  
 Arg Tyr Gly Ser Thr Ser Glu Leu Gly Ile Tyr Glu Met Arg Gln Asp  
 260 265 270  
 15 Gly Leu Arg Gly Val Glu Asn Pro Ser Glu His Leu Ile Thr Arg Asn  
 275 280 285  
 Arg Glu Asp Leu Ser Gly Ile Ala Ile Ala Val Ala Met Glu Gly Ile  
 290 295 300  
 Arg Pro Ile Leu Ile Glu Ala Gln Ala Leu Val Ser Ser Ala Ile Tyr  
 305 310 315 320  
 20 Ala Asn Pro Gln Arg Ser Ala Thr Gly Phe Asp Ile Arg Arg Met Asn  
 325 330 335  
 Met Leu Leu Ala Val Leu Glu Lys Arg Ala Gly Phe Lys Leu Ile Gln  
 340 345 350  
 25 Lys Asp Val Phe Leu Asn Ile Ala Gly Gly Ile Lys Ile Ala Asp Pro  
 355 360 365  
 Ala Thr Asp Leu Ala Val Ile Ser Ala Val Leu Ala Ser Ser Leu Asp  
 370 375 380  
 Ile Val Ile Pro Pro Ala Val Cys Met Thr Gly Glu Val Gly Leu Ser  
 385 390 395 400  
 30 Gly Glu Ile Arg Pro Val Ser Arg Ile Glu Gln Arg Ile Thr Glu Ala  
 405 410 415  
 Arg Arg Ile Gly Phe Lys Glu Ile Leu Val Pro Ala Asp Asn Phe Arg  
 420 425 430  
 35 Gln Glu Asp Ala Gly Arg Phe Gly Ile Arg Leu Val Pro Val Arg Lys  
 435 440 445  
 Val Glu Glu Ala Phe Arg His Leu Phe Ser Lys Gly Arg Glu  
 450 455 460

## (2) INFORMATION FOR SEQ ID NO:287

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 373 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc feature  
 (B) LOCATION 1...373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287

60 Gly Ser Cys Gly Ser Ser Pro Ala Ile Gly Arg Ser Gly Cys Ser Arg  
 1 5 10 15  
 Cys Asp Arg Arg Ile Gly His Gly Leu Ser Thr Ser Ala Phe Arg Thr  
 20 25 30  
 Tyr Ala Gly Leu Val Cys His Ser Arg Leu Arg Asp Gln Ser Ser Cys  
 35 40 45  
 65 Arg Val Cys Gly Met Arg Pro Ile Gly Gln Leu Phe Phe Pro Ser Cys  
 50 55 60  
 Pro Arg Arg Ser Ala Ser Asp Ala Gly Arg Thr Glu Arg Ile Gln Ser  
 65 70 75 80  
 70 Pro Leu Gln Asn Leu Leu Gln Glu Met Gln Phe Ser Pro Thr Asn Arg  
 85 90 95  
 Arg Asn Pro Phe Asp Asn Met Asn Ser Arg His Leu Thr Ile Thr Ile  
 100 105 110  
 Ile Ala Gly Leu Ser Leu Phe Val Leu Thr Leu Gly Gly Cys Ser Val  
 115 120 125  
 75 Ala Gln Gln Asp Thr Gln Trp Thr Leu Gly Gly Lys Leu Phe Thr Ser

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130 135 140  
 Ala Trp Ile Gln Arg Ser Ala Glu Tyr Gln Ala Leu Cys Ile Gln Ala  
 145 150 155 160  
 Tyr Asn Ile Ala Thr Glu Arg Val Asp Ala Leu Pro Ala Glu Arg Lys  
 165 170 175  
 5 Gln Gly Asp Arg Pro Tyr Ala Ile Val Thr Asp Ile Asp Glu Thr Ile  
 180 185 190  
 Leu Asp Asn Thr Pro Asn Ser Val Tyr Gln Ala Leu Arg Gly Lys Asp  
 195 200 205  
 10 Tyr Asp Glu Glu Thr Trp Gly Lys Trp Cys Ala Gln Ala Asp Ala Asp  
 210 215 220  
 Thr Leu Ala Gly Ala Leu Ser Phe Phe Leu His Ala Ala Asn Lys Gly  
 225 230 235 240  
 15 Ile Glu Val Phe Tyr Val Thr Asn Arg Arg Asp Asn Leu Arg Glu Ala  
 245 250 255  
 Thr Leu Gln Asn Leu Gln Arg Tyr Gly Phe Pro Phe Ala Asp Glu Glu  
 260 265 270  
 His Leu Leu Thr Thr His Gly Pro Ser Asp Lys Glu Pro Arg Arg Leu  
 275 280 285  
 20 Lys Ile Gln Glu Gln Tyr Glu Ile Val Leu Leu Ile Gly Asp Asn Leu  
 290 295 300  
 Gly Asp Phe His His Phe Asn Thr Lys Glu Glu Ser Gly Arg Lys  
 305 310 315 320  
 25 Gln Ala Leu Gly Leu Thr Ala Gly Glu Phe Gly Arg His Phe Ile Met  
 325 330 335  
 Leu Pro Asn Pro Asn Tyr Gly Ser Trp Glu Pro Ala Trp Tyr Gly Gly  
 340 345 350  
 Lys Tyr Pro Pro Leu Pro Glu Arg Asp Lys Ala Leu Lys Gln Leu His  
 355 360 365  
 30 Ser Gln Asn Ser Arg  
 370

## (2) INFORMATION FOR SEQ ID NO:288

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 426 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 40 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 45 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...426  
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:288

Arg Trp Gly Phe Ser Asn Phe Val Ala Met Ser Thr Asn Ile Asp Val  
 1 5 10 15  
 55 Gln Gln Ile Lys Gln Arg Phe Gly Ile Ile Gly Ser Ser Pro Leu Met  
 20 25 30  
 Glu His Ala Ile Arg Val Ala Ala Gln Val Ala Pro Thr Asp Met Ser  
 35 40 45  
 60 Val Leu Val Thr Gly Glu Ser Gly Ser Gly Lys Glu Phe Phe Pro Gln  
 50 55 60  
 Ile Ile His Tyr Tyr Ser Ala Arg Lys His His Ser Tyr Ile Ala Val  
 65 70 75 80  
 Asn Cys Gly Ala Ile Pro Glu Gly Thr Ile Asp Ser Glu Leu Phe Gly  
 85 90 95  
 65 His Arg Lys Gly Ser Phe Thr Gly Ala Val Ser Asp Arg Lys Gly Tyr  
 100 105 110  
 Phe Glu Glu Ala Ser Gly Gly Thr Ile Phe Leu Asp Glu Val Gly Glu  
 115 120 125  
 70 Leu Pro Leu Pro Thr Gln Ala Arg Leu Leu Arg Val Leu Glu Thr Gly  
 130 135 140  
 Glu Phe Ile Pro Val Gly Ala Ser Gln Ser Gln Lys Thr Asp Val Arg  
 145 150 155 160  
 Ile Val Ala Ala Thr Asn Val Asn Leu Lys Glu Ala Val Ala Asn Gly  
 165 170 175  
 75 Lys Phe Arg Glu Asp Leu Phe Phe Arg Leu Asn Thr Val Pro Ile Glu

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      180      185      190
Val Pro Ala Leu Arg Met Arg Pro Asp Asp Val Pro Leu Leu Phe Arg
      195      200      205
5 Arg Phe Ala Ala Asp Ser Ala Glu Lys Tyr Arg Met Pro Pro Leu Arg
      210      215      220
Leu Ser Asp Glu Ala Arg Thr Ile Leu Met Arg Tyr Arg Trp Pro Gly
      225      230      235      240
Asn Val Arg Glu Leu Arg Asn Ile Thr Asp Arg Leu Ser Ile Leu Glu
      245      250      255
10 Glu Glu Arg Thr Val Ser Ala Glu Thr Ile Thr Arg Tyr Leu Asp Ala
      260      265      270
Glu Gly Met Gln Asp Leu His Pro Val Val Ile Arg Arg Asn Glu Thr
      275      280      285
15 Thr Glu Ala Asp Lys Gln Ile Pro His Tyr Glu Arg Glu Ile Ile Tyr
      290      295      300
Gln Val Leu Tyr Asp Met Lys Lys Glu Ile Ala Asp Leu Lys Gly Met
      305      310      315      320
Met Asn Arg Leu Ala His His Glu Gln Pro Ser Trp Pro Val Gly Ser
      325      330      335
20 Asp Val Trp Gly Asn Asp Asp Lys Arg Thr Ala Asp Pro Lys Trp Gly
      340      345      350
Val Ser Thr His Lys Ala Pro Ile Ala Asn Ala Ala Glu Pro Val Glu
      355      360      365
25 Pro Ile Gln Glu Ala Ser Glu Tyr Thr Glu Asp Pro Val Ser Leu Glu
      370      375      380
Glu Val Glu Lys Lys Met Ile Ser Leu Ala Leu Glu Arg His Gly Gly
      385      390      395      400
Arg Arg Lys Gln Thr Ala Glu Glu Leu Lys Ile Ser Glu Arg Thr Leu
      405      410      415
30 Tyr Arg Lys Ile Lys Glu Tyr Gly Leu Glu
      420      425

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(2) INFORMATION FOR SEQ ID NO:289

- 35 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 653 amino acids  
 (B) TYPE: amino acid  
 (C) TOPOLOGY: linear
- 40 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES
- 45 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...653
- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:289

```

Lys Asn Leu Pro Arg Tyr Ala Pro Ala Phe Gly Arg Asn Arg Lys Arg
1 5 10 15
55 Glu Gln Pro Asp Pro Asp Asn Asp Asp Ser Arg Gly Arg Ser His Arg
      20 25 30
Gln Ser Gly Arg Ala Val Thr Val Val Cys Arg Arg Ile Gln Thr Pro
      35 40 45
60 Leu Pro His Met Ile Leu Leu Phe Gly Gly Thr Thr Glu Gly Arg Ala
      50 55 60
Ala Ala Arg Val Leu Asp Glu Ala Gly Ser Pro Phe Phe Tyr Ser Thr
      65 70 75 80
Lys Gly Asn Leu Gln Glu Ile Gln Ser Ser His Gly His Arg Leu Thr
      85 90 95
65 Gly Ala Met Thr Val Ala Asp Met Val Ser Phe Cys Arg Lys Glu Glu
      100 105 110
Ile Arg Leu Ile Val Asp Ala Ala His Pro Phe Ala Glu Glu Leu His
      115 120 125
70 Ala Ser Val Ala Glu Ala Ser Glu Gln Thr Gly Ile Pro Val Val Arg
      130 135 140
Tyr Glu Arg Gln Tyr Pro Pro Arg Glu Glu Gly Ile Val Trp Cys Ala
      145 150 155 160
Asn Tyr Asp Thr Ala Ala Glu Arg Met Leu Gly Asp Gly Val Gln Arg
      165 170 175
75 Leu Leu Met Leu Thr Gly Val Asn Thr Ile Pro Lys Leu Ala Ala Phe

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180 185 190  
 Trp Lys Glu Arg Thr Thr Phe Cys Arg Ile Leu Lys Arg Asp Glu Ser  
 195 200 205  
 Val Ala Leu Ala Glu Lys Asn Gly Phe Pro Ala Glu Arg Ile Val Phe  
 210 215 220  
 Phe Glu Pro His Ala Asp Glu Glu Leu Met Gln Ala Val Arg Pro Asp  
 225 230 235 240  
 Ala Ile Ile Thr Lys Glu Ser Gly Glu Ser Gly Tyr Phe Arg Glu Lys  
 245 250 255  
 10 Ile Glu Ala Ala Arg Arg Met Gly Ile Arg Ile Tyr Ala Val Val Arg  
 260 265 270  
 Pro Pro Leu Pro Pro Ser Phe Ile Pro Val Gly Gly Pro Val Gly Leu  
 275 280 285  
 15 Arg Arg Ala Val Glu Arg Leu Val Pro Gly Phe Phe Ser Leu Arg Ser  
 290 295 300  
 Gly Phe Thr Thr Gly Thr Thr Ala Thr Ala Val Val Ala Ala Met  
 305 310 315 320  
 Tyr Arg Leu Met Gly Leu Gly Ser Leu Ala Glu Ala Pro Val Glu Leu  
 325 330 335  
 20 Pro Ser Gly Glu Ile Val Ser Leu Pro Ile Ala Glu Ile Arg Glu Glu  
 340 345 350  
 Glu Asp Ala Val Val Ser Ala Val Leu Lys Asp Ala Gly Asp Asp Pro  
 355 360 365  
 25 Asp Val Thr Asn Gly Met Ala Val Cys Ala Thr Ile Arg Leu Asn Pro  
 370 375 380  
 Glu His Glu Glu Val Arg Phe Leu Gln Gly Glu Gly Val Gly Val Val  
 385 390 395 400  
 Thr Leu Pro Gly Leu Gly Leu Glu Val Gly Gly Pro Ala Ile Asn Leu  
 405 410 415  
 30 Val Pro Arg Arg Met Met Thr Ala Glu Val Arg Arg Leu Tyr Ala Gln  
 420 425 430  
 Gly Gly Val Asp Ile Thr Ile Ser Val Pro Glu Gly Arg Glu Ala Ala  
 435 440 445  
 35 Thr Gln Thr Phe Asn Pro Arg Leu Gly Ile Arg Asp Gly Ile Ser Ile  
 450 455 460  
 Ile Gly Thr Ser Gly Val Val Lys Pro Phe Ser Ala Glu Ala Phe Val  
 465 470 475 480  
 Gly Ala Ile Arg Lys Gln Val Gly Ile Ala Thr Ala Leu Gly Ala Asn  
 485 490 495  
 40 His Ile Val Leu Asn Ser Gly Ala Lys Ser Glu Arg Tyr Val Lys Gly  
 500 505 510  
 Ala Tyr Pro Ala Leu Ile Pro Gln Ala Phe Val Gln Tyr Gly Asn Phe  
 515 520 525  
 45 Val Gly Glu Ser Leu Ser Cys Val Ala Ser Phe Pro Ser Val Arg Ser  
 530 535 540  
 Val Thr Val Gly Ile Met Leu Gly Lys Ala Val Lys Leu Ala Glu Gly  
 545 550 555 560  
 Tyr Leu Asp Thr His Ser Lys Lys Val Val Met Asn Arg Asp Phe Leu  
 565 570 575  
 50 His Glu Leu Ala Arg Gln Ala Gly Cys Ser Glu Asp Ile His Ala Ile  
 580 585 590  
 Ile Asp Ser Leu Asn Leu Ala Arg Glu Leu Trp Thr Met Pro Ser Ala  
 595 600 605  
 55 Glu Asp Ser Asp Arg Leu Leu Arg Lys Ile Ala Glu Arg Ser Trp Glu  
 610 615 620  
 Thr Cys Arg Pro Ser Val Pro Ser Ala Glu Leu Glu Leu Leu Ile  
 625 630 635 640  
 Asp Glu Ser Gly Ala Ile Arg Phe Arg Ile Gly Gly Glu  
 645 650

(2) INFORMATION FOR SEQ ID NO:290

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 451 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

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(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...451

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:290

5  
1 Gln Gln Arg Pro His Arg Ile Ile Met Leu Arg Thr Phe Arg Ile Gly  
1 5 10 15  
Gly Ile His Pro Pro Glu Asn Lys Leu Ser Ala Gly Lys Pro Val Glu  
20 25 30  
10 Val Leu Pro Ile Pro Ser Gln Val Val Ile Pro Leu Gly Gln His Ile  
35 40 45  
Gly Ala Pro Ala Thr Ala Thr Val Lys Lys Gly Asp Glu Val Lys Val  
50 55 60  
15 Gly Thr Ile Ile Ala Gln Ala Gly Gly Phe Val Ser Ala Asn Ile His  
65 70 75 80  
Ser Ser Val Ser Gly Lys Val Leu Lys Ile Asp Asn Val Tyr Asp Ser  
85 90 95  
Ser Gly Tyr Pro Lys Pro Ala Val Phe Ile Ser Val Glu Gly Asp Glu  
100 105 110  
20 Trp Glu Glu Gly Ile Asp Arg Ser Pro Ala Ile Val Lys Glu Cys Asn  
115 120 125  
Leu Asp Ala Lys Glu Ile Val Ala Lys Ile Ser Ala Ala Gly Ile Val  
130 135 140  
25 Gly Leu Gly Gly Ala Thr Phe Pro Thr His Val Lys Leu Ser Pro Pro  
145 150 155 160  
Pro Gly Asn Lys Ala Glu Ile Leu Ile Ile Asn Ala Val Glu Cys Glu  
165 170 175  
Pro Tyr Leu Thr Ser Asp His Val Leu Met Leu Glu His Gly Glu Glu  
180 185 190  
30 Ile Met Ile Gly Val Ser Ile Leu Met Lys Ala Ile Gln Val Asn Lys  
195 200 205  
Ala Val Ile Gly Val Glu Asn Asn Lys Lys Asp Ala Ile Ala His Leu  
210 215 220  
35 Thr Lys Leu Ala Thr Ala Tyr Pro Gly Ile Glu Val Met Pro Leu Lys  
225 230 235 240  
Val Gln Tyr Pro Gln Gly Gly Glu Lys Gln Leu Ile Asp Ala Val Ile  
245 250 255  
Arg Lys Gln Val Lys Ser Gly Ala Leu Pro Ile Ser Thr Gly Ala Val  
260 265 270  
40 Val Gln Asn Val Gly Thr Val Phe Ala Val Tyr Glu Ala Val Gln Lys  
275 280 285  
Asn Lys Pro Leu Val Glu Arg Ile Val Thr Val Thr Gly Lys Lys Leu  
290 295 300  
45 Ser Arg Pro Ser Asn Leu Leu Val Arg Ile Gly Thr Pro Ile Ala Ala  
305 310 315 320  
Leu Ile Glu Ala Ala Gly Gly Leu Pro Glu Asn Thr Gly Lys Ile Ile  
325 330 335  
Gly Gly Gly Pro Met Met Gly Arg Ala Leu Leu Ser Pro Asp Val Pro  
340 345 350  
50 Val Thr Lys Gly Ser Ser Gly Val Leu Ile Leu Asp Arg Glu Glu Ala  
355 360 365  
Val Arg Lys Pro Met Arg Asp Cys Ile Arg Cys Ala Lys Cys Val Gly  
370 375 380  
55 Val Cys Pro Met Gly Leu Asn Pro Ala Phe Leu Met Arg Asp Thr Leu  
385 390 395 400  
Tyr Lys Ser Trp Glu Thr Ala Glu Lys Gly Asn Val Val Asp Cys Ile  
405 410 415  
Glu Cys Gly Ser Cys Ser Phe Thr Cys Pro Ala Asn Arg Pro Leu Leu  
420 425 430  
60 Asp Tyr Ile Arg Gln Ala Lys Lys Thr Val Met Gly Ile Gln Arg Ala  
435 440 445  
Arg Lys Gln  
450

65 (2) INFORMATION FOR SEQ ID NO:291

(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 489 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

70 (11) MOLECULE TYPE: protein

75 (111) HYPOTHETICAL: YES

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## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...489

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:291

10 Met Asn Ser Gln Lys Lys Glu Ala Phe Asn Met Lys Arg Ile Gln Leu  
 1 5 10 15  
 Thr Leu Ile Ala Leu Phe Ala Ala Val Ala Gly Leu Val Ala Gln Asn  
 20 25 30  
 15 Ala Tyr Glu Gly Val Ile Ser Tyr Lys Ile Ser Leu Asp Lys Thr Gly  
 35 40 45  
 Asn Lys Val Val Leu Asn Gly Ala Ala Asp Met Ser Asn Leu Lys Leu  
 50 55 60  
 Lys Ser Thr Gln Met Ile Ile Val Thr Pro Ile Leu Arg Ser Glu Asp  
 65 70 75 80  
 20 Gly Thr Ser Arg Val Glu Phe Pro Ser Val Val Ile Thr Gly Arg Asn  
 85 90 95  
 Arg Thr Lys Ala Leu Lys Arg Glu Ile Ala Phe Ser Ser Ala Leu Pro  
 100 105 110  
 25 Gln Ala Lys His Ala Ala Gln Tyr Ile Arg Arg His Asn Gly Lys Ser  
 115 120 125  
 Glu Gln Phe Ala Phe Thr Gly Glu His Ala Tyr Ala Ser Trp Met Met  
 130 135 140  
 Asp Ala Lys Phe Val Val Arg Glu Glu Val Arg Gly Cys Ala Lys Cys  
 145 150 155 160  
 30 Pro Val Gly Leu Ser Ser Asn Ile Val Pro Phe Asp Pro Leu Phe Asn  
 165 170 175  
 Pro Ala Glu Ala Pro Tyr Leu Leu Ala His Ile Thr Pro Ala Glu Glu  
 180 185 190  
 35 Val Glu Lys Gln Arg Glu Ser Ser Phe Asp Ala Tyr Ile Asn Phe Lys  
 195 200 205  
 Val Asn Lys Ala Asp Val Leu Pro Glu Tyr Arg Asn Asn Lys Ala Glu  
 210 215 220  
 Leu Glu Lys Ile Lys Glu Phe Val Ser Thr Val Lys Ala Asn Pro Asn  
 225 230 235 240  
 40 Tyr Ser Val Asn Lys Met Ile Ile Glu Gly Phe Ala Ser Pro Glu Ala  
 245 250 255  
 Ser Ile Ala His Asn Lys Ala Leu Ser Glu Arg Arg Ala Lys Arg Leu  
 260 265 270  
 45 Ala Glu Glu Leu Val Arg Lys Tyr Gly Lys Thr Leu Pro Asn Ile Thr  
 275 280 285  
 Thr Glu Phe Gly Gly Glu Asp Trp Lys Gly Leu Lys Leu Ala Ile Glu  
 290 295 300  
 Lys Ser Asp Ile Ala Asp Arg Asp Arg Val Leu Glu Ile Ile Asn Ser  
 305 310 315 320  
 50 Asp Lys Tyr Ala Asp Asp Ala Arg Glu Gln Ala Leu Lys Gln Leu  
 325 330 335  
 Ser Ser Tyr Arg Tyr Ile Leu Asp Gln Ile Tyr Pro Asn Leu Arg Arg  
 340 345 350  
 55 Asn Thr Ile Thr Met Gly Tyr Ile Val Arg Asp Tyr Thr Leu Glu Glu  
 355 360 365  
 Ala Arg Glu Ile Ile Lys Thr Ala Pro Lys Glu Leu Ser Glu Ala Glu  
 370 375 380  
 Met Tyr Arg Val Ala Met Ser Tyr Pro Glu Gly His Gln Glu Arg Leu  
 385 390 395 400  
 60 Phe Ala Leu Asn Thr Thr Leu Lys Tyr Phe Pro Glu Ser Val Thr Gly  
 405 410 415  
 Arg Ile Asn Leu Ala Val Ala Ala Phe Asn Gly Gly Asp Val Gln Gln  
 420 425 430  
 65 Ala Ile Ala Leu Leu Ser Pro Ile Gln Thr Glu Lys Gly Val Ser Asn  
 435 440 445  
 Ile Leu Gly Ala Ala Tyr Ala Arg Thr Gly Asp Phe Ala Arg Ala Glu  
 450 455 460  
 Thr Phe Phe Arg Lys Ala Val Ala Glu Gly Asp Ala Asn Ala Gln Arg  
 465 470 475 480  
 70 Asn Leu Asp Met Leu Leu Gly Lys Lys  
 485

## (2) INFORMATION FOR SEQ ID NO:292

75

## (1) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 384 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

- 5 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 10 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...384  
 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:292
- Asp Met Ala Glu Lys Arg Asp Tyr Tyr Glu Val Leu Gly Val Ser Lys  
 1 5 10 15  
 20 Asn Ala Thr Asp Asp Glu Leu Lys Lys Ala Tyr Arg Lys Lys Ala Ile  
 20 25 30  
 Gln Tyr His Pro Asp Lys Asn Pro Gly Asp Lys Glu Ala Glu Glu His  
 35 40 45  
 25 Phe Lys Glu Val Ala Glu Ala Tyr Asp Val Leu Ser Asp Pro Gln Lys  
 50 55 60  
 Arg Ser Gln Tyr Asp Gln Phe Gly His Ala Gly Leu Gly Gly Ala Ala  
 65 70 75 80  
 Gly Gly Gly Phe Ser Gly Gly Gly Met Ser Met Glu Asp Ile Phe Ser  
 85 90 95  
 30 Arg Phe Gly Asp Leu Phe Gly Gly Phe Gly Gly Phe Gly Gly Phe Ser  
 100 105 110  
 Asp Met Gly Gly Gly Ser Arg Arg Arg Val Arg Arg Gly Ser Asp Leu  
 115 120 125  
 35 Arg Val Arg Val Lys Leu Ser Leu Ala Asp Ile Ser Lys Gly Val Glu  
 130 135 140  
 Lys Lys Val Lys Val Lys Lys Gln Val Val Cys Ser Lys Cys Arg Gly  
 145 150 155 160  
 Asp Gly Thr Glu Glu Ala Asn Gly Lys Thr Thr Cys Gln Thr Cys His  
 165 170 175  
 40 Gly Thr Gly Val Val Thr Arg Val Ser Asn Thr Phe Leu Gly Ala Met  
 180 185 190  
 Gln Thr Gln Ser Thr Cys Pro Thr Cys His Gly Glu Gly Glu Ile Ile  
 195 200 205  
 45 Thr Lys Pro Cys Ser Lys Cys Lys Gly Glu Gly Val Glu Ile Gly Glu  
 210 215 220  
 Glu Val Ile Ser Phe His Ile Pro Ala Gly Val Ala Glu Gly Met Gln  
 225 230 235 240  
 Met Ser Val Asn Gly Lys Gly Asn Ala Ala Pro Arg Gly Gly Val Asn  
 245 250 255  
 50 Gly Asp Leu Ile Val Val Ile Ala Glu Glu Pro Asp Pro Asn Leu Ile  
 260 265 270  
 Arg Asn Gly Asn Asp Leu Ile Tyr Asn Leu Leu Ile Ser Val Pro Leu  
 275 280 285  
 55 Ala Ile Lys Gly Gly Ser Val Glu Val Pro Thr Ile Asp Gly Arg Ala  
 290 295 300  
 Lys Ile Arg Ile Glu Ala Gly Thr Gln Pro Gly Lys Met Leu Arg Leu  
 305 310 315 320  
 Arg Asn Lys Gly Leu Pro Ser Val Asn Gly Tyr Gly Met Gly Asp Gln  
 325 330 335  
 60 Leu Val Asn Val Asn Val Tyr Ile Pro Glu Ser Ile Asp Ala Lys Asp  
 340 345 350  
 Glu Gln Ala Ile Ala Ala Met Glu Asn Ser Asp Ser Phe Lys Pro Thr  
 355 360 365  
 65 Asp Ala Ala Arg Lys Asp Ile Asp Lys Lys Tyr Arg Glu Met Leu Asp  
 370 375 380
- (2) INFORMATION FOR SEQ ID NO:293
- 70 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 309 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 75 (ii) MOLECULE TYPE: protein



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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293

Arg Phe Asp Ser Thr Thr Asn Val Ser Gln Ile Asn Leu Arg Thr Glu  
 1 5 10 15  
 Met Lys Lys Leu Ile Leu Ala Thr Leu Gly Leu Met Ala Ile Ala Met  
 20 25 30  
 Leu Ser Cys Ser Ser Asn Asn Lys Asp Leu Glu Asn Lys Gly Glu Ala  
 35 40 45  
 Thr Leu Leu Val Thr Phe Gly Ser Ser Tyr Lys Ala Pro Arg Glu Thr  
 50 55 60  
 Tyr Ala Lys Ile Glu Lys Thr Phe Ala Ala Ala Tyr Pro Asp Gln Arg  
 65 70 75 80  
 Ile Ser Trp Thr Tyr Thr Ser Ser Ile Ile Arg Lys Lys Leu Ala Gln  
 85 90 95  
 Gln Gly Ile Tyr Ile Asp Ala Pro Asp Glu Ala Leu Glu Lys Leu Ala  
 100 105 110  
 Arg Leu Gly Tyr Lys Lys Ile Asn Val Gln Ser Leu His Val Ile Pro  
 115 120 125  
 Gly Arg Glu Tyr Asp Glu Met Ile Asp Phe Val Asn Lys Phe Lys Ala  
 130 135 140  
 Ala His Ser Asp Ile Thr Val Lys Val Gly Ala Pro Leu Phe Asp Thr  
 145 150 155 160  
 Asp Glu Asp Met Arg Glu Val Ala Glu Ile Leu His Lys Arg Phe Gln  
 165 170 175  
 Gln Thr Ile Glu Lys Gly Glu Ala Ile Val Phe Met Gly His Gly Thr  
 180 185 190  
 Glu His Ala Ala Asn Asp Arg Tyr Ala Arg Ile Asn Lys Ile Met Lys  
 195 200 205  
 Asn Tyr Ser Lys Phe Met Ile Val Gly Thr Val Glu Ser Asp Pro Ser  
 210 215 220  
 Ile Asn Asp Val Ile Ala Glu Leu Lys Glu Thr Gly Ala Thr Ala Val  
 225 230 235 240  
 Thr Met Met Pro Leu Met Ser Val Ala Gly Asp His Ala Thr Asn Asp  
 245 250 255  
 Met Ala Gly Asp Glu Asp Asp Ser Trp Lys Thr Leu Leu Thr Asn Ala  
 260 265 270  
 Gly Tyr Thr Val Ser Ile Asp Lys Leu Asp Asn Gly Asn Phe Ser Ala  
 275 280 285  
 Leu Gly Asp Ile Glu Glu Ile Arg Asn Ile Trp Leu Lys His Met Lys  
 290 295 300  
 Ala Thr Ser Ala Arg  
 305

(2) INFORMATION FOR SEQ ID NO:294

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 491 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294

Arg Arg Asp Ala Arg Arg Gln Leu Val Arg Arg Arg Arg Lys Glu Leu  
 1 5 10 15  
 Ser Gly Thr Ala Asn Thr Arg Cys Arg Arg Arg Val Phe Pro Glu Arg

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20 25 30  
 Arg Ser Ala Ile Arg Trp Cys Phe Pro Arg Leu Arg Asp Gly Leu Gln  
 35 40 45  
 Pro Ile Arg Phe Gly Ser Leu Ala Asn Pro Gln Gln Leu Ser Arg  
 50 55 60  
 Gly Val Arg Leu Arg Ser Phe Glu Ser Arg Arg Gln Pro Ile Cys Arg  
 65 70 75 80  
 Phe Gln Gly Ile Gln Gly Lys Arg Arg Asp Ile Leu Gln Pro Glu Gly  
 85 90 95  
 10 Asn Ser Leu Leu Arg Thr His Ala His Ala Ser Arg Leu Gly Ala Gly  
 100 105 110  
 Arg Ser Tyr Arg Tyr Leu Ala Pro Arg Thr Thr Ser Arg Pro Pro Thr  
 115 120 125  
 15 Ala Phe Leu Leu Phe Ala Pro Met Thr Ser Val Ser His Leu Arg Thr  
 130 135 140  
 Ile Ser Val Ala Gly Ile Leu Ala Ala Leu Gly Gly Ala Val Leu Ile  
 145 150 155 160  
 Leu Phe Gly Val Asn Leu Phe Leu Gly Ser Val Ala Ile Pro Met Ser  
 165 170 175  
 20 Glu Ile Phe Arg His Leu Phe Ser Asp Arg Pro Glu Gly Gly Glu Ala  
 180 185 190  
 Leu Val His Tyr Asn Ile Leu Trp Lys Ser Arg Leu Pro Glu Ala Leu  
 195 200 205  
 25 Thr Ala Ala Phe Ala Gly Ala Gly Leu Ser Val Ser Gly Leu Gln Met  
 210 215 220  
 Gln Thr Val Phe Arg Asn Pro Leu Ala Gly Pro Ser Val Leu Gly Ile  
 225 230 235 240  
 Ser Ser Gly Ala Ser Leu Gly Val Ala Leu Val Val Leu Leu Ser Gly  
 245 250 255  
 30 Ser Leu Gly Gly Val Ala Leu Ser Ser Leu Gly Tyr Met Gly Glu Val  
 260 265 270  
 Ala Met Asn Ile Ala Ala Ala Val Gly Ser Leu Ala Val Met Gly Leu  
 275 280 285  
 35 Ile Val Phe Val Ser Thr Lys Val Arg Ser His Val Thr Leu Leu Ile  
 290 295 300  
 Ile Gly Val Met Ile Gly Tyr Val Ala Thr Ala Val Ile Gly Val Phe  
 305 310 315 320  
 Lys Phe Phe Ser Ile Glu Glu Asp Ile Arg Ala Tyr Val Ile Trp Gly  
 325 330 335  
 40 Leu Gly Ser Phe Ser Arg Ala Thr Asp Ser Gln Leu Ser Phe Phe Ala  
 340 345 350  
 Ile Leu Met Leu Ile Phe Ile Pro Ala Gly Met Leu Leu Val Lys Gln  
 355 360 365  
 45 Leu Asn Leu Leu Leu Leu Gly Glu Ser Tyr Ala Arg Asn Leu Gly Leu  
 370 375 380  
 Asn Thr Arg Arg Ala Arg Leu Leu Val Ile Ser Ser Ala Gly Leu Leu  
 385 390 395 400  
 Ile Ala Thr Val Thr Ala Tyr Cys Gly Pro Ile Gly Phe Leu Gly Met  
 405 410 415  
 50 Ala Val Pro His Leu Ala Arg Val Ile Phe His Thr Ser Asp His Arg  
 420 425 430  
 Ile Leu Met Pro Ala Thr Cys Leu Ile Gly Ser Ala Leu Ala Leu Phe  
 435 440 445  
 55 Cys Asn Ile Ile Ala Arg Met Pro Gly Phe Glu Gly Ala Leu Pro Val  
 450 455 460  
 Asn Ser Val Thr Ala Leu Val Gly Ala Pro Ile Ile Val Thr Val Leu  
 465 470 475 480  
 Phe Arg Arg Arg Arg Phe Lys Glu Glu Thr Asp  
 485 490

- 60 (2) INFORMATION FOR SEQ ID NO:295
- 65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 763 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- 70 (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- 75 (ix) FEATURE:

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(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...763

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:295

5  
His Phe Leu Val Thr Ile Met Arg Thr Lys Thr Ile Phe Phe Ala Ile  
1 5 10 15  
Ile Ser Phe Ile Ala Leu Leu Ser Ser Ser Leu Ser Ala Gln Ser Lys  
20 25 30  
10 Ala Val Leu Thr Gly Ser Val Ser Asp Ala Glu Thr Gly Glu Pro Leu  
35 40 45  
Ala Gly Ala Arg Ile Glu Val Lys His Thr Asn Ile Val Ala Gly Ala  
50 55 60  
15 Asp Ala Gly Gly His Phe Glu Ile Lys Asn Leu Pro Ala Gly Gln His  
65 70 75 80  
Thr Ile Ile Cys Ser Leu Gly Gly Tyr Gly Gln Lys Glu Glu Val Val  
85 90 95  
Ala Ile Glu Ala Gly Gln Thr Lys Thr Ile Ser Phe Ala Leu Arg Leu  
100 105 110  
20 Arg Thr Asn Asn Leu Glu Glu Val Val Val Thr Gly Thr Gly Thr Arg  
115 120 125  
Tyr Arg Leu Val Asp Ala Pro Val Ala Thr Glu Val Leu Thr Ala Lys  
130 135 140  
25 Asp Ile Ala Ser Phe Ser Ala Pro Thr Ser Glu Ala Leu Leu Gln Gly  
145 150 155 160  
Leu Ser Pro Ser Phe Asp Phe Gly Pro Asn Leu Met Gly Ser Phe Met  
165 170 175  
Gln Leu Asn Gly Leu Ser Ser Lys Tyr Ile Leu Ile Leu Ile Asp Gly  
180 185 190  
30 Lys Arg Val Tyr Gly Asp Val Gly Gly Gln Ala Asp Leu Ser Arg Ile  
195 200 205  
Ser Pro Asp Gln Ile Glu Arg Ile Glu Leu Val Lys Gly Ala Ser Ser  
210 215 220  
35 Ser Leu Tyr Gly Ser Asp Ala Ile Ala Gly Val Ile Asn Val Ile Thr  
225 230 235 240  
Lys Lys Asn Thr Asn Arg Leu Ser Ala Tyr Thr Ser His Arg Ile Ser  
245 250 255  
Lys Tyr Asn Asp Arg Gln Thr Asn Thr Ser Leu Asp Ile Asn Ile Gly  
260 265 270  
40 Lys Phe Ser Ser Asn Thr Asn Tyr Phe Phe Tyr His Thr Asp Gly Trp  
275 280 285  
Gln Asn Ser Pro Phe Glu Ile Lys Lys Lys Lys Gly Ser Gly Glu Pro  
290 295 300  
45 Val Leu Glu Glu Thr Tyr Lys Lys Thr Phe Arg Ala Gln Glu Asn Gln  
305 310 315 320  
Gly Val Ser Gln Ser Leu Ser Tyr Tyr Ala Thr Asn Asn Leu Ser Phe  
325 330 335  
Ser Gly Asn Val Gln Tyr Asn Lys Arg Gln Ile Phe Thr Pro Thr Phe  
340 345 350  
50 Ser Glu Lys Lys Ala Tyr Asp Met Asp Tyr Arg Ala Leu Thr Ala Ser  
355 360 365  
Leu Gly Thr Asn Tyr Leu Phe Pro Asn Gly Leu His Thr Leu Ser Phe  
370 375 380  
55 Asp Ala Val Tyr Asp Arg Phe Arg Phe Gly Tyr Leu Tyr His Asp Lys  
385 390 395 400  
Asp Ser Ser Glu Ser Leu Ile Asn Asn Gln Gly Gln Thr Glu Gln Pro  
405 410 415  
Thr Phe Phe Pro Gly Gln Leu Arg Asn Lys Asn Asp Gln Ile Arg Tyr  
420 425 430  
60 Thr Ala Glu Ala Arg Gly Val Phe Thr Leu Pro Tyr Ala Gln Lys Leu  
435 440 445  
Thr Gly Gly Leu Glu Tyr Phe Arg Glu Glu Leu Ile Ser Pro Tyr Asn  
450 455 460  
65 Leu Ile Thr Asp Lys Ala Asp Ala Ser Thr Leu Ser Ala Tyr Val Gln  
465 470 475 480  
Asp Glu Trp Lys Pro Leu Asp Trp Phe Asn Met Thr Ala Gly Phe Arg  
485 490 495  
Leu Val His His Gln Glu Phe Gly Thr Arg Met Thr Pro Lys Val Ser  
500 505 510  
70 Ile Leu Ala Lys Tyr Gly Pro Leu Asn Phe Arg Ala Thr Tyr Ala Asn  
515 520 525  
Gly Tyr Lys Thr Pro Thr Leu Lys Glu Leu Phe Ala Arg Asn Glu Leu  
530 535 540  
75 Thr Thr Met Gly Ser His Asn Leu Tyr Leu Gly Asn Ala Asp Leu Lys  
545 550 555 560

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Pro Gln Met Ser Asp Tyr Tyr Ala Leu Gly Leu Glu Tyr Asn Gln Gly  
 565 570 575  
 Pro Ile Ser Phe Ser Ala Thr Val Tyr Asp Asn Glu Leu Arg Asn Leu  
 580 585 590  
 5 Ile Ser Phe Met Asp Ile Pro Thr Ser Pro Glu His Glu Ala Gln Gly  
 595 600 605  
 Ile Lys Lys Thr Lys Gln Tyr Ala Asn Ile Gly Lys Ala Arg Ser Arg  
 610 615 620  
 10 Gly Leu Asp Val Leu Cys Asp Ala Ser Ile Gly Trp Gly Ile Lys Leu  
 625 630 635 640  
 Gly Ala Gly Tyr Ser Leu Val Glu Ala Lys Asn Leu Gln Thr Asp Glu  
 645 650 655  
 Trp Leu Glu Gly Ala Ala Arg His Arg Ala Asn Val His Ala Asp Trp  
 660 665 670  
 15 Val His Tyr Trp Gly Gln Tyr Arg Leu Gly Val Ser Leu Phe Gly Arg  
 675 680 685  
 Ile Gln Ser Glu Arg Tyr Tyr Lys Asp Gly Asn Ala Pro Asp Tyr Thr  
 690 695 700  
 20 Leu Trp Arg Leu Ala Thr Ser His Arg Phe Ala His Phe Arg His Ile  
 705 710 715 720  
 Ile Leu Asp Gly Thr Leu Gly Ile Asp Asn Leu Phe Asp Tyr Val Asp  
 725 730 735  
 Asp Arg Pro Met Gly Val Asn Tyr Ala Thr Val Thr Pro Gly Arg Thr  
 740 745 750  
 25 Phe Phe Ala Gln Ile Ala Ile Arg Phe Asn Asn  
 755 760

## (2) INFORMATION FOR SEQ ID NO:296

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 365 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 35 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 40 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...365  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:296

Cys Cys Ala Arg Leu Arg Asp Thr Ser Pro Arg Lys Lys Ser Phe Arg  
 1 5 10 15  
 50 Asn Asp Thr Val Phe Pro Tyr Phe Val Ile His Leu Ile Lys His Ile  
 20 25 30  
 Ile Ile Met Thr Asp Asn Lys Gln Arg Asn Ile Val Phe Pro Ala Phe  
 35 40 45  
 55 Leu Leu Leu Leu Gly Val Ile Ala Val Val Thr Ile Val Gly Phe Phe  
 50 55 60  
 Met Leu Arg Pro Ala Glu Ile Ile Gln Gly Gln Ile Glu Val Thr  
 65 70 75 80  
 Glu Tyr Arg Val Ser Ser Lys Val Pro Gly Arg Ile Lys Glu Leu Arg  
 85 90 95  
 60 Val Ser Glu Gly Gln Gln Val Gln Ala Gly Asp Thr Leu Ala Val Ile  
 100 105 110  
 Glu Ala Pro Asp Val Ala Ala Lys Met Glu Gln Ala Lys Ala Ala Glu  
 115 120 125  
 65 Ala Ala Ala Gln Ala Gln Asn Ala Lys Ala Leu Lys Gly Ala Arg Ser  
 130 135 140  
 Glu Gln Ile Gln Ala Ala Tyr Glu Met Trp Gln Lys Ala Gln Ala Gly  
 145 150 155 160  
 Val Ala Ile Ala Thr Lys Thr His Gln Arg Val Gln Asn Leu Tyr Asp  
 165 170 175  
 70 Gln Gly Val Val Pro Ala Gln Lys Leu Asp Glu Ala Thr Ala Gln Arg  
 180 185 190  
 Asp Ala Ala Ile Ala Thr Gln Lys Ala Ala Glu Ala Gln Tyr Asn Met  
 195 200 205  
 75 Ala Arg Asn Gly Ala Glu Arg Glu Asp Lys Leu Ala Ala Ser Ala Leu  
 210 215 220

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Val Asp Arg Ala Arg Gly Ala Val Ala Glu Val Glu Ser Tyr Ile Asn  
 225 230 235 240  
 Glu Thr Tyr Leu Ile Ala Pro Arg Ala Gly Glu Val Ser Glu Ile Phe  
 245 250 255  
 5 Pro Lys Ala Gly Glu Leu Val Gly Thr Gly Ala Pro Ile Met Asn Ile  
 260 265 270  
 Ala Glu Met Gly Asp Met Trp Ala Ser Phe Ala Val Arg Glu Asp Phe  
 275 280 285  
 10 Leu Ser Ser Met Thr Met Gly Ala Val Leu Glu Thr Val Val Pro Ala  
 290 295 300  
 Leu Asn Glu Glu Lys Val Arg Phe Lys Ile Thr Phe Ile Lys Asn Met  
 305 310 315 320  
 Gly Thr Tyr Ala Ala Trp Lys Ala Thr Lys Thr Thr Gly Gln Tyr Asp  
 325 330 335  
 15 Leu Lys Thr Phe Glu Val Lys Ala Thr Leu Ala Asp Lys Asp Lys Ala  
 340 345 350  
 Gln Lys Leu Arg Pro Gly Met Ser Val Ile Ile Arg Lys  
 355 360 365  
 20 (i2) INFORMATION FOR SEQ ID NO:297  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 320 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 25 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...320  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:297  
 40 Pro Gln Ser Ser Pro Asp Arg Arg Ser Phe Gln Asn Val Met Asn Lys  
 1 5 10 15  
 Tyr His Ser Gln Ser Val Leu Glu Val Gly Lys Ile Gly Ile Val Ile  
 20 25 30  
 45 Ile Phe Ala Pro Ile Val Arg Asn Val His Gln Gln Pro Pro Phe Leu  
 35 40 45  
 Ser His Lys Ser Ile Met Arg Ile Val Ser Asn Phe Leu Phe Val Ser  
 50 55 60  
 Phe Ser Val Leu Leu Phe Ala Ser Cys Arg Ser Gln Arg Glu Lys Val  
 65 70 75 80  
 50 Val Tyr Leu Gln Asp Ile Gln Thr Phe Asn Arg Glu Ile Ile Ala Lys  
 85 90 95  
 Pro Tyr Asp Val Lys Ile Glu Lys Asp Asp Val Leu Asn Ile Leu Val  
 100 105 110  
 55 Ser Ser Arg Asp Pro Glu Leu Ser Thr Pro Tyr Asn Gln Val Leu Thr  
 115 120 125  
 Thr Arg Ala Leu Ala Arg Asn Gly Tyr Gly Thr Asn Ser Asn Glu Gly  
 130 135 140  
 Phe Leu Val Asp Ser Lys Gly Tyr Ile Asn Tyr Pro Ile Leu Gly Gln  
 145 150 155 160  
 60 Ile Tyr Val Glu Gly Leu Thr Arg Thr Glu Leu Glu Lys Glu Ile Gln  
 165 170 175  
 Lys Arg Ile Ile Ser Ser Gly Phe Ile Lys Asp Pro Thr Val Thr Val  
 180 185 190  
 65 Gln Leu Gln Asn Phe Lys Val Ser Val Leu Gly Glu Val Asn His Pro  
 195 200 205  
 Gly Ser Met Ser Val Lys Gly Glu Arg Ile Thr Leu Leu Glu Ala Ile  
 210 215 220  
 Gly Met Ala Gly Asp Leu Thr Ile Tyr Gly Arg Arg Asp Arg Val Phe  
 225 230 235 240  
 70 Val Ile Arg Glu Thr Asp Gly His Arg Glu Val Phe Gln Thr Asp Leu  
 245 250 255  
 Arg Lys Ala Asp Leu Leu Ala Ser Pro Val Tyr Tyr Leu His Gln Asn  
 260 265 270  
 75 Asp Val Ile Tyr Val Glu Pro Asn Asp Lys Lys Thr Gln Met Ser Glu  
 275 280 285

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Ile Asn Gln Asn Asn Val Asn Val Trp Leu Ser Val Thr Ser Thr  
 290 295 300  
 Leu Val Ser Ile Ser Thr Leu Thr Ile Thr Ile Ile Asp Lys Thr Lys  
 305 310 315 320

5

(2) INFORMATION FOR SEQ ID NO:298

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 582 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(11) MOLECULE TYPE: protein

15

(111) HYPOTHETICAL: YFS

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

20

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...582

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298

Ser Lys Ile Val Leu Arg Lys Phe Cys Thr Leu Ala Arg Met Lys Lys  
 1 5 10 15  
 Thr Asn Leu Phe Leu Ser Leu Leu Val Ile Phe Ile Thr Gly Ser Phe  
 20 25 30  
 Met Thr Ala Cys Ala Gln Lys Ser Lys Thr Asn Lys Leu Thr Glu Glu  
 35 40 45  
 Asp Arg Ser Arg Asn Glu Tyr Val Gln Ser Met Asp Val Leu Ser Asn  
 50 55 60  
 Ile Ile Gly Asn Val Arg Leu Tyr Phe Val Asp Thr Ile Ser Ile Lys  
 65 70 75 80  
 His Met Thr Arg Arg Gly Ile Asp Ala Met Leu Gly Gly Leu Asp Pro  
 85 90 95  
 Tyr Thr Glu Tyr Ile Pro Tyr Glu Glu Met Asp Glu Leu Lys Leu Met  
 100 105 110  
 Thr Thr Gly Glu Tyr Ala Gly Val Gly Ala Ile Ile Ser Gln Arg Pro  
 115 120 125  
 Asp Ser Ala Val Ile Ile Gln Arg Pro Met Glu Gly Met Pro Ala Asp  
 130 135 140  
 Glu Ala Gly Leu Ile Ala Gly Asp Arg Ile Leu Thr Ile Asp Gly Lys  
 145 150 155 160  
 Asp Phe Arg Lys Ser Thr Thr Pro Lys Val Ser Gln Ala Leu Lys Gly  
 165 170 175  
 Ile Ala Gly Thr Val Ala Lys Val Thr Val Met Arg Tyr Gly Glu Thr  
 180 185 190  
 Lys Pro Arg Thr Phe Ser Val Lys Arg Gln Lys Val Ile Met Asn Ser  
 195 200 205  
 Val Thr Tyr Ser Gly Met Leu Asp Gly Ser Ile Gly Tyr Ile Arg Leu  
 210 215 220  
 Asn Asn Phe Thr Asp Lys Ser Ala Glu Glu Val Arg Thr Ala Leu Leu  
 225 230 235 240  
 Asp Leu Arg Asp Lys Gln Gly Ala Lys Gly Leu Ile Leu Asp Leu Arg  
 245 250 255  
 Gly Asn Gly Gly Gly Leu Met Gln Ala Ala Ile Glu Ile Val Asn Leu  
 260 265 270  
 Phe Val Pro Lys Gly Lys Glu Val Val Thr Thr Lys Gly Arg Ile Ala  
 275 280 285  
 Glu Ser Ala Ser Val Phe Arg Thr Leu Thr Glu Pro Ile Asp Thr Lys  
 290 295 300  
 Leu Pro Ile Val Val Leu Ile Asp Gly Gln Ser Ala Ser Ser Ser Glu  
 305 310 315 320  
 Ile Val Ala Gly Ala Leu Gln Asp Met Asp Arg Ala Val Leu Met Gly  
 325 330 335  
 Gln Lys Ser Tyr Gly Lys Gly Leu Val Gln Thr Thr Arg Gln Leu Pro  
 340 345 350  
 Tyr Asn Gly Val Ile Lys Leu Thr Thr Ala Lys Tyr Tyr Ile Pro Ser  
 355 360 365  
 Gly Arg Cys Ile Gln Arg Leu Asp Tyr Ser Arg Thr Asn Arg Thr Gly  
 370 375 380  
 Met Ala Thr Ala Ile Pro Asp Ser Leu His Lys Ile Phe Tyr Thr Ala  
 385 390 395 400

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Ala Gly Arg Arg Val Glu Asp Ala Gly Gly Ile Leu Pro Asp Ile Glu  
 405 410 415  
 Val Lys Gln Asp Thr Ala Ala Thr Leu Leu Tyr Tyr Met Ala Ile Asn  
 420 425 430  
 5 Asn Asp Val Phe Asp Phe Val Thr Gly Tyr Val Leu Lys His Lys Thr  
 435 440 445  
 Ile Ala Lys Pro Glu Asp Phe Ser Ile Thr Asn Glu Asp Tyr Ala Ala  
 450 455 460  
 10 Phe Cys Lys Met Met Glu Glu Lys Lys Phe Asp Tyr Asp Arg Gln Ser  
 465 470 475 480  
 Gly Lys Met Leu Asp Lys Leu Glu Glu Leu Ala Lys Ile Glu Gly Tyr  
 485 490 495  
 Leu Pro Glu Ala Asn Ser Glu Leu Lys Ala Leu Arg Glu Lys Leu Lys  
 500 505 510  
 15 Pro Asn Leu Ser Arg Asp Leu Leu Arg Phe Lys Lys Glu Ile Thr Asn  
 515 520 525  
 Tyr Leu Asn Asn Glu Ile Val Thr Arg Tyr Tyr Glu Arg Gly Ser  
 530 535 540  
 20 Ile Arg Gln Ser Leu Pro Glu Asp Lys Val Val Lys Glu Ala Ile Lys  
 545 550 555 560  
 Leu Leu Lys Asp His Pro Glu Gln Ile Arg Gln Ile Leu Ala Ala Pro  
 565 570 575  
 Lys Ala Glu Asn Lys Gly  
 580  
 25  
 (2) INFORMATION FOR SEQ ID NO:299  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 985 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30  
 (ii) MOLECULE TYPE: protein  
 35  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 40  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...985  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:299  
 45  
 Val Thr Asp Lys Met Gln Asn Lys Gly Phe Val Ile Val Ile Thr Ser  
 1 5 10 15  
 Ala Leu Ala Ile Ile Cys Ala Phe Tyr Leu Ser Phe Ser Phe Val Thr  
 20 25 30  
 50 Asn Arg Tyr Glu Lys Lys Ala Lys Ala Met Gly Asp Val Ala Gly Met  
 35 40 45  
 Ala Tyr Leu Asp Ser Met Ser Asn Glu Lys Val Trp Phe Gly Tyr Thr  
 50 55 60  
 55 Leu Lys Glu Ala Gln Ala Gln Gln Ile Gly Leu Gly Leu Asp Leu Lys  
 65 70 75 80  
 Gly Gly Met Asn Val Ile Leu Lys Leu Asn Ala Ser Asp Leu Leu Arg  
 85 90 95  
 Asn Leu Ser Asn Lys Ser Leu Asp Pro Asn Phe Asn Lys Ala Leu Glu  
 100 105 110  
 60 Asn Ala Ala Lys Ser Thr Glu Gln Ser Asp Phe Ile Asp Ile Phe Val  
 115 120 125  
 Lys Glu Tyr Arg Lys Leu Asp Pro Asn Gly Arg Leu Ala Val Ile Phe  
 130 135 140  
 65 Gly Ser Gly Asp Leu Arg Asp Gln Ile Thr Ala Lys Ser Thr Asp Ala  
 145 150 155 160  
 Asp Val Val Arg Leu Leu Lys Glu Lys Tyr Asn Ser Ala Val Glu Ala  
 165 170 175  
 Ser Phe Asn Val Leu Arg Ala Arg Ile Asp Ala Phe Gly Val Val Ala  
 180 185 190  
 70 Pro Asn Leu Gln Arg Leu Glu Gly Gln Gly Arg Ile Leu Val Glu Leu  
 195 200 205  
 Pro Gly Val Lys Asp Pro Glu Arg Val Arg Thr Leu Leu Gln Arg Ser  
 210 215 220  
 75 Ala Asn Leu Gln Phe Trp Arg Thr Tyr Lys Phe Glu Glu Val Ser Gly  
 225 230 235 240

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Asp Leu Ile Ala Ala Asn Asp Arg Leu Ser Glu Leu Ala Met Asn Asn  
 Thr Asp Ala Thr Pro Glu Thr Glu Pro Ala Thr Thr Asp Ser Val Ala  
 245 250 255  
 5 Ala Thr Ala Asp Ser Ala Ala Val Gln Ala Val Ala Asp Ser Ala Thr  
 260 265 270  
 Val Ala Gln Lys Glu Ala Lys Asp Ala Thr Arg Lys Asp Ala Leu Phe  
 275 280 285  
 10 Ser Leu Leu Thr Pro Val Asn Arg Gly Gly Ala Val Val Gly Val Ala  
 290 295 300  
 Arg Arg Ala Asn Met Ala Gln Ile Ser Glu Met Leu Gln Gln Ala His  
 305 310 315 320  
 Asp Leu Lys Val Thr Arg Glu Asp Val Leu Phe Leu Trp Gly Ala Lys  
 325 330 335  
 15 Ala Ile Glu Asp Pro Glu Thr Lys Lys Glu Thr Asp Leu Tyr Glu Leu  
 340 345 350  
 Tyr Ala Ile Arg Thr Asn Arg Thr Gly Asp Pro Asp Leu Gly Gly Asp  
 355 360 365  
 20 Val Val Thr Ser Ala Lys Ser Asp Ile Gln Asn Asp Phe Gly Arg Ser  
 370 375 380  
 Glu Pro Ile Val Ser Met Thr Met Asn Glu Glu Gly Ala Arg Lys Trp  
 385 390 395 400  
 Ala Arg Ile Thr Lys Asp Asn Val Gly Arg Ala Ile Ala Ile Val Leu  
 405 410 415  
 25 Asp Gly Val Val Tyr Ser Ala Pro Asn Val Asn Asp Glu Ile Thr Gly  
 420 425 430  
 Gly Arg Ser Gln Ile Ser Gly His Phe Thr Val Glu Glu Ala Gly Asp  
 435 440 445  
 30 Leu Ala Asn Val Leu Asn Ser Gly Lys Met Asp Ala Thr Val Ser Ile  
 450 455 460  
 Glu Gln Glu Asn Val Ile Gly Pro Thr Leu Gly Ala Glu Ser Ile Lys  
 465 470 475 480  
 Ala Gly Phe Leu Ser Phe Leu Leu Ala Leu Val Ile Leu Met Cys Tyr  
 485 490 495  
 35 Met Cys Leu Ala Tyr Gly Phe Leu Pro Gly Leu Ile Ala Asn Gly Ala  
 500 505 510  
 Leu Ile Val Asn Ser Phe Phe Thr Leu Gly Val Leu Ala Ser Phe His  
 515 520 525  
 40 Ala Val Leu Thr Leu Ser Gly Ile Ala Gly Leu Val Leu Thr Leu Gly  
 530 535 540  
 Met Ala Val Asp Ala Asn Val Leu Ile Phe Glu Arg Ile Lys Glu Glu  
 545 550 555 560  
 Leu Arg Ala Gly Lys Thr Pro Ile Arg Ala Val Thr Asp Gly Tyr Gly  
 565 570 575  
 45 Asn Ala Phe Ser Ala Ile Phe Asp Ser Asn Val Thr Thr Ile Ile Thr  
 580 585 590  
 Gly Ile Ile Leu Phe Leu Tyr Gly Thr Gly Pro Ile Arg Gly Phe Ala  
 595 600 605  
 50 Thr Thr Leu Ile Ile Gly Leu Ile Ala Ser Phe Ile Thr Ala Val Phe  
 610 615 620  
 Leu Thr Arg Ile Val Phe Glu Lys Leu Ala Lys Lys Gly Arg Leu Asp  
 625 630 635 640  
 Lys Ile Thr Phe Thr Thr Ser Ile Thr Arg Asn Leu Leu Val Asn Pro  
 645 650 655  
 55 Ser Tyr Asn Ile Leu Gly Lys Arg Lys Thr Gly Phe Ile Ile Pro Val  
 660 665 670  
 Ile Ile Ile Val Leu Gly Leu Ile Ala Ser Phe Thr Ile Gly Leu Asn  
 675 680 685  
 60 Arg Gly Ile Glu Phe Ser Gly Gly Arg Asn Tyr Val Val Lys Phe Asp  
 690 695 700  
 Gln Pro Val Ser Ser Glu Ala Val Arg Ser Ala Leu Ser Ser Pro Leu  
 705 710 715 720  
 Gln Glu Lys Val Leu Val Thr Ser Ile Gly Thr Glu Gly Thr Glu Val  
 725 730 735  
 65 Arg Ile Ser Thr Asn Tyr Lys Ile Gln Glu Glu Ser Glu Glu Thr Glu  
 740 745 750  
 Ala Glu Ile Thr Asp Lys Leu Tyr Gln Ser Leu Lys Gly Phe Tyr Thr  
 755 760 765  
 70 Gln Gln Pro Thr Ala Asp Gln Phe Leu Asp Asn Ile Ile Ser Ser Gln  
 770 775 780  
 Lys Val Ser Pro Ser Met Ser Ser Asp Ile Thr Arg Gly Ala Ile Trp  
 785 790 795 800  
 Ala Val Leu Leu Ser Met Ile Phe Met Ala Ile Tyr Ile Leu Ile Arg  
 805 810 815  
 75 Phe Arg Asp Ile Ser Phe Ser Ala Gly Val Phe Val Ser Val Ala Ala  
 820 825 830



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5                   835                   840                   845  
 Thr Thr Phe Cys Ile Ile Ala Leu Tyr Ala Leu Leu Trp Lys Ile Leu  
 850                   855                   860  
 Pro Phe Thr Met Glu Ile Asp Gln Asn Phe Ile Ala Ala Ile Leu Ala  
 865                   870                   875                   880  
 Ile Ile Gly Tyr Ser Leu Asn Asp Thr Val Val Val Phe Asp Arg Ile  
 885                   890                   895  
 Arg Glu Thr Met Lys Leu Tyr Pro Asn Arg Asp Arg Tyr Gln Val Ile  
 900                   905                   910  
 10   Asn Asp Ala Leu Asn Ser Thr Leu Gly Arg Thr Leu Asn Thr Ser Leu  
 915                   920                   925  
 Thr Thr Phe Ile Val Met Leu Val Ile Phe Ile Phe Gly Gly Ala Thr  
 930                   935                   940  
 15   Met Arg Ser Phe Thr Phe Ser Ile Leu Leu Gly Ile Val Ile Gly Thr  
 945                   950                   955                   960  
 Tyr Ser Thr Leu Phe Val Ala Thr Pro Leu Ala Tyr Glu Ile Gln Lys  
 965                   970                   975  
 Arg Lys Leu Asn Lys Ala Ala Lys Lys  
 980                   985  
 20   (2) INFORMATION FOR SEQ ID NO:300  
       (i) SEQUENCE CHARACTERISTICS:  
           (A) LENGTH: 1046 amino acids  
           (B) TYPE: amino acid  
           (D) TOPOLOGY: linear  
       (ii) MOLECULE TYPE: protein  
       (iii) HYPOTHETICAL: YES  
       (vi) ORIGINAL SOURCE:  
           (A) ORGANISM: Porphyromonas gingivalis  
       (ix) FEATURE:  
           (A) NAME/KEY: misc\_feature  
           (B) LOCATION 1...1046  
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:300  
 40   Asp Phe Pro Trp Val Arg Val Lys Pro Glu Lys Lys Arg Lys Gln His  
       1                   5                   10                   15  
   Asn Ser Asn Asn Phe Lys Phe Asn Ala Lys Glu Lys Ser Met Lys Arg  
       20                   25                   30  
 45   Met Thr Leu Phe Phe Leu Cys Leu Leu Thr Ser Ile Gly Trp Ala Met  
       35                   40                   45  
   Ala Gln Asn Arg Thr Val Lys Gly Thr Val Ile Ser Ser Glu Asp Asn  
       50                   55                   60  
 50   Glu Pro Leu Ile Gly Ala Asn Val Val Val Val Gly Asn Thr Thr Ile  
       65                   70                   75                   80  
   Gly Ala Ala Thr Asp Leu Asp Gly Asn Phe Thr Leu Ser Val Pro Ala  
       85                   90                   95  
   Asn Ala Lys Met Leu Arg Val Ser Tyr Ser Gly Met Thr Thr Lys Glu  
       100                   105                   110  
 55   Val Ala Ile Ala Asn Val Met Lys Ile Val Leu Asp Pro Asp Ser Lys  
       115                   120                   125  
   Val Leu Glu Gln Val Val Val Leu Gly Tyr Gly Thr Gly Gln Lys Leu  
       130                   135                   140  
 60   Ser Thr Val Ser Gly Ser Val Ala Lys Val Ser Ser Glu Lys Leu Ala  
       145                   150                   155                   160  
   Glu Lys Pro Val Ala Asn Ile Met Asp Ala Leu Gln Gly Gln Val Ala  
       165                   170                   175  
   Gly Met Gln Val Met Thr Thr Ser Gly Asp Pro Thr Ala Val Ala Ser  
       180                   185                   190  
 65   Val Glu Ile His Gly Thr Gly Ser Leu Gly Ala Ser Ser Ala Pro Leu  
       195                   200                   205  
   Tyr Ile Val Asp Gly Met Gln Thr Ser Leu Asp Val Val Ala Thr Met  
       210                   215                   220  
 70   Asn Pro Asn Asp Phe Glu Ser Met Ser Val Leu Lys Asp Ala Ser Ala  
       225                   230                   235                   240  
   Thr Ser Ile Tyr Gly Ala Arg Ala Ala Asn Gly Val Val Phe Ile Gln  
       245                   250                   255  
   Thr Lys Lys Gly Lys Met Ser Glu Arg Gly Arg Ile Thr Phe Asn Ala  
       260                   265                   270  
 75   Ser Tyr Gly Ile Ser Gln Ile Leu Asn Thr Lys Pro Leu Asp Asn Met

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	275		280		285
	Met Thr Gly Asp Glu Leu Leu Asp Phe Gln Val Lys Ala Gly Phe Trp				
	290	295	300		
5	Gly Asn Asn Gln Thr Val Gln Lys Val Lys Asp Met Ile Leu Ala Gly				
	305	310	315		320
	Ala Glu Asp Leu Tyr Gly Asn Tyr Asp Ser Leu Lys Asp Glu Tyr Gly				
		325	330		335
	Lys Thr Leu Phe Pro Val Asp Phe Asn His Asp Ala Asp Trp Leu Lys				
		340	345		350
10	Ala Leu Phe Lys Thr Ala Pro Thr Ser Gln Gly Asp Ile Ser Phe Ser				
		355	360		365
	Gly Gly Ser Gln Gly Thr Ser Tyr Tyr Ala Ser Ile Gly Tyr Phe Asp				
		370	375		380
15	Gln Glu Gly Met Ala Arg Glu Pro Ala Asn Phe Lys Arg Tyr Ser Gly				
		385	390		400
	Arg Leu Asn Phe Glu Ser Arg Ile Asn Glu Trp Leu Lys Val Gly Ala				
		405	410		415
	Asn Leu Ser Gly Ala Ile Ala Asn Arg Arg Ser Ala Asp Tyr Phe Gly				
		420	425		430
20	Lys Tyr Tyr Met Gly Ser Gly Thr Phe Gly Val Leu Thr Met Pro Arg				
		435	440		445
	Tyr Tyr Asn Pro Phe Asp Val Asn Gly Asp Leu Ala Asp Val Tyr Tyr				
		450	455		460
25	Met Tyr Gly Ala Thr Arg Pro Ser Met Thr Glu Pro Tyr Phe Ala Lys				
		465	470		480
	Met Arg Pro Phe Ser Ser Glu Ser His Gln Ala Asn Val Asn Gly Phe				
		485	490		495
	Ala Gln Ile Thr Pro Ile Lys Gly Leu Thr Leu Lys Ala Gln Ala Gly				
		500	505		510
30	Val Asp Ile Thr Asn Thr Arg Thr Ser Ser Lys Arg Met Pro Asn Asn				
		515	520		525
	Pro Tyr Asp Ser Thr Pro Leu Gly Glu Arg Arg Glu Arg Ala Tyr Arg				
		530	535		540
35	Asp Val Ser Lys Ser Phe Thr Asn Thr Ala Glu Tyr Lys Phe Ser Ile				
		545	550		555
	Asp Glu Lys His Asp Leu Thr Ala Leu Met Gly His Glu Tyr Ile Glu				
		565	570		575
	Tyr Glu Gly Asp Val Ile Gly Ala Ser Ser Lys Gly Phe Glu Ser Asp				
		580	585		590
40	Lys Leu Met Leu Leu Ser Gln Gly Lys Thr Gly Asn Ser Leu Ser Leu				
		595	600		605
	Pro Glu His Arg Val Ala Glu Tyr Ala Tyr Leu Ser Phe Phe Ser Arg				
		610	615		620
45	Phe Asn Tyr Gly Phe Asp Lys Trp Met Tyr Ile Asp Phe Ser Val Arg				
		625	630		635
	Asn Asp Gln Ser Ser Arg Phe Gly Ser Asn Asn Arg Ser Ala Trp Phe				
		645	650		655
	Tyr Ser Val Gly Gly Met Phe Asp Ile Tyr Asn Lys Phe Ile Gln Glu				
		660	665		670
50	Ser Asn Trp Leu Ser Asp Leu Arg Leu Lys Met Ser Tyr Gly Thr Thr				
		675	680		685
	Gly Asn Ser Glu Ile Gly Asn Tyr Asn His Gln Ala Leu Val Thr Val				
		690	695		700
55	Asn Asn Tyr Thr Glu Asp Ala Met Gly Leu Ser Ile Ser Thr Ala Gly				
		705	710		715
	Asn Pro Asp Leu Ser Trp Glu Lys Gln Ser Gln Phe Asn Phe Gly Leu				
		725	730		735
	Ala Ala Gly Ala Phe Asn Asn Arg Leu Ser Ala Glu Val Asp Phe Tyr				
		740	745		750
60	Val Arg Thr Thr Asn Asp Met Leu Ile Asp Val Pro Met Pro Tyr Ile				
		755	760		765
	Ser Gly Phe Phe Ser Gln Tyr Gln Asn Val Gly Ser Met Lys Asn Thr				
		770	775		780
65	Gly Val Asp Leu Ser Leu Lys Gly Thr Ile Tyr Gln Asn Lys Asp Trp				
		785	790		795
	Asn Val Tyr Ala Ser Ala Asn Phe Asn Tyr Asn Arg Gln Glu Ile Thr				
		805	810		815
	Lys Leu Phe Phe Gly Leu Asn Lys Tyr Met Leu Pro Asn Thr Gly Thr				
		820	825		830
70	Ile Trp Glu Ile Gly Tyr Pro Asn Ser Phe Tyr Met Ala Glu Tyr Ala				
		835	840		845
	Gly Ile Asp Lys Lys Thr Gly Lys Gln Leu Trp Tyr Val Pro Gly Gln				
		850	855		860
75	Val Asp Ala Asp Gly Asn Lys Val Thr Thr Ser Gln Tyr Ser Ala Asp				
		865	870		875
					880



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Lys Thr Glu Val Trp Ile Cys Pro Leu Thr Asn Pro Asp Gly Ala Tyr  
 260 265 270  
 Arg Ala Gly Asn His Thr Val Gln Gly Ala Thr Arg Tyr Asn Ala Asn  
 275 280 285  
 5 Asn Val Asp Leu Asn Arg Asn Phe Lys Asp Asp Val Ala Gly Asp His  
 290 295 300  
 Pro Asp Gly Lys Pro Trp Gln Pro Glu Ala Thr Ala Phe Met Asp Leu  
 305 310 315 320  
 10 Glu Gly Asn Thr Ser Phe Val Leu Gly Ala Asn Ile His Gly Gly Thr  
 325 330 335  
 Glu Val Val Asn Tyr Pro Trp Asp Asn Lys Lys Glu Arg His Ala Asp  
 340 345 350  
 Asp Glu Trp Tyr Lys Leu Ile Ser Arg Asn Tyr Ala Ala Cys Gln  
 355 360 365  
 15 Ser Ile Ser Ala Ser Tyr Met Thr Ser Glu Thr Asn Ser Gly Ile Ile  
 370 375 380  
 Asn Gly Ser Asp Trp Tyr Val Ile Arg Gly Ser Arg Gln Asp Asn Ala  
 385 390 395 400  
 20 Asn Tyr Phe His Arg Leu Arg Glu Ile Thr Leu Glu Ile Ser Asn Thr  
 405 410 415  
 Lys Leu Val Pro Ala Ser Gln Leu Pro Lys Tyr Trp Asn Leu Asn Lys  
 420 425 430  
 Glu Ser Leu Leu Ala Leu Ile Glu Glu Ser Leu Tyr Gly Ile His Gly  
 435 440 445  
 25 Thr Val Thr Ser Ala Ala Asn Gly Gln Pro Leu Lys Cys Gln Ile Leu  
 450 455 460  
 Ile Glu Asn His Asp Lys Arg Asn Ser Asp Val Tyr Ser Asp Ala Thr  
 465 470 475 480  
 30 Thr Gly Tyr Tyr Val Arg Pro Ile Lys Ala Gly Thr Tyr Thr Val Lys  
 485 490 495  
 Tyr Lys Ala Glu Gly Tyr Pro Glu Ala Thr Arg Thr Ile Thr Ile Lys  
 500 505 510  
 Asp Lys Glu Thr Val Ile Met Asp Ile Ala Leu Gly Asn Ser Val Pro  
 515 520 525  
 35 Leu Pro Val Pro Asp Phe Thr Ala Ser Pro Met Thr Ile Ser Val Gly  
 530 535 540  
 Glu Ser Val Gln Phe Gln Asp Gln Thr Thr Asn Pro Thr Asn Trp  
 545 550 555 560  
 40 Glu Trp Thr Phe Glu Gly Gly Gln Pro Ala Met Ser Thr Glu Gln Asn  
 565 570 575  
 Pro Leu Val Ser Tyr Ser His Pro Gly Gln Tyr Asp Val Thr Leu Lys  
 580 585 590  
 Val Trp Asn Ala Ser Gly Ser Asn Thr Ile Thr Lys Glu Lys Phe Ile  
 595 600 605  
 45 Thr Val Asn Ala Val Met Pro Val Ala Glu Phe Val Gly Thr Pro Thr  
 610 615 620  
 Glu Ile Glu Glu Gly Gln Thr Val Ser Phe Gln Asn Gln Ser Thr Asn  
 625 630 635 640  
 50 Ala Thr Asn Tyr Val Trp Ile Phe Asp Gly Gly Thr Pro Ala Thr Ser  
 645 650 655  
 Glu Asp Glu Asn Pro Thr Val Leu Tyr Ser Lys Ala Gly Gln Tyr Asp  
 660 665 670  
 Val Thr Leu Lys Ala Ile Ser Ala Ser Gly Glu Thr Val Lys Thr Lys  
 675 680 685  
 55 Glu Lys Tyr Ile Thr Val Lys Lys Ala Pro Val Pro Ala Pro Val Ala  
 690 695 700  
 Asp Phe Glu Gly Thr Pro Arg Lys Val Lys Lys Gly Glu Thr Val Thr  
 705 710 715 720  
 60 Phe Lys Asp Leu Ser Thr Asn Asn Pro Thr Ser Trp Leu Trp Val Phe  
 725 730 735  
 Glu Gly Gly Ser Pro Ala Thr Ser Thr Glu Gln Asn Pro Val Val Thr  
 740 745 750  
 Tyr Asn Glu Thr Gly Lys Tyr Asp Val Gln Leu Thr Ala Thr Asn Glu  
 755 760 765  
 65 Gly Gly Ser Asn Val Lys Lys Ala Glu Asp Tyr Ile Glu Val Ile Leu  
 770 775 780  
 Asp Asp Ser Val Glu Asp Ile Val Ala Gln Thr Gly Ile Val Ile Arg  
 785 790 795 800  
 70 Pro Gln Asn Gly Thr Lys Gln Ile Leu Ile Glu Ala Asn Ala Ala Ile  
 805 810 815  
 Lys Ala Ile Val Leu Tyr Asp Ile Asn Gly Arg Val Val Leu Lys Thr  
 820 825 830  
 Thr Pro Asn Gln Leu Arg Ser Thr Val Asp Leu Ser Ile Leu Pro Glu  
 835 840 845  
 75 Gly Ile Tyr Thr Ile Asn Ile Lys Thr Glu Lys Ser Ala Arg Thr Glu

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850  
Lys Ile His Ile Gly  
865

855

860

- 5 (2) INFORMATION FOR SEQ ID NO:302
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 106 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...106
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:302
- 25 Leu Ser Tyr Ser Gly Glu Ser Asp Ala Lys Glu Ser Asp Gln Asn Cys  
1 5 10 15  
Arg Lys Cys Thr Phe Ile Gly Phe Glu Lys Arg Val Asn Thr Met Arg  
20 25 30  
30 Leu Ile Lys Ala Phe Leu Val Gln Leu Leu Leu Leu Pro Ile Phe Phe  
35 40 45  
Tyr Lys Arg Phe Ile Ser Pro Leu Thr Pro Pro Ser Cys Arg Phe Thr  
50 55 60  
Pro Ser Cys Ser Ser Tyr Ala Ile Glu Ala Leu Arg Lys Tyr Gly Pro  
65 70 75 80  
35 Gly Lys Gly Leu Leu Ser Ile Lys Arg Ile Leu Arg Cys His Pro  
85 90 95  
Trp Gly Gly Ser Gly Tyr Asp Pro Val Pro  
100 105
- 40 (2) INFORMATION FOR SEQ ID NO:303
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 861 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...861
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:303
- 60 Leu Glu Met Ala Tyr Asp Phe Thr Gln Thr Phe Arg Asn Ser Leu Glu  
1 5 10 15  
Tyr Ser Tyr Gln Glu Ala Thr Arg Leu Gly Val Val Ala Val Thr Gln  
20 25 30  
65 Asp Met Leu Val Leu Gly Ile Ile Arg Asp Gly Asp Asn Gly Ala Ile  
35 40 45  
Asp Ile Met Arg His Tyr Gly Ile Asn Leu Tyr Glu Leu Lys Arg Leu  
50 55 60  
Ile Glu Leu Glu Ala Ile Ala Glu Ser Leu Pro Ala Ser Pro Glu Gly  
65 70 75 80  
70 Ser Pro Ile Phe Thr Pro Ser Ala Arg Glu Ala Ile Asp Asp Ala Thr  
85 90 95  
Asp Ile Cys Ala Asp Met Glu Asp Glu Ala Val Ser Pro Val His Leu  
100 105 110  
75 Leu Leu Ser Ile Leu Asn Ser Thr Gln Glu Ser Leu Val Gln Lys Ile  
115 120 125

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Phe Met Lys Gln Gly Ile Lys Tyr Asp Thr Ile Leu Ser Asp Tyr Phe  
 130 135 140  
 Gly Gln Arg Asn Pro Ser Glu Gly Lys Ser Pro Ser Glu Met Glu Ile  
 145 150 155  
 5 Leu Asp Gly Tyr Gln Asp Asn Asp Phe Asp Asp Glu Glu Asp Glu Ser  
 165 170 175  
 Ser Pro Pro Ser Gly Asn Ser Gly Thr Gly Gly Gly Ser Gly Asp Ala  
 180 185 190  
 10 Pro Glu Gln Asn Thr Gly Gly Gly Asp Thr Thr Thr Thr Arg Ser  
 195 200 205  
 Gly Gly Asp Thr Pro Ala Leu Asp Thr Phe Gly Thr Asp Ile Thr Ala  
 210 215 220  
 Met Ala Ala Ala Gly Lys Leu Asp Pro Val Val Gly Arg Glu Gln Glu  
 225 230 235  
 15 Ile Glu Arg Val Ile Gln Ile Leu Ser Arg Arg Lys Lys Asn Asn Pro  
 245 250 255  
 Val Leu Ile Gly Glu Pro Gly Val Gly Lys Ser Ala Ile Val Glu Gly  
 260 265 270  
 20 Leu Ala Glu Arg Ile Val Asn Arg Lys Val Ser Arg Ile Leu Phe Asp  
 275 280 285  
 Lys Arg Ile Ile Ser Leu Asp Leu Ala Gln Met Val Ala Gly Thr Lys  
 290 295 300  
 Tyr Arg Gly Gln Phe Glu Glu Arg Leu Lys Ala Val Leu Asp Glu Leu  
 305 310 315  
 25 Lys Lys Asn Pro Gln Ile Ile Leu Phe Ile Asp Glu Ile His Thr Ile  
 325 330 335  
 Val Gly Ala Gly Ser Ala Ala Gly Ser Met Asp Thr Ala Asn Met Leu  
 340 345 350  
 30 Lys Pro Ala Leu Ala Arg Gly Gln Val Gln Cys Ile Gly Ala Thr Thr  
 355 360 365  
 Leu Asp Glu Tyr Arg Lys Asn Ile Glu Lys Asp Gly Ala Leu Glu Arg  
 370 375 380  
 Arg Phe Gln Lys Val Pro Ile Ala Pro Ser Thr Ala Glu Glu Thr Leu  
 385 390 395  
 35 Thr Ile Leu Gln Asn Ile Lys Glu Lys Tyr Glu Asp Tyr His Gly Val  
 405 410 415  
 Arg Tyr Thr Asp Glu Ala Ile Lys Ala Ala Val Glu Leu Thr Asp Arg  
 420 425 430  
 40 Tyr Val Ser Asp Arg Phe Phe Pro Asp Lys Ala Ile Asp Ala Met Asp  
 435 440 445  
 Glu Ala Gly Ala Ser Val His Ile Thr Asn Val Val Ala Pro Lys Glu  
 450 455 460  
 Ile Glu Ile Leu Glu Ala Glu Leu Ala Ser Val Arg Glu Asn Lys Leu  
 465 470 475  
 45 Ser Ala Val Lys Ala Gln Asn Tyr Glu Leu Ala Ala Ser Phe Arg Asp  
 485 490 495  
 Gln Glu Arg Arg Thr Gln Gln Gln Ile Ala Glu Glu Lys Lys Lys Trp  
 500 505 510  
 50 Glu Glu Gln Met Ser Lys His Arg Glu Thr Val Asp Glu Asn Val Val  
 515 520 525  
 Ala His Val Val Ala Leu Met Thr Gly Val Pro Ala Glu Arg Leu Ser  
 530 535 540  
 Thr Gly Glu Gly Glu Arg Leu Arg Thr Met Ala Asp Asp Leu Lys Thr  
 545 550 555  
 55 Lys Val Val Gly Gln Asp Thr Ala Ile Glu Lys Met Val His Ala Ile  
 565 570 575  
 Gln Arg Asn Arg Leu Gly Leu Arg Asn Glu Lys Lys Pro Ile Gly Ser  
 580 585 590  
 60 Phe Leu Phe Leu Gly Pro Thr Gly Val Gly Lys Thr Tyr Leu Ala Lys  
 595 600 605  
 Lys Leu Ala Glu Tyr Leu Phe Glu Asp Glu Asn Ala Met Ile Arg Val  
 610 615 620  
 Asp Met Ser Glu Tyr Met Glu Lys Phe Ser Val Ser Arg Leu Val Gly  
 625 630 635  
 65 Ala Pro Pro Gly Tyr Val Gly Tyr Glu Glu Gly Gly Gln Leu Thr Glu  
 645 650 655  
 Arg Val Arg Arg Lys Pro Tyr Ser Val Val Leu Leu Asp Glu Ile Glu  
 660 665 670  
 70 Lys Ala His Ala Asp Val Phe Asn Leu Leu Leu Gln Val Met Asp Glu  
 675 680 685  
 Gly Gln Leu Thr Asp Ser Leu Gly Arg Arg Val Asn Phe Lys Asn Thr  
 690 695 700  
 Val Ile Ile Ile Thr Ser Asn Val Gly Thr Arg Gln Leu Lys Asp Phe  
 705 710 715  
 75 Gly Gln Gly Ile Gly Phe Arg Ser Glu Lys Asp Glu Glu Ala Asn Lys

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290 295 300  
 Trp Gln Lys Arg Ile Asn Thr Thr Val Phe Val Pro Glu Ser Met Tyr  
 305 310 315 320  
 Ala Asn Lys Leu Met Arg Leu Leu Met Gln Arg Lys Lys Ser Ile Ala  
 325 330 335  
 5 Ile Val Ile Asp Glu Leu Gly Gly Thr Ala Gly Met Val Thr Leu Glu  
 340 345 350  
 Asp Leu Val Glu Glu Ile Phe Gly Asp Ile Glu Asp Glu His Asp Thr  
 355 360 365  
 10 Arg Lys Ile Ile Ala Lys Gln Leu Gly Pro His Thr Tyr Leu Val Ser  
 370 375 380  
 Gly Arg Met Glu Ile Asp Asp Val Asn Glu Arg Phe Gly Leu Ser Leu  
 385 390 395 400  
 15 Pro Glu Ser Asp Asp Tyr Leu Thr Val Ala Gly Phe Ile Leu Asn Ser  
 405 410 415  
 His Gln Asn Ile Pro Gln Ala Asn Glu Val Val Glu Ile Ala Pro Tyr  
 420 425 430  
 Thr Phe Thr Ile Leu Arg Ser Ser Ser Thr Lys Ile Glu Leu Val Lys  
 435 440 445  
 20 Met Ser Ile Asp Asp Gln Ser Asn  
 450 455

(2) INFORMATION FOR SEQ ID NO:305

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 299 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 35 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...299  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:305

Leu Lys Lys Glu Ile Thr Met Lys Gln Asn Tyr Phe Lys Arg Val Cys  
 1 5 10 15  
 45 Ser Leu Leu Trp Leu Val Leu Pro Met Leu Ile Met Pro Leu Glu Val  
 20 25 30  
 Ala Ala Gln Glu Ile Ile Pro Asn Glu Glu Val Leu Glu Ser Leu Thr  
 35 40 45  
 50 Phe Val Ala Pro Val Glu Glu Thr Asp Ala Ile Glu Ala Glu Val Glu  
 50 55 60  
 Ala Leu Gln Glu Ile Val Ala Thr Glu Glu Ile Ala Glu Gln Ala Val  
 65 70 75 80  
 Arg Ser Tyr Thr Tyr Thr Val Tyr Arg Asp Gly Val Lys Ile Ala Ser  
 85 90 95  
 55 Gly Leu Thr Glu Pro Thr Phe Leu Asp Glu Asp Val Pro Ala Gly Glu  
 100 105 110  
 His Thr Tyr Cys Val Glu Val Gln Tyr Gln Gly Gly Val Ser Asp Lys  
 115 120 125  
 60 Val Cys Val Asp Val Glu Val Lys Asp Phe Lys Pro Val Thr Asn Leu  
 130 135 140  
 Thr Gly Thr Ala Ser Asn Asp Glu Val Ser Leu Asp Trp Asp Gly Val  
 145 150 155 160  
 Glu Glu Lys Ala Glu Glu Pro Ala Ser Asp Lys Ala Val Ser Tyr Asn  
 165 170 175  
 65 Val Tyr Lys Asn Gly Thr Leu Ile Gly Asn Thr Ala Glu Thr His Tyr  
 180 185 190  
 Val Glu Thr Gly Val Ala Asn Gly Thr Tyr Ile Tyr Glu Val Glu Val  
 195 200 205  
 70 Lys Tyr Pro Asp Gly Val Ser Pro Lys Val Ala Val Thr Val Thr Val  
 210 215 220  
 Thr Asn Ser Ser Leu Ser Asn Val Asp Gly Gln Ala Pro Tyr Thr Leu  
 225 230 235 240  
 Arg Val Glu Gly Lys Lys Ile Ile Ala Glu Ala His Gly Met Ile Thr  
 245 250 255  
 75 Leu Tyr Asp Ile Asn Gly Arg Thr Val Ala Val Ala Pro Asn Arg Leu



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260  
 Glu Tyr Met Ala Gln Thr Gly Phe Tyr Ala Val Arg Phe Asp Val Gly  
 275  
 280  
 290  
 Asn Lys His His Val Ser Lys Ile Gln Val Arg  
 295

(2) INFORMATION FOR SEQ ID NO:306

10 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 377 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature  
 (B) LOCATION 1...377

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:306

30 Leu Phe Asn His Lys Lys Ser Trp Tyr Glu Thr Phe Gln Phe Tyr Leu  
 1 5 10 15  
 Val Val Phe Arg Ser Gly Phe Ile Leu Cys Glu Asn Thr Leu Ala  
 20 25 30  
 Gln Gln Lys Thr Glu Glu Phe Ala Pro Val Ser Asp Leu Arg Ala Glu  
 35 40 45  
 Ala Tyr Gly Ser Thr Val Phe Leu His Trp Thr Pro Pro Tyr Asp Asn  
 50 55 60  
 35 Pro Met Ile Pro Leu Ser Glu Ser Phe Glu Ser Gly Ile Pro Ala Ile  
 65 70 75 80  
 Trp Lys Thr Ile Asp Ala Asp Gly Asp Gly Tyr Asn Trp Met His Leu  
 85 90 95  
 40 Thr Asn Phe Thr Gly Gln Ser Gly Leu Cys Val Ser Ser Ala Ser Tyr  
 100 105 110  
 Ile Gly Gly Val Gly Ala Leu Thr Pro Asp Asn Tyr Leu Ile Thr Pro  
 115 120 125  
 Glu Leu Lys Leu Pro Thr Asp Ala Leu Val Glu Ile Ile Tyr Trp Val  
 130 135 140  
 45 Cys Thr Gln Asp Leu Thr Ala Pro Ser Glu His Tyr Ala Val Tyr Ser  
 145 150 155 160  
 Ser Ser Thr Gly Asn Asn Ala Ala Asp Phe Val Asn Leu Leu Tyr Glu  
 165 170 175  
 50 Glu Thr Leu Thr Ala Lys Arg Ile Gln Ser Pro Glu Leu Ile Arg Gly  
 180 185 190  
 Asn Arg Thr Gln Gly Val Trp Tyr Gln Arg Lys Val Val Leu Pro Asn  
 195 200 205  
 Asp Thr Lys Tyr Val Ala Phe Arg His Phe Asn Ser Thr Asp Asn Phe  
 210 215 220  
 55 Trp Leu Asn Leu Asp Glu Val Ser Ile Leu Tyr Thr Pro Leu Pro Arg  
 225 230 235 240  
 Arg Ala Pro Cys Pro His Pro Gly Gly Tyr Thr Tyr Ser Val Phe Arg  
 245 250 255  
 60 Asp Gly Gln Lys Ile Ala Ser Gly Leu Ser Ala Leu Ala Tyr Ile Asp  
 260 265 270  
 Thr Asp Val Pro Tyr Gly Thr Gln Asp Tyr Cys Val Gln Val Asn Tyr  
 275 280 285  
 Leu Gln Gly Asp Ser Tyr Lys Val Cys Lys Asn Ile Val Val Ala Asn  
 290 295 300  
 65 Ser Ala Asn Ile Tyr Gly Ala Asp Lys Pro Phe Ala Leu Thr Val Val  
 305 310 315 320  
 Gly Lys Thr Ile Val Ala Ser Ala Phe Lys Gly Glu Ile Thr Leu Tyr  
 325 330 335  
 70 Asp Ile Arg Gly Arg Leu Ile Ala Ser Gly Cys Asp Thr Leu Arg Tyr  
 340 345 350  
 Lys Ala Glu Asn Gly Phe Tyr Leu Ile Lys Ile Gln Val Asn Gly Thr  
 355 360 365  
 Val Tyr Thr Glu Lys Ile Gln Ile Gln  
 370 375

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

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(31) SEQUENCE DESCRIPTION: SEQ ID NO:307

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55 (2) INFORMATION FOR SEQ ID NO:308
      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 295 amino acids
          (B) TYPE: amino acid
60      (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: protein

      (iii) HYPOTHETICAL: YES

      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Porphyromonas gingivalis

      (ix) FEATURE:
70      (A) NAME/KEY: misc_feature
          (B) LOCATION 1...295

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:308

75 Thr Lys Lys Thr Leu Met Lys Lys Leu Phe Leu Ser Leu Thr Ser Leu

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1      5      10      15
Val Met Val Phe Ala Val Ala Ser Cys Asp Ile Ile Asp Lys Asp Gln
20      25      30
5 Thr Leu Leu Pro Ala Pro Thr Asn Val Thr Pro Asp Asn Pro Asp Asp
35      40      45
Asn Pro Ser Glu Ile Asp Ile Thr Gln Thr His Thr Glu Lys Tyr Val
50      55      60
Leu Ala Glu Glu Phe Thr Gly Gln Lys Cys Leu Asn Cys Pro Lys Gly
65      70      75      80
10 His Arg Lys Leu Ala Ala Leu Lys Glu Gln Tyr Gly Lys Arg Leu Thr
85      90      95
Val Val Gly Ile His Ala Gly Pro Gly Ser Leu Val Pro Pro Leu Phe
100      105      110
15 Arg Thr Glu Ala Gly Asp Ala Tyr Tyr Ser Lys Phe Ala Asn Asn Thr
115      120      125
Pro Leu Pro Ala Leu Met Val Ser Arg Lys Lys Phe Gly Ser Ser Tyr
130      135      140
Val Tyr Asp Lys Ser Tyr Lys Thr Trp Asp Val Pro Ile Ala Glu Gln
145      150      155      160
20 Met Glu Gln Lys Ala Lys Ile Asn Ile Phe Ala Val Ala Glu Tyr Thr
165      170      175
Asp Thr Gln Lys Ile Lys Val Thr Val Lys Gly Lys Ile Leu Glu Gly
180      185      190
Asn Thr Leu Pro Lys Ser Met Val Gln Val Tyr Leu Leu Glu Asp Lys
195      200      205
25 Leu Ile Ala Pro Gln Val Asp Gly Asn Thr Thr Val Glu Asn Tyr Glu
210      215      220
His Asn His Val Leu Arg Gly Ala Val Asn Gly Ile Trp Gly Glu Glu
225      230      235      240
30 Phe Val Asn Leu Lys Asp Tyr Leu Tyr Thr Tyr Ala Val Glu Pro Leu
245      250      255
Ser Gly Met Ser Phe Val Ala Glu Asn Tyr Ser Ile Val Ala Phe Val
260      265      270
35 Tyr Asp Val Gln Thr Phe Glu Val Tyr Asp Val Val His Val Lys Ile
275      280      285
Asn Pro Gln Ser Asp Gly Lys
290      295

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## (2) INFORMATION FOR SEQ ID NO:309

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...230

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:309

```

60 Thr Asn Lys Lys Glu Glu Thr Met Lys Lys Ser Ser Val Val Ala Ser
1      5      10      15
Val Leu Ala Val Ala Leu Val Phe Ala Gly Cys Gly Leu Asn Asn Met
20      25      30
Ala Lys Gly Gly Leu Ile Gly Ala Gly Val Gly Gly Ala Ile Gly Ala
35      40      45
65 Gly Val Gly Asn Val Ala Gly Asn Thr Ala Val Gly Ala Ile Val Gly
50      55      60
Thr Ala Val Gly Gly Ala Ala Gly Ala Leu Ile Gly Lys Lys Met Asp
65      70      75      80
Lys Gln Lys Lys Glu Leu Glu Ala Ala Val Pro Asp Ala Thr Ile Gln
95      100      105      110
70 Thr Val Asn Asp Gly Glu Ala Ile Leu Val Thr Phe Asp Ser Gly Ile
100      105      110
Leu Phe Ala Thr Asn Ser Ser Thr Leu Ser Pro Asn Ser Arg Thr Ala
115      120      125
75 Leu Thr Lys Phe Ala Ala Asn Met Asn Lys Asn Pro Asp Thr Asp Ile

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130 135 140  
 Arg Ile Val Gly His Thr Asp Asn Thr Gly Ser Asp Lys Ile Asn Asp  
 145 150 155 160  
 Pro Leu Ser Glu Arg Arg Ala Ala Ser Val Tyr Ser Phe Leu Asn Ser  
 5 165 170 175  
 Gln Gly Val Ser Met Ser Arg Met Ala Ala Glu Gly Arg Gly Ser His  
 180 185 190  
 Glu Pro Val Ala Asp Asn Ser Thr Val Ala Gly Arg Ser Ala Asn Arg  
 195 200 205  
 10 Arg Val Glu Val Tyr Ile Leu Pro Asn Ala Lys Met Ile Glu Gln Ala  
 210 215 220  
 Gln Gln Gly Thr Leu Lys  
 225 230

15 (2) INFORMATION FOR SEQ ID NO:310

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...342

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310

35 Asn Arg Asn Arg Asn Met Ser Lys Lys Ser Ile Leu Leu Leu Cys Cys  
 1 5 10 15  
 Ser Leu Cys Phe Ile Ser Ala Thr Lys Ala Val Thr Pro Val Arg Asn  
 20 25 30  
 40 Val Arg Asn Ser Gln Val Asn Ser Lys Ala Lys Thr Glu Arg Thr Lys  
 35 40 45  
 Pro Ser Asp Ser Val Arg Tyr Ile Ser Asn Met Ile Ala Asp Arg Leu  
 50 55 60  
 Glu Phe Arg Asn Lys Ile Ser Ser Glu Lys Glu Val Arg Lys Ala Glu  
 65 70 75 80  
 45 Tyr Glu Asn Arg Leu Ala Met Glu Ala Leu Asn Tyr Pro Ala Ile Asp  
 85 90 95  
 Leu Tyr Gly Glu Asp Ser Trp Ser Glu Tyr Val Asn Pro Phe Val Gly  
 100 105 110  
 50 Ala Gly Thr Asp Val Glu Ile Pro Asn Ser Tyr Asp Ile Asp Cys Ser  
 115 120 125  
 Ser Phe Val Met Pro Val Glu Asp Lys Gln Val Thr Ser Gln Phe Gly  
 130 135 140  
 Tyr Arg Arg Arg Phe Gly Arg Met His Tyr Gly Ile Asp Leu Ser Val  
 145 150 155 160  
 55 Asn Arg Gly Asp Thr Ile Arg Ala Ala Phe Asp Gly Lys Val Arg Val  
 165 170 175  
 Arg Ser Tyr Glu Ala Arg Gly Tyr Gly Tyr Tyr Ile Val Leu Arg His  
 180 185 190  
 60 Pro Asn Gly Leu Glu Thr Val Tyr Gly His Met Ser Arg Gln Leu Val  
 195 200 205  
 Asp Glu Asn Gln Ile Val Arg Ala Gly Gln Pro Ile Gly Leu Gly Gly  
 210 215 220  
 Ser Thr Gly Arg Ser Thr Gly Pro His Leu His Phe Glu Thr Arg Phe  
 225 230 235 240  
 65 Met Gly Ile Pro Ile Asn Pro Ser Thr Ile Ile Asp Phe Asp Asn Gly  
 245 250 255  
 Val Pro Leu Arg Asp Ile Tyr Thr Phe Lys Arg Gly Ser Asn Ser Arg  
 260 265 270  
 70 Tyr Ala Lys Ala Ser Lys Thr Ser Ser Arg Tyr Ala Lys Lys Gly Lys  
 275 280 285  
 Lys Gly Arg Gln Ala Ser Ser Pro Met Thr Tyr Arg Ile Lys Lys Gly  
 290 295 300  
 Asp Thr Leu Glu Thr Ile Ala Lys Arg His Gly Thr Ser Val Gln Lys  
 305 310 315 320  
 75 Leu Cys Ala Thr Asn Gly Ile Gly Lys Ser Lys Ile Leu Thr Pro Gly

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325  
Lys Ala Leu Arg Ile Lys 330 335  
340

## 5 (2) INFORMATION FOR SEQ ID NO:311

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 159 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

15 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

20 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311

25 Pro Ser Lys Thr Ile Ile Lys Thr Met Ala Lys Ile Asn Phe Tyr Ala  
1 5 10 15  
Glu Gly Val Ser Leu Pro Arg Ile Arg Arg Ile Val Gly Lys Trp  
20 25 30  
Ile Ala Glu Val Cys Ser Arg Tyr Gly Lys Ala Val Gly Glu Ile Ser  
35 40 45  
Tyr Leu Phe Cys Asp Asp Glu Tyr Ile Leu Lys Ala Asn Gln Glu Phe  
50 55 60  
Leu Asp His Asp Tyr Tyr Thr Asp Ile Ile Thr Phe Asp Ser Cys Glu  
65 70 75 80  
35 Ala Asp Thr Val Asn Gly Asp Leu Leu Ile Ser Leu Asp Thr Val Arg  
85 90 95  
Ser Asn Ala Arg Ala Leu Asp Leu Arg Tyr Glu Asp Glu Leu His Arg  
100 105 110  
40 Val Ile Ile His Gly Ile Leu His Leu Cys Gly Leu Lys Asp Lys Ser  
115 120 125  
Lys Lys Asp Glu Ala Gln Met Arg Ala Ala Glu Glu Lys Ala Leu Val  
130 135 140  
Met Leu Arg Glu Thr Ile Gly Ser Glu Leu Ser Leu Leu His Thr  
145 150 155

## 45 (2) INFORMATION FOR SEQ ID NO:312

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 395 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

60 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312

65 Lys Ser Lys Thr Met Lys Val Lys Tyr Leu Met Leu Thr Leu Val Gly  
1 5 10 15  
Ala Ile Ala Leu Asn Ala Ser Ala Gln Glu Asn Thr Val Pro Ala Thr  
20 25 30  
70 Gly Gln Leu Pro Ala Lys Asn Val Ala Phe Ala Arg Asn Lys Ala Gly  
35 40 45  
Ser Asn Trp Phe Val Thr Leu Gln Gly Gly Val Ala Ala Gln Phe Leu  
50 55 60  
Asn Asp Asn Asn Asn Lys Asp Leu Met Asp Arg Leu Gly Ala Ile Gly  
65 70 75 80

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Ser Leu Ser Val Gly Lys Tyr His Ser Pro Phe Phe Ala Thr Arg Leu  
 85 90 95  
 Gln Ile Asn Gly Gly Gln Ala His Thr Phe Leu Gly Lys Asn Gly Glu  
 100 105 110  
 5 Gln Glu Ile Asn Thr Asn Phe Gly Ala Ala His Phe Asp Phe Met Phe  
 115 120 125  
 Asp Val Val Asn Tyr Phe Ala Pro Tyr Arg Glu Asn Arg Phe Phe His  
 130 135 140  
 10 Leu Ile Pro Trp Val Gly Val Gly Tyr Gln His Lys Phe Ile Gly Ser  
 145 150 155 160  
 Glu Trp Ser Lys Asp Asn Val Glu Ser Leu Thr Ala Asn Val Gly Val  
 165 170 175  
 Met Met Ala Phe Arg Leu Gly Lys Arg Val Asp Phe Val Ile Glu Ala  
 180 185 190  
 15 Gln Ala Ala His Ser Asn Leu Asn Leu Ser Arg Ala Tyr Asn Ala Lys  
 195 200 205  
 Lys Thr Pro Val Phe Glu Asp Pro Ala Gly Arg Tyr Tyr Asn Gly Phe  
 210 215 220  
 20 Gln Gly Met Ala Thr Ala Gly Leu Asn Phe Arg Leu Gly Ala Val Gly  
 225 230 235 240  
 Phe Asn Ala Ile Unk Pro Met Asp Tyr Ala Leu Ile Asn Asp Leu Asn  
 245 250 255  
 Gly Gln Ile Asn Arg Leu Arg Ser Glu Val Glu Glu Leu Ser Lys Arg  
 260 265 270  
 25 Pro Val Ser Cys Pro Glu Cys Pro Glu Val Thr Pro Val Thr Lys Thr  
 275 280 285  
 Glu Asn Ile Leu Thr Glu Lys Ala Val Leu Phe Arg Phe Asp Ser His  
 290 295 300  
 30 Val Val Asp Lys Asp Gln Leu Ile Asn Leu Tyr Asp Val Ala Gln Phe  
 305 310 315 320  
 Val Lys Glu Thr Asn Glu Pro Ile Thr Val Val Gly Tyr Ala Asp Pro  
 325 330 335  
 Thr Gly Asn Thr Gln Tyr Asn Glu Lys Leu Ser Glu Arg Arg Ala Lys  
 340 345 350  
 35 Ala Val Val Asp Val Leu Thr Gly Lys Tyr Gly Val Pro Ser Glu Leu  
 355 360 365  
 Ile Ser Val Glu Trp Lys Gly Asp Ser Thr Gln Pro Phe Ser Lys Lys  
 370 375 380  
 40 Ala Trp Asn Arg Val Val Ile Val Arg Ser Lys  
 385 390 395

(2) INFORMATION FOR SEQ ID NO:313

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 387 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...387  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:313

Tyr Lys Met Thr Tyr Arg Ile Met Lys Ala Lys Ser Leu Leu Leu Ala  
 1 5 10 15  
 Leu Ala Gly Leu Ala Cys Thr Phe Ser Ala Thr Ala Gln Glu Ala Thr  
 20 25 30  
 65 Thr Gln Asn Lys Ala Gly Met His Thr Ala Phe Gln Arg Asp Lys Ala  
 35 40 45  
 Ser Asp His Trp Phe Ile Asp Ile Ala Gly Gly Ala Gly Met Ala Leu  
 50 55 60  
 70 Ser Gly Trp Asn Asn Asp Val Asp Phe Val Asp Arg Leu Ser Ile Val  
 65 70 75 80  
 Pro Thr Phe Gly Ile Gly Lys Trp His Glu Pro Tyr Phe Gly Thr Arg  
 85 90 95  
 75 Leu Gln Phe Thr Gly Phe Asp Ile Tyr Gly Phe Pro Gln Gly Ser Lys  
 100 105 110

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Glu Arg Asn His Asn Tyr Phe Gly Asn Ala His Leu Asp Phe Met Phe  
 115 120 125  
 Asp Leu Thr Asn Tyr Phe Gly Val Tyr Arg Pro Asn Arg Val Phe His  
 130 135 140  
 5 Ile Ile Pro Trp Ala Gly Ile Gly Phe Gly Tyr Lys Phe His Ser Glu  
 145 150 155 160  
 Asn Ala Asn Gly Glu Lys Val Gly Ser Lys Asp Asp Met Thr Gly Thr  
 165 170 175  
 Val Asn Val Gly Leu Met Leu Lys Phe Arg Leu Ser Arg Val Val Asp  
 180 185 190  
 10 Phe Asn Ile Glu Gly Gln Ala Phe Ala Gly Lys Met Asn Phe Ile Gly  
 195 200 205  
 Thr Lys Arg Gly Lys Ala Asp Phe Pro Val Met Ala Thr Ala Gly Leu  
 210 215 220  
 15 Thr Phe Asn Leu Gly Lys Thr Glu Trp Thr Glu Ile Val Pro Met Asp  
 225 230 235 240  
 Tyr Ala Leu Val Asn Asp Leu Asn Asn Gln Ile Asn Ser Leu Arg Gly  
 245 250 255  
 20 Gln Val Glu Glu Leu Ser Arg Arg Pro Val Ser Cys Pro Glu Cys Pro  
 260 265 270  
 Glu Pro Thr Gln Pro Thr Val Thr Arg Val Val Val Asp Asn Val Val  
 275 280 285  
 Tyr Phe Arg Ile Asn Ser Ala Lys Ile Asp Arg Asn Gln Glu Ile Asn  
 290 295 300  
 25 Val Tyr Asn Thr Ala Glu Tyr Ala Lys Thr Asn Asn Ala Pro Ile Lys  
 305 310 315 320  
 Val Val Gly Tyr Ala Asp Glu Lys Thr Gly Thr Ala Ala Tyr Asn Met  
 325 330 335  
 30 Lys Leu Ser Glu Arg Arg Ala Lys Ala Val Ala Lys Met Leu Glu Lys  
 340 345 350  
 Tyr Gly Val Ser Ala Asp Arg Ile Thr Ile Glu Trp Lys Gly Ser Ser  
 355 360 365  
 Glu Gln Ile Tyr Glu Glu Asn Ala Trp Asn Arg Ile Val Val Met Thr  
 370 375 380  
 35 Ala Ala Glu  
 385

(2) INFORMATION FOR SEQ ID NO:314

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 195 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 50 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...195  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:314

Val Ile Gly Ile Ile Met Glu Phe Phe Met Leu Phe Ile Ala Ala Val  
 1 5 10 15  
 60 Phe Val Asn Asn Val Val Leu Ser Gln Phe Leu Gly Ile Cys Pro Phe  
 20 25 30  
 Leu Gly Val Ser Lys Lys Val Asp Thr Ser Ile Gly Met Gly Ala Ala  
 35 40 45  
 65 Val Thr Phe Val Leu Ala Leu Ala Thr Leu Val Thr Phe Leu Ile Gln  
 50 55 60  
 Lys Phe Val Leu Asp Arg Phe Gly Leu Gly Phe Met Gln Thr Ile Ala  
 65 70 75 80  
 Phe Ile Leu Val Ile Ala Ala Leu Val Gln Met Val Glu Ile Ile Leu  
 85 90 95  
 70 Lys Lys Val Ser Pro Pro Leu Tyr Gln Ala Leu Gly Val Phe Leu Pro  
 100 105 110  
 Leu Ile Thr Thr Asn Cys Cys Val Leu Gly Val Ala Ile Leu Val Ile  
 115 120 125  
 75 Gln Lys Asp Tyr Thr Leu Leu Gln Ser Phe Val Tyr Ala Ile Ser Thr  
 130 135 140



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Ala Ile Gly Phe Thr Leu Ala Met Val Thr Phe Ala Gly Ile Arg Glu  
 145 150 155 160  
 Gln Leu Asp Met Thr Asn Leu Pro Lys Ala Met Lys Gly Ile Pro Ser  
 165 170 175  
 5 Ala Leu Leu Ala Ala Gly Ile Leu Ala Met Ala Phe Met Gly Phe Ser  
 180 185 190  
 Gly Ile Ala  
 195

10 (2) INFORMATION FOR SEQ ID NO:315

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 876 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...876

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:315

30 Tyr Arg Ser Tyr Arg Gly Ile Gly Ser Gly Thr His Ser Pro Asn Leu  
 1 5 10 15  
 Lys Asn Arg Leu Lys Arg Ile Gly Ile Arg Ile Pro Asn Arg His Tyr  
 20 25 30  
 Ile His Ile Lys Pro Ile Lys Pro Lys Asn Lys Met Lys Gln Leu Asn  
 35 40 45  
 Ile Ile Ser Phe Ile Ile Ala Phe Leu Phe Leu Gly Thr Ser Ala Ser  
 50 55 60  
 Ala Gln Gln Ser Gly Gly Ser Val Thr Gly Thr Val Val Asp Lys Ser  
 65 70 75 80  
 40 Ser Lys Glu Pro Ile Ala Tyr Val Gln Val Phe Val Lys Gly Thr Thr  
 85 90 95  
 Leu Gly Thr Ser Thr Asp Ala Asn Gly Asn Tyr Ser Ile Lys Gly Ile  
 100 105 110  
 Pro Ser Gly Asn Gln Thr Ile Val Ala Arg Leu Met Gly Tyr Ser Thr  
 115 120 125  
 45 Cys Glu Glu Lys Val His Ile Glu Lys Gly Gly Ser Arg His Val Asp  
 130 135 140  
 Leu Tyr Leu Thr Glu Glu Ile Leu Ser Leu Asp Gly Val Val Val Ser  
 145 150 155 160  
 50 Ala Asn Arg Asn Glu Thr Phe Arg Arg Gln Ala Pro Ser Leu Val Thr  
 165 170 175  
 Val Leu Ser Pro Glu Leu Phe Leu Lys Thr Asn Ser Thr Asn Leu Ser  
 180 185 190  
 Gln Gly Leu Lys Phe Gln Pro Gly Leu Arg Val Glu Asp Asn Cys Gln  
 195 200 205  
 55 Asn Cys Gly Phe Asn Gln Val Arg Ile Asn Gly Leu Glu Gly Ala Tyr  
 210 215 220  
 Ser Gln Ile Leu Ile Asp Ser His Pro Ile Phe Ser Ser Leu Ala Gly  
 225 230 235 240  
 60 Val Tyr Gly Leu Glu Gln Met Pro Ala Asn Met Ile Glu Arg Val Glu  
 245 250 255  
 Val Ile Arg Gly Gly Gly Ser Ala Leu Phe Gly Ser Asn Ala Val Gly  
 260 265 270  
 Gly Val Ile Asn Val Ile Thr Lys Glu Pro Leu Arg Asn Ser Ala Glu  
 275 280 285  
 65 Ile Ser His Ser Thr Met Thr Phe Asp His Ala Lys Gly Trp Gly Ser  
 290 295 300  
 Phe Gln Asn Thr Thr Gln Phe Asn Gly Ser Met Leu Thr Glu Asp Arg  
 305 310 315 320  
 70 Lys Ala Gly Val Met Val Phe Gly Gln His Asn Tyr Arg Pro Gly Gln  
 325 330 335  
 Asp Ile Asp Gly Asp Asn Phe Thr Glu Leu Pro Asn Leu Arg Asn Arg  
 340 345 350  
 75 Ser Leu Gly Phe Arg Ser Tyr Tyr Lys Thr Gly Leu Tyr Ser Lys Ala  
 355 360 365

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Thr Leu Glu Tyr His Ser Met Gln Glu Tyr Arg Arg Gly Gly Asp Arg  
 370 375 380  
 Leu Asp Asn Pro Pro Phe Glu Ala Gln Ile Ala Glu Tyr Leu Gln His  
 385 390 395 400  
 5 Tyr Ile Asn Gly Gly Ser Phe Lys Phe Asp Gln Gly Phe Ser Gly Gly  
 405 410 415  
 Lys Asp Phe Phe Ser Leu Tyr Ala Ser Ala Gln Asp Val Gln Arg Arg  
 420 425 430  
 10 Ser Tyr Tyr Gly Gly Gly Asp Tyr Thr Glu Asn Leu Leu Asn Gly Ala  
 435 440 445  
 Val Gln Ser Gly Ser Thr Glu Ser Asp Glu Tyr Asn Asp Ala Phe Thr  
 450 455 460  
 Ala Leu Thr Ser Tyr Gly Thr Thr Lys Gly Phe Asp Leu Gln Gly Gly  
 465 470 475 480  
 15 Gly Met Tyr Arg His Thr Phe Gly Glu Asn Trp Asp Phe Thr Gly Gly  
 485 490 495  
 Leu Glu Tyr Ile Tyr Gly Gln Leu Asp Asp Arg Ser Gly Tyr Arg Pro  
 500 505 510  
 20 Ser Lys Ile Asp Gln Asn Thr Ser Thr Phe Ser Gln Tyr Asp Gln Leu  
 515 520 525  
 Glu Tyr Lys Thr Glu Lys Leu Ser Ala Leu Ile Gly Ala Arg Ile Asp  
 530 535 540  
 Tyr Val Leu Leu Asn Gln Asp Gly Lys Arg Tyr Ile Asp Pro Leu Phe  
 545 550 555 560  
 25 Ile Phe Ser Pro Arg Ala Asn Val Arg Tyr Asn Pro Asn Lys Asn Leu  
 565 570 575  
 Ser Phe Arg Leu Ser Tyr Ser Glu Gly Phe Arg Ala Pro Gln Tyr Phe  
 580 585 590  
 30 Asp Glu Asp Leu His Val Glu Leu Ala Gly Gly Thr Pro Ile Ser Arg  
 595 600 605  
 Val Leu Ser Pro Asn Leu Lys Glu Glu Arg Ser Arg Ser Ile Ser Ala  
 610 615 620  
 Ser Phe Asp Tyr Tyr His Arg Ala Asp Glu Trp Gln Phe Asn Ile Met  
 625 630 635 640  
 35 Gly Glu Ala Phe Ser Thr Phe Ile Ser Asn Gln Phe Lys Pro Ser Asp  
 645 650 655  
 Lys Val Glu Thr Thr Ser Asp Gly Lys Glu Trp Ile Ile Arg Thr Ile  
 660 665 670  
 40 Tyr Asn Asp Lys Asp Gly Val Ser Lys Val Tyr Gly Val Asn Leu Glu  
 675 680 685  
 Gly Arg Ile Ala Tyr Asn Lys Ser Phe Asp Leu Gln Leu Gly Gly Thr  
 690 695 700  
 Trp Gln Arg Ser Arg Tyr Gly Ser Ile Tyr Thr Thr Ala Val Glu Ala Asp  
 705 710 715 720  
 45 Lys Thr Thr Gly Gln Ala Glu Ile Ser Val Lys Asp Tyr Val Arg Thr  
 725 730 735  
 Pro Asn Leu Tyr Gly Tyr Phe Val Ala Thr Val Arg Pro Thr Glu His  
 740 745 750  
 50 Phe Ala Ile Asn Leu Ser Gly Thr Phe Thr Gly Lys Met Asp Val Val  
 755 760 765  
 His Glu Ala Tyr Glu Gly Asp Ile Pro Ala Glu His Ile Ala Pro Asp  
 770 775 780  
 Gly Ser Phe Asp Phe Glu Met Asn Gly Gln Gln Phe Lys Gly Leu Ala  
 785 790 795 800  
 55 Glu Gly His Ala Lys Leu Val Lys Thr Pro Ala Phe Ala Asp Ile Asp  
 805 810 815  
 Leu Lys Leu Ser His Asp Phe His Leu Ala Ser Thr Met Thr Leu Glu  
 820 825 830  
 60 Leu Asn Ala Gly Ile Gln Asn Ile Phe Asn Ser Tyr Gln Lys Asp Thr  
 835 840 845  
 Asp Lys Gly Pro Gly Arg Ala Ser Thr Tyr Val Tyr Gly Pro Met Gln  
 850 855 860  
 Pro Arg Arg Ile Phe Val Gly Thr Lys Ile Asn Phe  
 865 870 875

(2) INFORMATION FOR SEQ ID NO:316

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 899 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

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## (VI) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

5

## (IX) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...899

## (XII) SEQUENCE DESCRIPTION: SEQ ID NO:316

10 Ile Leu Asn His Leu Arg Lys Thr Met Tyr Lys Lys Ile Ile Ala Val  
1 5 10 15  
Ala Ala Leu Phe Cys Ala Ser Ile Gly Ile Leu Lys Gly Gln Ser Ser  
20 25 30  
15 Asp Leu Thr Pro Gln Asp Thr Ile Tyr Ser Pro Glu Ile Ser Tyr Ala  
35 40 45  
Lys Pro Ile His Lys Thr Ile Ala Ser Ile Glu Ile Glu Gly Met Arg  
50 55 60  
20 Ser Phe Asp Asp Phe Val Leu Arg Asn Leu Ser Gly Leu Ala Val Gly  
65 70 75 80  
Asp Glu Val Leu Ile Pro Gly Asp Ala Met Ser Ala Ala Val Asn Arg  
85 90 95  
Ile Met Arg Gln Gly Tyr Phe Ser Asn Val Arg Ile Ile Ala Asp Lys  
100 105 110  
25 Tyr Val Gly Asn Lys Val Tyr Leu Lys Ile Ile Val Thr Glu Arg Pro  
115 120 125  
Arg Ile Ser Lys Val Thr Phe Ser Gly Val Lys Lys Ser Glu Arg Glu  
130 135 140  
30 Asp Leu Glu Met Lys Ile Gly Leu Arg Glu Gly Ile Gln Met Thr Arg  
145 150 155 160  
Asn Asn Glu Asp Lys Val Arg Gln Ile Val Gln Lys Tyr Phe Ser Glu  
165 170 175  
Lys Gly Tyr Arg Asp Ala Ser Ile Arg Ile Thr Gln Glu Pro Asp Leu  
180 185 190  
35 Ser Lys Asp Gly Phe Val Asn Val Leu Ile Ser Ile Glu Lys Lys Ser  
195 200 205  
Lys Thr Lys Val Asn Glu Ile Tyr Phe Ser Gly Asn Lys Ala Leu Ser  
210 215 220  
40 Asn His Lys Leu Arg Met Ala Met Lys Asn Thr Asn Ala Lys Phe Ser  
225 230 235 240  
Leu Arg Lys His Ile Arg Ser Ser Phe Leu Lys Leu Phe Ser Thr His  
245 250 255  
Lys Phe Val Glu Glu Ser Tyr Arg Glu Asp Leu Val Arg Leu Ile Glu  
260 265 270  
45 Lys Tyr Gln Glu Tyr Gly Tyr Arg Asp Ala Glu Ile Leu Thr Asp Ser  
275 280 285  
Val Val Lys Ala Pro Asp Gly Lys Arg Val Asp Ile Tyr Leu Asn Ile  
290 295 300  
50 Glu Glu Gly Gln Lys Tyr Ile Lys Asp Val Asn Phe Val Gly Asn  
305 310 315 320  
Ser Gln Tyr Pro Ser Glu Tyr Leu Glu Arg Val Leu Gly Ile Lys Ser  
325 330 335  
Gly Asp Val Tyr Asn Gln Arg Arg Leu Ala Lys Arg Leu Asn Glu Asp  
340 345 350  
55 Glu Asp Ala Val Gly Asn Leu Tyr Tyr Asn Asn Gly Tyr Ile Phe Ala  
355 360 365  
Trp Val Asp Pro Val Glu Thr Asn Val Val Gly Asp Ser Val Ser Leu  
370 375 380  
60 Asp Ile Arg Ile Ala Glu Gly Lys Gln Ala Asn Ile Asn Lys Val Ile  
385 390 395 400  
Ile Lys Gly Asn Thr Val Val Tyr Glu Asp Val Val Arg Arg Glu Leu  
405 410 415  
Tyr Thr Lys Pro Gly Gln Leu Phe Ser Arg Glu Asp Ile Ile Asn Ser  
420 425 430  
65 Ile Arg Leu Ile Asn Gln Leu Gly His Phe Asp Ala Glu Lys Ser Ile  
435 440 445  
Pro Arg Pro Ile Pro Asn Pro Glu Thr Gly Thr Val Asp Ile Glu Tyr  
450 455 460  
70 Asp Leu Val Pro Arg Ser Ser Asp Gln Leu Glu Leu Ser Val Gly Trp  
465 470 475 480  
Ser Gln Ser Gly Leu Leu Phe Arg Gly Ala Ile Lys Phe Thr Asn Phe  
485 490 495  
Ser Val Gly Asn Leu Leu His Pro Ser Met Tyr Lys Lys Gly Ile Ile  
500 505 510  
75 Pro Gln Gly Asp Gly Gln Thr Leu Ser Leu Ser Ala Gln Thr Asn Gly

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515 520 525  
 Lys Tyr Tyr Gln Gln Tyr Ser Val Thr Phe Met Asp Pro Trp Phe Gly  
 530 535 540  
 Gly Lys Arg Pro Asp Met Phe Ser Phe Ser Ala Phe Tyr Ser Lys Thr  
 545 550 555 560  
 Thr Ala Ile Asp Ser Lys Phe Tyr Asn Ser Asn Ala Gly Asn Tyr Tyr  
 565 570 575  
 Asn Ala Tyr Tyr Asn Ser Tyr Tyr Asn Asn Tyr Asn Ser Tyr Tyr Asn  
 580 585 590  
 10 Gly Met Ser Asn Tyr Thr Gly Asp Leu Tyr Thr Gln Ala Ser Asp Pro  
 595 600 605  
 Asp Arg Ser Leu Gln Met Leu Gly Thr Ser Ile Gly Tyr Gly Lys Arg  
 610 615 620  
 15 Leu Thr Trp Pro Asp Asn Trp Phe Gln Ile Tyr Thr Ser Leu Asn Tyr  
 625 630 635 640  
 Thr Tyr Tyr Arg Leu Arg Asn Trp Ser Tyr Asn Thr Phe Gln Asn Phe  
 645 650 655  
 His His Gly Ser Ala Asn Asp Leu Asn Leu Glu Leu Arg Leu Ser Arg  
 660 665 670  
 20 Thr Ser Ile Asp Asn Pro Ile Tyr Thr Arg Ser Gly Ser Asp Phe Met  
 675 680 685  
 Val Ser Val Ala Ala Thr Leu Pro Tyr Ser Leu Trp Asp Asn His Asp  
 690 695 700  
 25 Tyr Ala Ser Gln Asn Leu Ser Val Ser Asp Arg Tyr Arg Phe Ile Glu  
 705 710 715 720  
 Tyr His Lys Trp Lys Phe Arg Gly Arg Val Phe Thr Pro Leu Leu Asn  
 725 730 735  
 Pro Ala Thr His Lys Tyr Thr Pro Val Leu Met Ser Arg Val Glu Gly  
 740 745 750  
 30 Ala Val Leu Gly Ser Tyr Asn Ser Asn Lys Lys Ser Pro Phe Gly Thr  
 755 760 765  
 Phe Tyr Met Gly Gly Asp Gly Met Ser Ser Tyr Tyr Gly Gly Tyr Met  
 770 775 780  
 35 Asn Glu Thr Ile Gly Leu Arg Gly Tyr Lys Asn Gly Ser Ile Ala Gly  
 785 790 795 800  
 Asn Asn Tyr Asp Tyr Ala Tyr Ala Tyr Met Arg Leu Thr Met Glu Leu  
 805 810 815  
 Arg Phe Pro Ile Leu Phe Glu Asn Ser Phe Asn Ala Trp Leu Leu Ala  
 820 825 830  
 40 Phe Ala Glu Ala Gly Asn Ala Trp Arg Ser Ile Asp Asn Tyr Asn Pro  
 835 840 845  
 Phe Asn Leu Lys Arg Ser Ala Gly Val Gly Leu Arg Val Thr Leu Pro  
 850 855 860  
 45 Met Val Gly Met Leu Gly Ile Asp Trp Gly Tyr Gly Phe Asp Arg Pro  
 865 870 875 880  
 Asp Asn Ser Leu Gln Arg Gly Gly Ser Asn Val His Phe Val Leu Gly  
 885 890 895  
 Gln Glu Phe  
 50  
 (2) INFORMATION FOR SEQ ID NO:317  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 177 amino acids  
 55 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 60 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 65 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...177  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:317  
 70 Gln Ile Asn Met Asn Gly Asp Met Lys Arg Phe Leu Ile Leu Ile Gly  
 1 5 10 15  
 Phe Ala Leu Ala Val Ala Phe Ser Gly Phe Ser Gln Lys Phe Ala Leu  
 20 25 30  
 75 Val Asp Met Glu Tyr Ile Leu Arg Asn Ile Pro Asp Tyr Glu Met Met

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35 40 45  
 Asn Glu Gln Leu Glu Gln Val Ser Lys Lys Trp Gln Asn Glu Ile Glu  
 50 55 60  
 5 Ala Leu Glu Asn Glu Ala Gln Ser Met Tyr Lys Lys Tyr Gln Ser Asp  
 65 70 75 80  
 Leu Val Phe Leu Ser Ala Ala Gln Lys Lys Thr Gln Glu Glu Ala Ile  
 85 90 95  
 Val Lys Lys Glu Gln Gln Ala Ser Glu Leu Lys Arg Lys Tyr Phe Gly  
 100 105 110  
 10 Pro Glu Gly Glu Leu Tyr Lys Lys Arg Ser Asp Leu Met Lys Pro Ile  
 115 120 125  
 Gln Asp Glu Ile Trp Asn Ala Ile Lys Glu Ile Ala Lys Arg Asn Asn  
 130 135 140  
 15 Tyr Gln Met Val Leu Asp Arg Gly Thr Ser Gly Ile Ile Phe Ala Ser  
 145 150 155 160  
 Pro Ser Ile Asp Ile Ser Asp Leu Val Leu Ser Lys Met Gly Phe Ser  
 165 170 175  
 Lys

20

(2) INFORMATION FOR SEQ ID NO:318

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 170 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...170

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318

Arg Ile Asn Lys Gln His Glu Met Lys Lys Phe Phe Leu Met Leu Leu  
 1 5 10 15  
 Met Ala Leu Pro Leu Ser Leu Leu Ala Gln Lys Val Ala Val Val Asn  
 20 25 30  
 45 Thr Glu Glu Ile Ile Ser Lys Met Pro Glu Gln Val Ala Ala Thr Lys  
 35 40 45  
 Gln Leu Asn Glu Leu Ala Glu Lys Tyr Arg Leu Asp Leu Lys Ser Met  
 50 55 60  
 50 Asp Asp Glu Phe Ala Lys Lys Thr Glu Glu Phe Val Lys Glu Lys Asp  
 65 70 75 80  
 Ser Leu Leu Glu Asn Ile Arg Asn Arg Arg Gln Gln Glu Leu Gln Asp  
 85 90 95  
 Ile Gln Thr Arg Tyr Gln Gln Ser Tyr Gln Thr Met Gln Glu Asp Leu  
 100 105 110  
 55 Gln Lys Arg Gln Gln Gln Leu Phe Ala Pro Ile Gln Gln Lys Val Ala  
 115 120 125  
 Asp Ala Ile Lys Lys Val Gly Asp Glu Glu Asn Cys Ala Tyr Ile Met  
 130 135 140  
 60 Glu Ala Gly Met Met Leu Tyr Thr Gly Ala Thr Ala Ile Asp Leu Thr  
 145 150 155 160  
 Ala Lys Val Lys Ala Lys Leu Gly Ile Lys  
 165 170

65

(2) INFORMATION FOR SEQ ID NO:319

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 828 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:

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(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...828

5

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:319

10 Ile Met Lys Glu Ala Ile Pro Arg Lys Asn Lys Tyr Ile Lys Leu Asn  
 1 5 10 15  
 Gly Ile Tyr Arg Leu Ser Phe Ile Leu Cys Cys Leu Leu Cys Ser  
 20 25 30  
 Gln Ala Ala Met Ala Gln Gly Val Arg Val Ser Gly Tyr Val Leu Asp  
 35 40 45  
 15 Arg Gly Glu Lys Pro Ile Pro Phe Ala Gly Val Lys Val Arg Gly Thr  
 50 55 60  
 Gly Thr Gly Ala Thr Thr Asn Leu Lys Gly Tyr Tyr Glu Phe Arg Met  
 65 70 75 80  
 20 Lys Ala Thr Thr Asp Ser Ile Thr Ile Glu Phe Ser Ser Met Gly Tyr  
 85 90 95  
 Gln Gly Val Ser Arg Ser Phe Pro Ser Leu Thr Lys Asp Thr Arg Leu  
 100 105 110  
 Asn Val Arg Leu Ala Glu Ala Glu Met Glu Leu Ser Ser Val Thr Val  
 115 120 125  
 25 Gln Ala Thr Lys Arg Arg Leu Asn Thr Met Glu Arg Val Asn Thr Arg  
 130 135 140  
 Asp Leu Arg Val Asn Ala Gly Pro Thr Gly Gly Val Glu Ser Leu Ile  
 145 150 155 160  
 30 Ser Thr Tyr Ala Gly Val Thr Gln Asn Asn Glu Leu Ser Ser Gln Tyr  
 165 170 175  
 Ser Val Arg Gly Gly Ser Tyr Asp Glu Asn Met Val Tyr Val Asn Gly  
 180 185 190  
 Val Glu Val Tyr Arg Pro Leu Leu Val Arg Ser Ala Gln Gln Glu Gly  
 195 200 205  
 35 Leu Ser Phe Val Asn Pro Asp Leu Thr Gln Ser Val Gln Phe Ser Ala  
 210 215 220  
 Gly Gly Phe Thr Ala Asp Tyr Gly Asp Lys Met Ser Ser Val Leu Asp  
 225 230 235 240  
 40 Ile Arg Tyr Lys Gln Pro Gln Glu Lys Glu Gly Ala Val Leu Leu Gly  
 245 250 255  
 Met Leu Gln Ser Ser Ala Tyr Tyr Gly Ser Ser Ala Gly Ala Phe Ser  
 260 265 270  
 Gln Ile Thr Gly Val Arg Tyr Lys Ser Ala Lys Ser Leu Leu Gly Thr  
 275 280 285  
 45 Thr Asp Thr Lys Ala Glu Tyr Asp Pro Ile Tyr Ala Asp Gly Gln Thr  
 290 295 300  
 Phe Met Thr Tyr Arg Phe Ser Pro Lys Leu Ser Val Ser Phe Leu Gly  
 305 310 315 320  
 50 Asn Ile Ser Gln Thr Arg Tyr Lys Phe Val Pro Gln Thr Arg Glu Thr  
 325 330 335  
 Ser Phe Gly Thr Leu Ser Asp Ala Lys Lys Leu Lys Ile Phe Phe Asp  
 340 345 350  
 Gly Gln Glu Gln Asp Arg Phe Leu Thr Tyr Phe Gly Ala Phe Ser Met  
 355 360 365  
 55 Asn Phe Val Pro Asp Asp Lys Gln Arg His Thr Val Thr Leu Ser Ala  
 370 375 380  
 Phe Asn Ser Asn Glu Arg Glu Thr Tyr Asp Ile Gln Gly Glu Tyr Phe  
 385 390 395 400  
 60 Leu Asn Asp Val Gln Leu Gly Ala Asp Gly Thr Ala Ser Met Ala Ser  
 405 410 415  
 Gly Ser Glu Asn Ser Asn Gly Leu Gly Ile Gly Arg Asn His Glu His  
 420 425 430  
 Ala Arg Asn Arg Leu Ser Tyr Arg Val Leu Asn Met Gly Tyr Arg Gly  
 435 440 445  
 65 Glu Met Lys Leu Asn Glu Lys His Arg Leu Gln Ala Gly Val Ser Ala  
 450 455 460  
 Gln Met Glu Lys Ile Ala Asp His Ile Ser Glu Trp Glu Arg Arg Asp  
 465 470 475 480  
 70 Ser Val Gly Tyr Asn Leu Pro His Ser Glu Thr Val Leu Leu Met Tyr  
 485 490 495  
 Asn Asn Leu Tyr Ala Asp Thr Gln Met Arg Gly Thr Arg Leu Ser Ala  
 500 505 510  
 Phe Val Gln Asp Arg Phe Asn Phe Ser Met Gly Gly Gly Thr Phe Ser  
 515 520 525  
 75 Leu Ile Pro Gly Ile Arg Ala Ser Trp Trp Ser Phe Asn Lys Glu Leu

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130 135 140  
 Leu Glu Gly Cys Leu Phe Ala Arg Gln Gln Lys Glu Tyr Pro Thr Arg  
 145 150 155 160  
 Tyr Arg Ile Arg Arg Ala Ala Glu Trp Asn Ser Ala Arg Gly Asp Phe  
 165 170 175  
 Gly Pro Ala Tyr Ala Pro Asp Ala Ser Ala Leu Tyr Phe Thr Ser Ser  
 180 185 190  
 Arg Ser Lys Asp Asp Gly Leu Asp Asn Ser Ser Ile Thr Gly Leu Lys  
 195 200 205  
 Pro Asn Asp Ile Tyr Ile Ile Lys Arg Asp Ala Gln Gly Arg Trp Gly  
 210 215 220  
 Arg Pro Asp Ser Val Ser Gly Gly Ile Asn Thr Pro Trp Asp Glu Gly  
 225 230 235 240  
 Val Pro Thr Ile Thr Pro Asp Gly Ser Thr Ile Tyr Tyr Thr Leu Ala  
 245 250 255  
 Gln Gln Gly Ala Asp Tyr Asp Arg Thr Val Gln Ile Tyr Ser Ala Ala  
 260 265 270  
 Arg Ser Gly Glu Gly Gly Trp Ser Asn Gly Ser Leu Val Asp Ile Met  
 275 280 285  
 Arg Asp Ser Leu Arg Met Ala Ala His Pro Ser Met Ser Ala Ser Gly  
 290 295 300  
 Asp Tyr Leu Tyr Phe Val Ser Asn Ile Gly Gly Ser Tyr Gly Gly Lys  
 305 310 315 320  
 Asp Ile Tyr Arg Val Lys Val Ser Asp Arg Ser Tyr Gly Ser Pro Glu  
 325 330 335  
 Asn Leu Gly Pro Asp Ile Asn Thr Pro Gly Asp Glu Met Phe Pro Phe  
 340 345 350  
 Ile Asp Gly Asp Ser Thr Leu Phe Phe Ala Ser Asp Gly His Ala Gly  
 355 360 365  
 Leu Gly Gly Leu Asp Ile Phe Lys Ala Thr Leu Asp Ser Thr Gly Gln  
 370 375 380  
 Trp His Val Val Asn Met Gly Gln Pro Val Asn Ser Ser Ala Asp Asp  
 385 390 395 400  
 Phe Gly Leu Ala Val Glu Pro Lys Gly Lys Asn Lys Glu Glu Ala Leu  
 405 410 415  
 Pro Asp Asn Gly Val Lys Gly Val Phe Cys Ser Asn Arg Gly Asp Ala  
 420 425 430  
 Arg Gly Trp Pro His Leu Phe His Phe Glu Leu Pro Ala Ile Tyr Thr  
 435 440 445  
 Glu Ile Gln Gly Tyr Val Met Asp Arg Glu Glu Asn Pro Ile Ala Gly  
 450 455 460  
 Ala Thr Val Arg Ile Val Gly Glu Arg Gly Pro Val Gly Gln Gly Phe  
 465 470 475 480  
 Val Thr Thr Arg Asp Asp Gly Ser Tyr Lys Met Ser Val Gln Gly Asp  
 485 490 495  
 Thr Arg Tyr Val Met Leu Ala Gly Ala Ser Gly Tyr Leu Asn Gln Tyr  
 500 505 510  
 Val Glu Leu Lys Thr Asp Thr Ala Lys Gln Ser Glu Thr Tyr Tyr Val  
 515 520 525  
 Asp Phe Phe Leu Ala Ser Arg Glu Lys Ala Glu Gly Leu Gln Asn Ile  
 530 535 540  
 Phe Tyr Asp Phe Asp Lys Ala Thr Leu Arg Pro Glu Ser Met Lys Ser  
 545 550 555 560  
 Leu Asp Glu Leu Ile Arg Ile Leu Thr Asp Asn Pro Asp Ile Arg Ile  
 565 570 575  
 Glu Leu Gly Ser His Ala Asp Arg Lys Gly Pro Asp Ala Tyr Asn Leu  
 580 585 590  
 Gly Leu Ser Asp Arg Arg Ala Lys Ser Val Val Asp Tyr Leu Thr Ser  
 595 600 605  
 Arg Gly Ile Ala Ala Asp Arg Leu Thr Trp Lys Gly Tyr Gly Lys Ser  
 610 615 620  
 Val Pro Lys Thr Val Thr Ala Lys Ile Ala Glu Arg His Asp Phe Leu  
 625 630 635 640  
 Lys Glu Gly Asp Val Leu Thr Glu Glu Phe Val Ala Pro Leu Thr Glu  
 645 650 655  
 Glu Gln Gln Ser Val Cys Asp Gln Leu Asn Arg Arg Thr Glu Phe Arg  
 660 665 670  
 Val Ile Glu Glu Glu Leu Arg  
 675

(2) INFORMATION FOR SEQ ID NO:321

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 772 amino acids

(B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

10 (ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321

15 Pro Ala Gln Pro Lys Thr Tyr Cys Ile Arg Tyr Phe Arg Arg Glu Val  
1 5 10 15  
Ser Pro Arg Arg Gln Thr Glu Arg Thr Leu Tyr Ala Asp Lys Met Arg  
20 20 25 30  
Arg His Ile Val Lys Cys Cys Pro Ser Ala Ser Ile Leu Leu Gln Glu  
35 40 45  
Tyr Ser Thr Thr Glu Leu Phe Ile His His Phe Asn Ile Ser Ile Ile  
50 55 60  
Met Lys Lys Phe Phe Phe Ala Leu Leu Ser Ile Gly Ile Ser Ala Gln  
65 70 75 80  
Ala Phe Ala Lys Thr Asp Asn Val Pro Thr Asp Ser Leu Arg Val His  
85 90 95  
Asn Leu Gln Thr Val Thr Val Tyr Ser Thr Arg Thr Ala Val Pro Leu  
100 105 110  
30 Lys Lys Ile Pro Ala Lys Met Glu Leu Ile Ser Ser Arg Asn Ile Lys  
115 120 125  
Gln Ser Gly Phe Asn Asn Met Thr Asp Ile Leu Lys Thr Gln Ser Ser  
130 135 140  
35 Leu Asp Val Ile Gln Tyr Pro Gly Phe Ser Ser Asn Ile Gly Ile Arg  
145 150 155 160  
Gly Phe Lys Pro Ser Gly Lys Tyr Val Thr Val Leu Val Asn Gly Ile  
165 170 175  
40 Pro Ala Gly Thr Asp Asn Ile Ser Thr Leu Asn Thr Ser Asn Ile Glu  
180 185 190  
Gln Ile Glu Ile Leu Lys Gly Pro Phe Ser Ser Ile Tyr Gly Thr Asn  
195 200 205  
Ala Met Gly Gly Val Val Asn Ile Ile Thr His Lys Ser Lys Asp Lys  
210 215 220  
45 Ile His Gly Asn Val Ser Leu Phe Gly Gly Ser Tyr Gln Thr Met Ala  
225 230 235 240  
Gly Ser Phe Asn Leu Gly Gly Arg Phe Glu Asp Ile Phe Ser Phe Asp  
245 250 255  
Leu Ser Leu Gly Leu Asp Lys Gln Asn Lys Asp Tyr Lys Thr Gly Ser  
260 265 270  
50 Asn Asn Phe Leu Ser Leu Ser Lys Leu Glu Glu Ala Ile Val Asp Val  
275 280 285  
Asn Ala Thr Lys Asn Lys Lys Met Lys Gly Ser Asp Tyr Thr Val Ala  
290 295 300  
55 Thr Gly Arg Leu Arg Phe Gly Ile Asp Phe Thr Pro Glu Trp Ser Leu  
305 310 315 320  
Asn Leu Tyr Gln Asn Val Phe Leu Gly Asp Ala Ile Pro Val Gly Gly  
325 330 335  
Ser Ile Trp Gly Val Tyr Gly Glu Ser Lys Lys Asn Leu Asn Arg Ser  
340 345 350  
60 Ser Thr Ser Phe Glu Leu Leu Gly Lys His Gly Cys His Thr Leu Gln  
355 360 365  
Phe Ser Pro Tyr Phe Asn Ile Glu Lys Ser Glu Asn Tyr Asn Asn Ala  
370 375 380  
65 Asp Pro Thr Gly Phe Ile Asn Tyr Lys Ser Asp Tyr Tyr Thr Tyr Gly  
385 390 395 400  
Ala Leu Leu Gln Asp Lys Ile Ser Phe Gly Gly Gln Asn Ile Val Leu  
405 410 415  
Gly Val Asp Ser Arg Asn Met Thr Met Glu Ser Glu Arg Phe Glu Gln  
420 425 430  
70 Ala Gly Val Asn Thr Lys Pro Tyr Asn Pro Gly Tyr Ala Thr Asn Asn  
435 440 445  
Ile Gly Leu Phe Gly Gln Ala Asn Phe Tyr Leu Leu Asn Asp Ala Leu  
450 455 460  
75 Ser Ile Ser Ala Gly Ala Arg Ala Asp Phe Met Phe Phe Asp Leu Lys  
465 470 475 480

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Ala Asn Glu Tyr Leu Asn Asn Glu Ala Lys Gln Glu Thr His Asn Val  
 485 490 495  
 Ile Asn Pro Asn Val Gly Ile Lys Tyr Glu Phe Val Lys Gly Leu Thr  
 500 505 510  
 5 Ala His Gly Thr Phe Gly Ser Ala Phe Ser Ala Pro Asp Ala Phe Gln  
 515 520 525  
 Lys Ala Gly Gln Tyr Val Gly Pro Phe Gly Thr Thr Ile Gly Asn Pro  
 530 535 540  
 10 Asp Leu Lys Pro Glu Lys Ser Met Thr Trp Asp Phe Gly Ile Gly Tyr  
 545 550 555 560  
 Ser Asn Ala Arg Cys Gly Ile Gln Ala Asp Val Thr Leu Thr Tyr Phe  
 565 570 575  
 His Thr Asp His Lys Asp Leu Ile Leu Ser Ser Pro Asp Tyr Ala Asn  
 580 585 590  
 15 Asn Ile Thr Thr Tyr Ile Asn Ala Asp Lys Ala Arg Met Ser Gly Ile  
 595 600 605  
 Glu Ala Leu Leu Ser Tyr Asp Phe Gly Ser Leu Phe Ala Asn Lys Phe  
 610 615 620  
 20 Ser Leu Arg Ala Phe Ala Asn Ala Thr Ile Met Leu Asn Ser Glu Met  
 625 630 635 640  
 Lys Lys Ser Gln Thr Asp Ala Pro Trp Ser Glu Met Tyr Tyr Val Arg  
 645 650 655  
 Lys Gln Asn Ile Thr Phe Gly Ile Glu Tyr Arg Gly Lys Glu Gly Leu  
 660 665 670  
 25 Glu Val Met Leu Asn Gly Arg Phe Met Gly Arg Arg Ile Glu Gln Asn  
 675 680 685  
 Trp Tyr Ala Tyr Tyr Pro Glu Val Arg Pro Glu Leu Gln Gln Leu Leu  
 690 695 700  
 30 Ala Ala Glu Glu Pro Glu Leu Ala Ala Gln Gly Leu Leu Arg His Pro  
 705 710 715 720  
 Gln Ala Met Val Phe Asn Ala Ser Ala Tyr Tyr His Met Asn Lys Tyr  
 725 730 735  
 Leu Thr Phe Gly Val Asn Leu Asn Asn Ile Leu Asp Glu Leu Tyr Thr  
 740 745 750  
 35 Glu Lys Asp Gly Tyr His Met Pro Gly Arg Asn Ile Met Gly Lys Val  
 755 760 765  
 Met Val Asn Phe  
 770

40 (2) INFORMATION FOR SEQ ID NO:322

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 484 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

50 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

55 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...484

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322

60 Gly Arg Ala Ser Ser Pro Tyr Arg Gln Met Asp Gly Ile Leu Asn Asp  
 1 5 10 15  
 Glu Tyr Arg Gln Ala Ser Met Asn Arg Phe Ser Asn His Trp Pro Cys  
 20 25 30  
 65 Ile Leu Val Gly Phe Val Leu Trp Phe Val Ser Ala Ser Arg Thr Val  
 35 40 45  
 Ala Gln Asn Ala Ser Glu Thr Thr Val Ser Tyr Asp Thr Asp Thr Ala  
 50 55 60  
 Val Leu Ser Glu Ala Asp Val Leu Arg Ile Ala Leu Ser Glu Asn Ala  
 65 70 75 80  
 70 Thr Val Lys Val Ala Asp Met Asp Val Arg Lys Gln Glu Tyr Ala Arg  
 85 90 95  
 Arg Ala Ala Arg Ala Asp Leu Phe Pro Lys Val Asp Leu Asn Gly Val  
 100 105 110  
 75 Tyr Ser His Thr Leu Lys Lys Gln Val Leu Tyr Ile Asp Met Pro Gly  
 115 120 125

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Phe Ser Ser Ser Glu Gly Ile Glu Met Gly Arg Thr His Asn Thr Gln  
 130 135 140  
 Gly Gly Val Asn Val Ser Met Pro Leu Val Ser Ala Gln Leu Trp Lys  
 145 150 155 160  
 5 Ser Ile Ala Met Thr Gly Glu Gln Leu Asp Leu Ala Leu Glu Lys Ala  
 165 170 175  
 Arg Ser Ser Arg Ile Asp Leu Val Ala Glu Val Lys Lys Ala Tyr Leu  
 180 185 190  
 10 Ser Val Leu Leu Ala Glu Asp Ser Tyr Gly Val Phe Lys Arg Ser Tyr  
 195 200 205  
 Asp Asn Ala Leu Ala Asn Tyr Lys Asn Ile Ser Asp Lys Phe Asp Arg  
 210 215 220  
 Gly Leu Val Ala Glu Tyr Asp Lys Ile Arg Ala Asn Val Gln Val Arg  
 225 230 235 240  
 15 Asn Ile Glu Pro Asn Leu Leu Gln Ala Gln Asn Ser Val Ala Leu Ala  
 245 250 255  
 Leu Trp Gln Leu Lys Val Leu Met Ser Met Glu Val Glu Thr Pro Ile  
 260 265 270  
 20 Arg Leu Ser Gly Ser Leu Ser Asp Tyr Lys Glu Gln Val Tyr Thr Gly  
 275 280 285  
 Tyr Phe Ala Ala Asp Thr Leu Ile Ser Asn Asn Ser Ser Leu Arg Gln  
 290 295 300  
 Leu Asp Ile Gln Arg Arg Leu Ala Val Ser Ala Asp Lys Leu Asn Lys  
 305 310 315 320  
 25 Tyr Ser Phe Leu Pro Thr Leu Asn Leu Gly Gly Gln Tyr Thr Tyr Ser  
 325 330 335  
 Leu Asn Ser Asn Asp Ile Lys Phe Trp Gly Glu Gly Gln Arg Trp Thr  
 340 345 350  
 30 Pro Phe Ser Thr Ile Ser Leu Ser Leu Tyr Ile Pro Ile Phe Asn Gly  
 355 360 365  
 Gly Lys Arg Leu Tyr Asn Val Lys Gln Ser Ala Leu Ser Ile Arg Gln  
 370 375 380  
 Ile Asp Leu Gln Arg Arg His Ile Glu Gln Ser Ile Arg Met Gly Ile  
 385 390 395 400  
 35 Lys Asn Gln Asn Asp Arg Leu Arg Thr Cys Met Gln Arg Phe Val Ala  
 405 410 415  
 Ser Glu Glu Ala Val Arg Ser Ala Glu Lys Gly Tyr Gln Ile Ala Glu  
 420 425 430  
 40 Lys Arg Tyr Gln Thr Gly Glu Gly Thr Leu Val Glu Leu Asn Asp Ala  
 435 440 445  
 Asp Val Ala Leu Leu Gln Ala Arg Leu Asn Tyr Asn Gln Ala Ile Phe  
 450 455 460  
 45 Asp Phe Met Thr Ala Lys Ala Glu Leu Asp Lys Met Asn Gly Met Gly  
 465 470 475 480  
 Ile Pro Glu Gln

## (C) INFORMATION FOR SEQ ID NO:323

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 540 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 55 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 60 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...540  
 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:323

Phe His Asn Phe Asp Phe Leu Asn Gly Ile Lys Leu Phe Ser Met Ala  
 1 5 10 15  
 70 Asn Asn Thr Leu Leu Ala Lys Thr Arg Tyr Val Cys Leu Val Gly  
 20 25 30  
 Phe Cys Trp Leu Met Ala Met Met His Leu Ser Gly Gln Glu Val Thr  
 35 40 45  
 75 Met Trp Gly Asp Ser His Gly Val Ala Pro Asn Gln Val Arg Arg Thr  
 50 55 60

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Leu Val Lys Val Ala Leu Ser Glu Ser Leu Pro Pro Gly Ala Lys Gln  
 65 70 75 80  
 Ile Arg Ile Gly Phe Ser Leu Pro Lys Glu Thr Glu Glu Lys Val Thr  
 85 90 95  
 5 Ala Leu Tyr Leu Leu Val Ser Asp Ser Leu Ala Val Arg Asp Leu Pro  
 100 105 110  
 Asp Tyr Lys Gly Arg Val Ser Tyr Asp Ser Phe Pro Ile Ser Lys Glu  
 115 120 125  
 10 Asp Arg Thr Thr Ala Leu Ser Ala Asp Ser Val Ala Gly Arg Arg Phe  
 130 135 140  
 Phe Tyr Leu Ala Ala Asp Ile Gly Pro Val Ala Ser Phe Ser Arg Ser  
 145 150 155 160  
 Asp Thr Leu Thr Ala Arg Val Glu Glu Val Ala Val Asp Gly Arg Pro  
 165 170 175  
 15 Leu Pro Leu Lys Glu Leu Ser Pro Ala Ser Arg Arg Leu Tyr Arg Gly  
 180 185 190  
 Tyr Glu Ala Leu Phe Val Pro Gly Asp Gly Gly Ser Arg Asn Tyr Arg  
 195 200 205  
 20 Ile Pro Ala Ile Leu Lys Thr Ala Asn Gly Thr Leu Ile Ala Met Ala  
 210 215 220  
 Asp Arg Arg Lys Tyr Asn Gln Thr Asp Leu Pro Glu Asp Ile Asp Ile  
 225 230 235 240  
 Val Met Arg Arg Ser Thr Asp Gly Gly Lys Ser Trp Ser Asp Pro Arg  
 245 250 255  
 25 Ile Ile Val Gln Gly Glu Gly Arg Asn His Gly Phe Gly Asp Val Ala  
 260 265 270  
 Leu Val Gln Thr Gln Ala Gly Lys Leu Leu Met Ile Phe Val Gly Gly  
 275 280 285  
 30 Val Gly Leu Trp Gln Ser Thr Pro Asp Arg Pro Gln Arg Thr Tyr Ile  
 290 295 300  
 Ser Glu Ser Arg Asp Glu Gly Leu Thr Trp Ser Pro Pro Arg Asp Ile  
 305 310 315 320  
 Thr His Phe Ile Phe Gly Lys Asp Cys Ala Asp Pro Gly Arg Ser Arg  
 325 330 335  
 35 Trp Leu Ala Ser Phe Cys Ala Ser Gly Gln Gly Leu Val Leu Pro Ser  
 340 345 350  
 Gly Arg Ile Thr Phe Val Ala Ala Ile Arg Glu Ser Gly Gln Glu Tyr  
 355 360 365  
 40 Val Leu Asn Asn Tyr Val Leu Tyr Ser Asp Asp Glu Gly Asp Thr Trp  
 370 375 380  
 Gln Leu Ser Asp Cys Ala Tyr Arg Arg Gly Asp Glu Ala Lys Leu Ser  
 385 390 395 400  
 Leu Met Pro Asp Gly Arg Val Leu Met Ser Ile Arg Asn Gln Gly Arg  
 405 410 415  
 45 Gln Glu Ser Arg Gln Arg Phe Phe Ala Leu Ser Ser Asp Asp Gly Leu  
 420 425 430  
 Thr Trp Glu Arg Ala Lys Gln Phe Glu Gly Ile His Asp Pro Gly Cys  
 435 440 445  
 50 Asn Gly Ala Met Leu Gln Val Lys Arg Asn Gly Arg Asp Gln Val Leu  
 450 455 460  
 His Ser Leu Pro Leu Gly Pro Asp Gly Arg Asp Gly Ala Val Tyr  
 465 470 475 480  
 Leu Phe Asp His Val Ser Gly Arg Trp Ser Ala Pro Val Val Val Asn  
 485 490 495  
 55 Ser Gly Ser Ser Ala Tyr Ser Asp Met Thr Leu Leu Ala Asp Gly Thr  
 500 505 510  
 Ile Gly Tyr Phe Val Glu Glu Gly Asp Glu Ile Ser Leu Val Phe Ile  
 515 520 525  
 60 Arg Phe Val Leu Asp Asp Leu Phe Asp Val Arg Gln  
 530 535 540

## (2) INFORMATION FOR SEQ ID NO:324

- 65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 293 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
  
 70 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
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## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...293

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:324

```

Lys Ser Pro Ser Asp Ser Ala Leu Pro Ser Val Trp Ser Ala Asn Thr
1      5      10      15
Ile Ser Gly Leu Val Gly Gly Lys Arg Ile Thr Leu Leu Ile Leu Tyr
10     20     25     30
Ser Met Ala Ile Arg Ser Ser Asn Ile Glu Ser Ile Gln Cys Phe Val
35     40     45     50
Met Lys Lys Glu Lys Leu Trp Ile Ala Ile Val Ala Gly Leu Ala Phe
55     60
Val Leu Gly Leu Tyr Ala Leu Gly Arg Ser Val Ala Gln Leu Arg Arg
15     70     75     80
Ser Gln Pro Ser Val Thr Thr Gly Met Ala Glu Arg Asn Phe Lys
85     90     95
Ser Asp Leu Ile Val Trp Thr Ala Ser Tyr Gln Leu Gln Met Met Asp
100    105    110
Leu Glu Ser Ala Tyr Lys Ala Leu Lys Glu Lys Gln Ile Leu Val Ala
115    120    125
Asp Tyr Leu Lys Asn Lys Gln Leu Pro Asp Ser Ser Tyr Ile Phe Ser
130    135    140
Ser Val Ala Ile Ser Lys Glu Tyr Asn Tyr Tyr Tyr Asp Pro Arg Gln
145    150    155    160
Glu Gln Asn Val Arg Thr Phe Ala Gly Tyr Leu Leu Ser Gln Thr Val
165    170    175
Thr Val Thr Ser Gln Asp Ile Glu His Val Glu Lys Ile Ser Arg Asp
180    185    190
Ile Thr Glu Leu Ile Asn Gln Gly Val Glu Ile Thr Ser Asp Arg Pro
195    200    205
Ala Tyr Tyr Tyr Thr Lys Leu Asn Asp Leu Lys Val Glu Met Leu Arg
210    215    220
Asn Ala Ser Glu Asp Ala Phe Asn Arg Ala Ser Val Ile Ala Glu Gly
225    230    235    240
Ser Gly Ser Ser Val Gly Lys Met Leu Ser Ser Ser Met Gly Val Phe
245    250    255
Gln Ile Val Gly Leu Asn Ser Asn Glu Asp Tyr Ser Trp Gly Gly Ser
260    265    270
Phe Asn Thr Ser Ser Lys Met Lys Thr Ala Ser Ile Thr Val Lys Ala
275    280    285
Ser Phe Ala Leu Lys
290

```

## 45 (2) INFORMATION FOR SEQ ID NO:325

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## 50 (ii) MOLECULE TYPE: protein

## 55 (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

## 60 (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...280

## 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:325

```

Gly Lys Leu Gln Met Lys Lys Thr Ile Ala Ile Ile Ala Ser Ala Leu
1      5      10      15
Leu Ala Leu Gly Ala Val Gly Cys Lys Lys Asn Ala Asp Thr Thr Ala
20     25     30
Val Ser Glu Lys Asp Ser Ile Ala Leu Ser Met Gly Ile Leu Tyr Gly
35     40     45
Gln Asp Phe Ala Asn Gln Phe Glu Met Ser Arg Leu Gln Gly Gln Pro
50     55     60
Ile Asp Ser Val Ala Phe Leu Asp Gly Phe Lys Tyr Gly Ile Asp Thr
65     70     75     80

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Thr Arg Phe Ser Tyr Asn Leu Gly Ala Ile Tyr Ala Ser Asn Ile Ala  
 85 90 95  
 Arg Gln Leu Ala His Asp Ser Ile Asp Ile Asp Lys Phe Tyr Ala Ala  
 100 105 110  
 5 Met Arg Ala Ala Leu Leu Lys Asp Thr Val Ser Ile Ala Met Lys Pro  
 115 120 125  
 Ala Asp Ala Gln Ala Phe Met Gln Arg Ile Gln Ala Lys Lys Gln Arg  
 130 135 140  
 10 Glu Asn Asn Met Lys Gln Phe Gly Gln Asn Ile Glu Lys Gly Asn Glu  
 145 150 155 160  
 Tyr Ile Asp Thr Phe Lys Lys Glu Asp Gly Val Thr Val Thr Thr  
 165 170 175  
 Gly Leu Ala Tyr Lys Thr Leu Gln Glu Gly Thr Gly Ala Thr Pro Ser  
 180 185 190  
 15 Leu Ala Asp Thr Val Arg Val Lys Tyr Val Gly Thr Leu Val Asp Gly  
 195 200 205  
 Lys Glu Phe Asp Lys Asn Glu Glu Gly Ile Glu Phe Ala Val Thr Gly  
 210 215 220  
 20 Val Ile Lys Gly Trp Thr Glu Met Leu Gln Leu Met Lys Val Gly Gln  
 225 230 235 240  
 Lys Val Arg Val Val Ile Pro Gln Glu Leu Ala Tyr Gly Glu Thr Gly  
 245 250 255  
 Asn Tyr Thr Ile Glu Pro Phe Ser Thr Leu Thr Phe Glu Met Glu Leu  
 260 265 270  
 25 Ile Gly Ile Lys Pro Gly Lys Lys  
 275 280

(2) INFORMATION FOR SEQ ID NO:326

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 803 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 35 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 40 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...803  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:326

Cys Arg Lys Gln Lys Leu Ser Asn Pro Lys Arg Ser Arg Tyr Pro Cys  
 1 5 10 15  
 50 Arg Arg Ile Ser Phe Arg Gln Ser Asp Lys Asn Pro Met Lys Val Leu  
 20 25 30  
 Arg Gln Val Phe Leu Pro Ile Leu Phe Val Leu Leu Thr Gly Ala Cys  
 35 40 45  
 55 Ser Thr Thr Lys Asn Leu Pro Glu Gly Glu Gln Leu Tyr Ile Gly Met  
 50 55 60  
 Gly Lys Thr Gln Ile Leu Arg Gln Asp Lys Ser His Ala Gly Gln Gln  
 65 70 75 80  
 Ala Leu Thr Glu Val Glu Ser Thr Leu Lys Val Thr Pro Asn Gly Ala  
 85 90 95  
 60 Ile Phe Gly Ser Ala Ser Ala Ser Leu Pro Lys Ile Pro Phe Gly Leu  
 100 105 110  
 Trp Leu Tyr Asn Ser Phe Val Gly Asp Ser Thr Val Ile Ser Lys Trp  
 115 120 125  
 65 Ile Phe Asp Lys Phe Ala Ala Lys Pro Val Phe Ile Ser Gln Val Lys  
 130 135 140  
 Ser Asp Ser Arg Ala Lys Val Ala Thr Asn Ile Leu Arg Glu His Gly  
 145 150 155 160  
 Tyr Phe Asp Ala Lys Val Lys Ser Ser Val Thr Thr Leu Lys Lys Asp  
 165 170 175  
 70 Ser Leu Lys Ala Lys Ile Ser Tyr Thr Val Asp Met Ala Ser Pro Tyr  
 180 185 190  
 His Tyr Asp Ser Ile Ile Pro Leu Pro Ile Ser Thr Phe Pro Asp Ser  
 195 200 205  
 75 Ile Leu Ala Tyr Arg Gln Thr Pro Ser Leu Ile Arg Lys Gly Asp Gln  
 210 215 220

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Phe Asn Leu Ala Lys Leu His Glu Glu Arg Gln Thr Ile Ser Ala Leu  
 235 230 235 240  
 Leu Arg Asp Asn Gly Tyr Tyr Tyr Phe Arg Pro Gln Asp Ile Ile Tyr  
 245 250 255  
 5 Glu Ala Asp Thr Leu Leu Val Arg Gly Ala Val Cys Leu Arg Ala Lys  
 260 265 270  
 Leu Ser Glu Asp Thr Pro Pro Gln Ala Met Arg Pro Trp Arg Ile Gly  
 275 280 285  
 10 Lys Arg Thr Ala Val Leu Leu Gly Met Asn Gly Glu Ser Pro Thr Asp  
 290 295 300  
 Ser Leu Glu Val Glu Asp Met Lys Val Leu Tyr Tyr Arg Lys Met Pro  
 305 310 315 320  
 Val Arg Pro Lys Ile Leu Ala Lys Arg Phe Arg Phe Ser Gly Asn  
 325 330 335  
 15 Leu Tyr Arg Gln Lys Asp Asp Glu Thr Thr Arg Lys Ser Leu Ala Arg  
 340 345 350  
 Leu Gly Ala Phe Ser Val Ile Asp Leu Asn Phe Leu Gln Arg Asp Ser  
 355 360 365  
 20 Ile Ser Gly Leu Leu Asp Val Arg Leu Leu Thr Thr Leu Asp Lys Pro  
 370 375 380  
 Trp Asp Ala Ser Leu Glu Thr Leu Phe Thr Ser Lys Ser Asn Asp Phe  
 385 390 395 400  
 Ile Gly Pro Gly Leu Asn Phe Ala Leu Ala Arg Arg Asn Val Phe Gly  
 405 410 415  
 25 Gly Gly Glu Asn Leu Ser Trp Asn Ile Gly Gly Ser Tyr Glu Trp Glu  
 420 425 430  
 Thr Gly Asn Arg Pro Glu Asn Ser Ser Asn Arg Leu Ile Asp Ile Asn  
 435 440 445  
 30 Ser Tyr Asn Met Asn Thr Ala Val Asn Leu Ser Phe Pro Ser Ile Val  
 450 455 460  
 Phe Pro Gly Leu Leu Asp Lys Tyr Tyr Tyr Tyr Pro Thr Thr Thr Thr  
 465 470 475 480  
 Phe Gln Ala Ser Ala Thr Ala Leu Asn Arg Ala His Tyr Phe Ser Met  
 485 490 495  
 35 Tyr Ser Phe Gly Phe Ser Thr Thr Tyr Glu Phe Gln Pro Ser Lys Glu  
 500 505 510  
 His Arg His Ala Ile Phe Pro Leu Lys Leu Asn Tyr Asn Leu Leu Gly  
 515 520 525  
 40 His Gln Thr Glu Thr Phe Gln Ala Ile Thr Ala Asn Asn Pro Pro Leu  
 530 535 540  
 Leu Leu Ser Leu Gln Ser Gln Phe Leu Ala Gln Met Gly Tyr Ile Tyr  
 545 550 555 560  
 Thr Phe Asn Lys Ser Val Ser Glu Lys Ser Pro His His Leu Trp Met  
 565 570 575  
 45 Gln Phe Gly Leu Ser Glu Ala Gly Asn Leu Leu Asn Leu Ile Tyr Leu  
 580 585 590  
 Ala Ala Gly Lys Lys Tyr Ser Asp Thr Lys Asn Phe Val Gly Val Pro  
 595 600 605  
 50 Phe Ser Gln Phe Ile Lys Ala Thr Gly Glu Leu Arg Phe Tyr Ser Tyr Thr  
 610 615 620  
 Ile Asp Arg Asn Gln Ser Leu Ala Thr Arg Phe Gly Thr Gly Val Ile  
 625 630 635 640  
 Tyr Ser Tyr Gly Asn Met Arg Val Ala Pro Tyr Ser Glu Gln Phe Tyr  
 645 650 655  
 55 Val Gly Gly Ala Asn Ser Ile Arg Ala Phe Thr Val Arg Ser Ile Gly  
 660 665 670  
 Pro Gly Arg Phe Asn Pro Asp Ser Asp Asn Gln Tyr Ser Tyr Leu Asp  
 675 680 685  
 60 Gln Val Gly Glu Phe Lys Leu Glu Ala Asn Val Glu Tyr Arg Gly Lys  
 690 695 700  
 Leu Phe Gly Asp Leu His Ala Ala Val Phe Leu Asp Ala Gly Asn Val  
 705 710 715 720  
 Trp Leu Leu Arg Glu Asp Ser Ser Arg Pro Gly Gly Ala Leu Ser Glu  
 725 730 735  
 65 Val Gly Ser Val Ser Asn Phe Leu Asn Ser Ile Ala Leu Gly Thr Gly  
 740 745 750  
 Val Gly Leu Arg Tyr Asp Leu Ala Phe Leu Val Val Arg Val Asp Val  
 755 760 765  
 70 Gly Phe Gly Leu His Leu Pro Tyr Asn Thr Gly Lys Lys Gly Tyr Tyr  
 770 775 780  
 Asn Ile Pro Arg Phe Lys Asp Ala Ile Gly Phe His Leu Ala Val Gly  
 785 790 795 800  
 Tyr Pro Phe

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## (C) INFORMATION FOR SEQ ID NO:327

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 783 amino acids  
(B) TYPE: amino acid  
(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (iii) HYPOTHETICAL: YES

## (iv) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

15 (ix) FEATURE:

(A) NAME/KEY: misc feature  
(B) LOCATION 1...783

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:327

20 Ser Leu Ser Pro Tyr Ile Arg Phe Pro Met Ser Ser His Ser Val Arg  
1 5 10 15  
Tyr Leu Ile Gly Ile Ala Gly Cys Leu Leu Met Leu Ala Ser Ser  
20 25 30  
25 Cys Ser Val Thr Arg Tyr Val Pro Asp Gly Ser Arg Leu Leu Asp Arg  
35 40 45  
Val Thr Ile Ala Ser Glu Thr Gly Ser Ile Ala Leu Pro Glu Asp Ile  
50 55 60  
30 Arg Asp Tyr Thr Leu Gln Gln Pro Asn Tyr Arg Leu Phe Gly Met Thr  
65 70 75 80  
Arg Trp Leu Leu Arg Val Tyr Ser Ser Ser Asn Pro Asn Ser Asn Ser  
85 90 95  
Trp Trp Asn Arg Ser Leu Arg Lys Met Gly Glu Pro Pro Val Leu Ile  
100 105 110  
35 Asp Ser Val Leu Thr Asp Arg Thr Ala Asn Arg Leu Ala Lys Ala Met  
115 120 125  
Ala Gly Asp Gly Phe Leu Asp Ala Thr Ala Arg Ala Val Val Asp Thr  
130 135 140  
40 Gly Leu Tyr Lys Lys Ala Arg Ile Thr Tyr Leu Ile Gln Pro Gly Ser  
145 150 155 160  
Arg Tyr Tyr Ile Arg Asn Met Ala Leu Asp Val Lys Asn Pro Leu Leu  
165 170 175  
Pro Pro Val Ala Leu Gly Asn Ser Leu Pro Ser Ala Tyr Lys Val Gly  
180 185 190  
45 Ile Ser Glu Gly Ser Pro Leu Ser Pro Ile Val Leu Asp Glu Glu Arg  
195 200 205  
Lys Ala Ile Ala Arg His Met Arg Asn Asn Gly Phe Trp Lys Phe Ser  
210 215 220  
50 Ala Glu Asp Val Tyr Tyr Glu Ala Asp Thr Thr Val Ser Gly Gly Ser  
225 230 235 240  
Gly Thr Lys Ser Ala Asp Leu Lys Leu Val Val Asn Gly Ile Gly Arg  
245 250 255  
Tyr Pro Tyr Arg Ile Gly Arg Val Phe Phe His Ala Asp Tyr Asp Pro  
260 265 270  
55 Leu Glu Ser Asp Phe Arg Val Gln Glu Leu Pro Arg Ile Asp Ser Ile  
275 280 285  
Ser Arg Gly Asp Tyr Thr Val Tyr Tyr Gly Ser Arg Gly Arg Tyr Ile  
290 295 300  
60 Arg Ala Ser Ala Leu Thr Arg Ser Val Ser Val Thr Pro Gly Ala Phe  
305 310 315 320  
Phe Cys Glu Asp Asp Val Glu Arg Ser Tyr Ile Lys Leu Asn Ala Leu  
325 330 335  
Pro Ile Val Arg Asn Val Asn Ile Arg Phe Val Glu His Asn Gly Lys  
340 345 350  
65 Asp Glu Ile Ala Leu Ala Asp Ser Ser Arg Leu Val Asp Cys Tyr Ile  
355 360 365  
Leu Thr Val Pro Ala Lys Ser Lys Ser Phe Glu Ala Glu Val Leu Gly  
370 375 380  
70 Thr Asn Ser Ala Gly Asp Phe Gly Ala Ala Leu Ser Leu Gly Phe Thr  
385 390 395 400  
Asp Arg Asn Leu Phe Arg Gly Ala Glu Met Phe Asn Ile Lys Leu Lys  
405 410 415  
Gly Ala Tyr Glu Ala Ile Arg Lys Gly Ser His Ser Phe Met Glu Tyr  
420 425 430  
75 Gly Val Glu Ser Ser Leu Arg Phe Pro Arg Leu Leu Phe Pro Phe Ile



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435 440 445  
 Ser Asp Glu Thr Arg Arg Arg Leu Arg Ala Ser Thr Glu Trp Lys Ile  
 150 455 460  
 5 Gly Tyr Asn Tyr Gln Thr Arg Pro Glu Phe Asp Arg Val Ile Leu Ser  
 465 470 475 480  
 Ala Gln Leu Asn Tyr Ser Trp Gln Thr Tyr Leu His Asn Arg Leu Arg  
 485 490 495  
 His Thr Ile Arg Leu Leu Asp Val Asp Tyr Leu His Leu Pro Tyr Ile  
 500 505 510  
 10 Asp Pro Asp Phe Ala Gln Ser Leu Pro Pro Thr Thr Ala Leu Tyr Asn  
 515 520 525  
 Tyr Thr Glu Gln Phe Ile Leu Gly Ser Ala Tyr Ile Leu Asn Tyr Thr  
 530 535 540  
 15 Thr Ala Ser Ser Met Glu Arg Thr Val Ser Asn Pro Phe Thr Ala Arg  
 545 550 555 560  
 Phe Ser Ile Gln Thr Ala Gly Asn Leu Leu Gln Ala Ile Ser Tyr Leu  
 565 570 575  
 Thr Asp Ser Pro Lys Asp Glu His Gly Leu Tyr Lys Met Phe Gly Leu  
 580 585 590  
 20 His Tyr Ala Gln Phe Val Lys Leu Asp Leu Asp Leu Ala Lys Thr Val  
 595 600 605  
 Leu Leu Glu Lys Asp Asn Thr Leu Ala Leu His Leu Gly Phe Gly Leu  
 610 615 620  
 25 Ala Phe Pro Tyr Gly Asn Ala Arg His Ile Pro Phe Glu Leu Arg Tyr  
 625 630 635 640  
 Phe Ala Gly Gly Ser Asn Ser Val Arg Gly Trp Ser Val Arg Thr Leu  
 645 650 655  
 Gly Pro Gly Ser Met Lys Met Thr Pro Asp Lys Thr Phe Phe Asp Gln  
 660 665 670  
 30 Met Gly Asp Ile Arg Leu Asp Leu Asn Val Glu Tyr Arg Thr Lys Leu  
 675 680 685  
 Phe Trp Lys Phe Arg Ala Ala Phe Val Asp Ala Gly Asn Val Trp  
 690 695 700  
 35 Thr Ile Lys Glu Tyr Glu Asn Gln Glu Asp Gly Leu Phe Arg Phe Asp  
 705 710 715 720  
 Arg Phe Tyr Lys Glu Ile Ala Leu Ala Tyr Gly Leu Gly Leu Arg Leu  
 725 730 735  
 Asp Phe Asp Tyr Phe Leu Val Arg Leu Asp Ala Gly Leu Lys Ala Tyr  
 740 745 750  
 40 Asp Pro Gln Gln Thr Gly Arg Tyr Lys Trp Ala Ile Thr Arg Pro Asn  
 755 760 765  
 Leu Ser Ser Asn Phe Ala Trp His Ile Ala Val Gly Tyr Pro Phe  
 770 775 780  
 45 (2) INFORMATION FOR SEQ ID NO:328  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 875 amino acids  
 50 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 55 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 60 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...875  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:328  
 65 Val Glu Ser Lys Leu Leu Cys Leu Met Arg Lys Arg Ile Leu Gln Leu  
 1 5 10 15  
 Phe Leu Thr Ala Leu Leu Leu Ala Leu Gly Ser Ser Leu Ala Ile Ala  
 20 25 30  
 70 Gln Thr Val Val Thr Gly Lys Val Ile Asp Ser Glu Thr Ser Glu Pro  
 35 40 45  
 Leu Ile Gly Val Ser Val Ser Thr Gly Gln Gly Ala Ser Leu Arg Gly  
 50 55 60  
 Val Thr Thr Asp Met Asp Gly Gly Phe Arg Phe Glu Val Pro Ala Lys  
 65 70 75 80  
 75 Ser Val Leu Thr Phe Arg Cys Val Gly Tyr Ala Thr Val Thr Arg Ser



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His Cys Gly Val Glu Ala Glu Val Ser Tyr Arg Pro Ile Arg Gln Ile  
 690 695 700  
 Asp Leu Arg Gly Met Phe Ser Leu Gly Asp Trp Thr Trp Gln Asn Asn  
 705 710 715 720  
 5 Val Ser Tyr Thr Ser Tyr Asp Glu Ala Gly Asn Glu Thr Gly Gln Asp  
 725 730 735  
 Ile Thr Tyr Ile Lys Gly Leu His Val Gly Asp Ala Ala Gln Met Thr  
 740 745 750  
 10 Ala Ala Val Ser Ala Asp Ile Glu Leu Phe Lys Gly Phe His Val Ile  
 755 760 765  
 Gly Lys Tyr Asn Phe Leu Gly Lys Asn Tyr Ala Gly Phe Asn Pro Ala  
 770 775 780  
 Thr Arg Asn Ala Gln Gln Tyr Glu Ala Asp Gly Lys Glu Ile Val Glu  
 785 790 795 800  
 15 Ser Trp Lys Leu Pro Asp Val Gly Leu Phe Asp Leu Ser Ala Ser Tyr  
 805 810 815  
 Asn Phe Lys Leu Gly Ser Leu Ser Thr Thr Phe Tyr Phe Asn Met Asp  
 820 825 830  
 20 Asn Val Ala Asp Lys Arg Tyr Val Ser Asp Ala Asp Asn Ile Ile  
 835 840 845  
 Gly Lys Lys His Asp Glu Ala Ser Ala Leu Val Trp Tyr Gly Phe Gly  
 850 855 860  
 Arg Thr Trp Ser Thr Gly Ile Arg Val Asn Phe  
 865 870 875  
 25 (2) INFORMATION FOR SEQ ID NO:329  
 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 460 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30 (ii) MOLECULE TYPE: protein  
 35 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 40 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...460  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:329  
 Asn Arg Cys Asn Pro Ser Arg Gln Tyr Phe His Leu Ser Gln Asn Asp  
 1 5 10 15  
 Val Gly Arg Ser Leu Arg Ala Phe Leu Ile His Leu Ser Met Lys Phe  
 20 25 30  
 50 Ser Ile Arg Leu Phe Leu Cys Ile Ile Phe Leu Leu Ser Ala Phe Ile  
 35 40 45  
 Leu Pro Ala Leu Gly Gln Lys Ser Lys Gln Val Gln Arg Leu Glu Lys  
 50 55 60  
 Gln Arg Lys Glu Ala Leu Lys Ala Ile Glu Lys Thr Asp Arg Glu Leu  
 65 70 75 80  
 Arg Asn Thr Lys Lys Asp Lys Gln Asp Lys Gln Lys His Leu Asn Leu  
 85 90 95  
 Leu Asn Lys Gln Val Ala Gln Arg Lys Gln Met Val Gln Leu Leu Asp  
 100 105 110  
 60 Asn Glu Val Lys Glu Leu Gln Ser Asp Ile Asp Ser Met Thr Gly Val  
 115 120 125  
 Cys His Gln Leu Ser Val Glu Glu Lys Ala Arg Ser Asp Glu Tyr Ala  
 130 135 140  
 Gln Ala Leu Gln Ser Met Gln Lys Arg Lys Arg Ser Leu Asp Arg Ile  
 145 150 155 160  
 65 Leu Phe Ile Ser Ser Ala Lys Ser Phe Asp Glu Gly Met Arg Arg Met  
 165 170 175  
 Arg Phe Leu Glu Gln Tyr Ala Ser Ala Tyr Lys Leu Ala Ser Val Arg  
 180 185 190  
 70 Leu Arg Asp Thr Arg Ser Lys Leu Glu Thr Glu Arg Ala Thr Val Glu  
 195 200 205  
 Asp Ala Lys Lys Glu Lys Gly His Leu Leu Val Ile Arg Glu Glu Glu  
 210 215 220  
 75 Lys Lys Lys Leu Glu Gly Gln Gln Ala Glu Gln Arg Arg Gln Val Gln  
 225 230 235 240

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Ile Val Asn Gly Ser Leu Ser Glu Phe Lys Phe Arg Tyr Val Asn Phe  
 210 215 220  
 Asp Lys Glu Thr Tyr Val Val Lys Pro Thr Thr Lys Pro Asp Asn Leu  
 225 230 235 240  
 5 Ile Ser Ser Ala Asn Gly Val Trp Pro Gln Ile Thr Asp Trp Thr Val  
 245 250 255  
 Trp Gly Ala Ser Leu Asn Thr Ser Pro Ala Pro Asp Ala Gly Thr Gly  
 260 265 270  
 10 Tyr Thr Leu Asp Ala Asn Gly Lys Val Thr Ala Leu Arg Ile Val Thr  
 275 280 285  
 Tyr Leu Asn Glu Arg Asp Ser Lys Gly Ala Thr Val Glu Val Ala Leu  
 290 295 300  
 Pro Arg Val Asp Asp Gly Thr Leu Pro Pro Glu Phe Gly Pro Glu  
 305 310 315 320  
 15 Leu Tyr Arg Leu Pro Leu Pro Asp Lys Ile Leu Arg Asn His Trp Tyr  
 325 330 335  
 Lys Tyr Glu Val Glu Ile  
 340

20 (2) INFORMATION FOR SEQ ID NO:331  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 329 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 25  
 (ii) MOLECULE TYPE: protein  
 30 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 35 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...329  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:331

40 Asn Leu Arg Thr Gln Pro Phe Phe Leu Val Asp Leu Gln Ser Met Ile  
 1 5 10 15  
 Arg Thr Ile Leu Ser Arg Tyr Val Ser Ser Asn Phe Trp Ser Arg Gly  
 20 25 30  
 45 Ala Thr Phe Phe Phe Thr Ile Phe Pro Ala Phe Ile Leu Ala Ala Thr  
 35 40 45  
 Ala Leu Pro Ala Cys Gly Gly Gly Thr Ala Ser Gly Ser Asp Arg Thr  
 50 55 60  
 Leu Ala Val Thr Ile Glu Pro Gln Lys Tyr Phe Ile Glu Ser Ile Ala  
 65 70 75 80  
 50 Asp Lys Ser Val Gln Val Val Ala Leu Val Pro Ala Gly Ser Asn Pro  
 85 90 95  
 Glu Glu Tyr Asp Pro Ser Pro Thr Val Met Lys Arg Leu Ser Glu Ala  
 100 105 110  
 55 Asp Ala Tyr Phe Tyr Ile Gly Gly Leu Gly Phe Glu Gln Arg Asn Leu  
 115 120 125  
 Ala Ala Ile Arg Asp Asn Asn Pro Lys Leu Pro Leu Phe Glu Met Gly  
 130 135 140  
 Lys Ala Leu Ala Asp Ala Gly Ser Ala Asp Leu His Gly Ser Cys Thr  
 145 150 155 160  
 60 Asp His Ser His Thr Asp Leu His Ala His Asp Pro His Tyr Trp Ser  
 165 170 175  
 Ser Val Val Gly Ala Lys Ala Leu Ser Arg Ala Ala Tyr Asp Ala Leu  
 180 185 190  
 65 Val Glu Leu Tyr Pro Asn Glu Lys Asp Lys Trp Asp Lys Gly His Asp  
 195 200 205  
 Arg Leu Asn Gly Arg Ile Asp Ser Val Lys Arg Leu Val Asp Thr Met  
 210 215 220  
 Phe Ala Asn Gly Lys Ala Asp Lys Ala Phe Val Ile Tyr His Pro Ser  
 225 230 235 240  
 70 Leu Ser Phe Phe Ala Gln Glu Phe Gly Leu Arg Gln Ile Val Ile Glu  
 245 250 255  
 Glu Asp Gly Lys Glu Pro Thr Ala Ala His Leu Arg Arg Val Ile Asp  
 260 265 270  
 75 Gln Ala Arg Ala Asp Gly Val Arg Ile Val Phe Ile Gln Pro Glu Phe  
 275 280 285

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Glu Thr Arg Gln Ala Glu Asp Ile Ala Arg Glu Ile Gly Ala Arg Pro  
 290 295 300  
 Val Arg Ile Asn Pro Leu Arg Ser Ser Trp Glu Glu Ile Leu His  
 305 310 315 320  
 5 Ile Ala Arg Ala Leu Ala His Glu Arg  
 325

(2) INFORMATION FOR SEQ ID NO:332

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 878 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...878

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:332

Ala Asp Ser Ile Arg Tyr Pro Leu Tyr Phe Phe Gly Arg Asn Arg Lys  
 1 5 10 15  
 30 Lys Cys Phe Arg Glu Pro Ile Pro Thr Leu Tyr Asn Lys Asn Met Ile  
 20 25 30  
 Gly Lys Lys Ile Phe Phe Ile Leu Leu Ala Leu Ile Ala Phe Ser Gly  
 35 35 40 45  
 Leu Asn Ala Ala Thr Asp Thr Glu Phe Lys Tyr Pro Thr Asp Ala Asn  
 50 55 60  
 Ile Ile Gly His Val Lys Asp Ser Lys Thr Gly Glu His Leu Val Gly  
 65 70 75 80  
 Ile Thr Ile Ala Ile Lys Gly Thr Thr Phe Gly Thr Ser Thr Asp Ala  
 85 90 95  
 40 Thr Gly His Tyr Tyr Leu Arg Asn Leu Arg Pro Gly Glu Ile Thr Leu  
 100 105 110  
 Ile Met Arg Gly Met Gly Tyr Lys Ser Gln Glu Arg Val Val Arg Val  
 115 120 125  
 45 Glu Lys Asp Lys Thr Ile Glu Val Asn Phe Glu Ala Glu Glu Asp Ala  
 130 135 140  
 Ile Asn Leu Asp Glu Val Val Ile Ser Ala Asn Arg Glu Leu Thr Leu  
 145 150 155 160  
 Arg Arg Leu Ala Pro Thr Leu Val Asn Val Leu Asn Glu Lys Val Phe  
 165 170 175  
 50 Ser Gln Val Asn Ala Ser Asn Leu Ala Gln Gly Leu Ser Phe Gln Pro  
 180 185 190  
 Gly Val Arg Val Glu Asn Asn Cys Gln Asn Cys Gly Phe Asn Gln Val  
 195 200 205  
 55 Arg Ile Asn Gly Leu Asp Gly Arg Tyr Ala Gln Ile Leu Ile Asp Ser  
 210 215 220  
 Arg Pro Ile Met Ser Ala Leu Ala Gly Val Tyr Gly Leu Glu Gln Ile  
 225 230 235 240  
 Pro Ala Asn Met Ile Glu Arg Val Glu Val Val Arg Gly Gly Ser  
 245 250 255  
 60 Ala Leu Tyr Gly Ser Ser Ala Ile Ala Gly Val Val Asn Ile Ile Thr  
 260 265 270  
 Lys Glu Pro Ser His Asn Ser Phe Thr Phe Asn Glu Ser Leu Ser Phe  
 275 280 285  
 65 Thr Gly Phe Ser Lys Leu Asp Asn Asn Thr Asn Phe Asn Ala Ser Ile  
 290 295 300  
 Val Ser Asp Asp Asn Arg Ala Gly Ala Met Val Phe Gly Gln Ala Arg  
 305 310 315 320  
 Tyr Arg Asn His Trp Asp Ala Asn Asn Asp Gly Tyr Ser Glu Leu Gly  
 325 330 335  
 70 Lys Ile Asp Ala Arg Ser Leu Gly Ala His Ser Tyr Leu Arg Leu Ser  
 340 345 350  
 Asp Tyr Ser Lys Leu Thr Gly Glu Phe His Thr Ile Ser Glu Phe Arg  
 355 360 365  
 75 Arg Gly Gly Asp Arg Ile Asp Leu Pro Pro His Val Val Gly Val Ala  
 370 375 380

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Glu Gln Thr Asp His Ser Val Phe Ser Gly Asn Leu Lys Tyr Asp Leu  
 385 390 395 400  
 Phe Ser Ser Asn Tyr Lys His His Phe Gln Ala Tyr Thr Ser Gly Gln  
 405 410 415  
 5 Ile Val Asn Arg Lys Ser Tyr Tyr Gly Ile Gly Glu Ile Asp Val  
 420 425 430  
 Asn Gly His Pro Gly Gly Thr Glu Gly Tyr Pro Ile Pro Gln Asp Gln  
 435 440 445  
 10 Tyr Gly Asn Asn Tyr Gly Val Thr Lys Gly Lys Thr Tyr Met Gly Gly  
 450 455 460  
 Ile Gln Tyr Ser Tyr Asp Leu Asp Lys Phe Leu Leu Met Pro Ser Gln  
 465 470 475 480  
 Leu Leu Phe Gly Ala Glu Tyr Thr Arg Asp Glu Leu Asn Asp Val Met  
 485 490 495  
 15 Pro Ile Leu Ser Trp Gln Thr Gly Glu Asp Ala Asn Gly Asn Thr Ile  
 500 505 510  
 Pro Leu Tyr Pro Glu Leu Asp Gln Asn Ile Asn Asn Tyr Ser Leu Phe  
 515 520 525  
 20 Gly Gln Asn Glu Trp Lys Asn Asp Arg Trp Ser Ile Leu Val Gly Ala  
 530 535 540  
 Arg Leu Asp Lys His Ser Glu Val Lys Asp Met Ile Leu Ser Pro Arg  
 545 550 555 560  
 Thr Thr Leu Arg Phe Asn Val Asn Pro Asp Ile Asn Leu Arg Ala Thr  
 565 570 575  
 25 Tyr Ala Lys Gly Phe Arg Ala Pro Gln Val Phe Asp Glu Asp Leu His  
 580 585 590  
 Val Gly Val Val Gly Gly Glu Ala Gln Lys Val Phe Asn Asp Pro Asn  
 595 600 605  
 30 Leu Lys Pro Glu Ile Ser His Ala Phe Ser Leu Ser Ala Asp Met Tyr  
 610 615 620  
 His Arg Phe Gly Asn Val Gln Thr Asn Phe Leu Val Glu Gly Phe Tyr  
 625 630 635 640  
 Thr Arg Leu Leu Asp Val Phe Thr Asn Glu Glu Gln Pro Asp Gln His  
 645 650 655  
 35 Asp Gly Ile Lys Arg Tyr Thr Arg Ile Asn Gly Ser Gly Ala Lys Val  
 660 665 670  
 Phe Gly Leu Asn Leu Glu Gly Lys Val Ala Tyr Lys Ser Phe Gln Leu  
 675 680 685  
 40 Gln Ala Gly Leu Thr Leu Ala Ser Asn Lys Tyr Asp Glu Ala Gln Glu  
 690 695 700  
 Trp Gly Leu Asn Thr Val Lys Asp Thr Asn Gly Ala Phe Val Thr Glu  
 705 710 715 720  
 Ala Asn Ala Asn Gly Gln Gln Glu Tyr Lys Asn Glu Ser Met Thr Asp  
 725 730 735  
 45 Thr Gln Ile Thr Arg Thr Pro Ser Val Tyr Gly Tyr Phe Thr Leu Ala  
 740 745 750  
 Tyr Asn Pro Ala His Ser Trp Asn Ile Ala Leu Thr Gly Ala Tyr Thr  
 755 760 765  
 50 Gly Gln Met Tyr Val Pro His Ala Ile Glu Tyr Gly Val Lys Ser Ala  
 770 775 780  
 Glu Leu Asp Ile Met Gln Asn Asn Pro Glu Ile Thr Asp Glu Thr Gly  
 785 790 795 800  
 Lys Ala Pro Arg Ile Asp Glu Leu Lys Lys Thr Pro Ala Phe Phe Asp  
 805 810 815  
 55 Leu Gly Leu Lys Val Gly Tyr Asp Phe His Val Phe Gln Ala Thr Glu  
 820 825 830  
 Val Gln Leu Tyr Val Gly Met Asn Asn Ile Phe Asn Ser Phe Gln Lys  
 835 840 845  
 60 Asp Phe Asp Arg Gly Ala Ala Arg Asp Ser Gly Tyr Ile Tyr Gly Pro  
 850 855 860  
 Thr Gln Pro Arg Thr Gly Tyr Met Gly Leu Val Val Lys Phe  
 865 870 875

(2) INFORMATION FOR SEQ ID NO:333

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 206 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...206

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333

10 Lys Gln Ile Val Met Thr Val Lys Arg Ala Val Arg Ile Ala Leu Leu  
1 5 10 15  
Thr Leu Ile Gly Ile Leu Phe Ser Ser Pro Ser Leu Val Arg Ala Gln  
20 25 30  
Ser Leu Phe Ser Thr Glu His Val Leu Gln Leu Tyr Asn Lys Ile Leu  
35 40 45  
15 Tyr Gly Glu Ser Ala Ala Asp Thr Val Ala Glu Lys Thr Ala Gly Glu  
50 55 60  
Ser Ala Phe Pro Phe Ile Asp Lys Leu Ile Asn Leu Gly Arg Thr Phe  
65 70 75 80  
Leu Gly Lys Pro Tyr Arg Tyr Arg Gly Pro Ser Pro Trp Pro Met Asp  
85 90 95  
20 Cys Ser Gly Tyr Val Ser Tyr Leu Tyr Ser Lys Phe Asp Ile Lys Leu  
100 105 110  
Pro Arg Gly Ala Ala Ala Gln Ser Gln Tyr Thr Asn Pro Ile Glu Arg  
115 120 125  
25 Glu Asp Val Arg Pro Gly Asp Leu Leu Phe Phe Lys Gly Arg Asn Ala  
130 135 140  
Arg Ser Asn Arg Ile Gly His Val Ala Leu Val Val Ser Val Asp Glu  
145 150 155 160  
Asp Asp Ile Thr Met Met His Ser Arg Asn Ser Arg Gly Ile Val Ile  
165 170 175  
30 Glu Lys Leu Asn Arg Ser Ala Tyr Phe Ser Arg Arg Leu Val Ser Tyr  
180 185 190  
Gly Arg Val Pro Gly Ala Lys Arg Val Ile Pro Arg Lys Ser  
195 200 205

35

(2) INFORMATION FOR SEQ ID NO:334

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 467 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: protein

45

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

50

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334

55

Lys Gly Thr Trp Asn Arg Lys Asn Arg Arg Glu Glu Met Lys Arg Thr  
1 5 10 15  
Ile Leu Leu Thr Ala Leu Thr Val Leu Ser Ser Leu Ser Leu Leu Arg  
20 25 30  
60 Ala Gln Asn Glu Ser Glu Ala Ser Thr Asn Pro Met Ser Gly Leu Ser  
35 40 45  
Leu Glu Asp Cys Ile Arg Ile Ala Lys Glu Arg Asn Leu Asn Leu Arg  
50 55 60  
65 Arg Gln Glu Ile Glu Gln Glu Asn Arg Ile Ile Ser Leu Asp Ala Ala  
65 70 75 80  
Arg His Ser Phe Leu Pro Ser Val Asn Ala Gly Ile Gly His Asn Tyr  
85 90 95  
Ser Phe Gly Arg Ser Lys Asp Lys Thr Gly Val Thr Val Asp Arg Ser  
100 105 110  
70 Ser Met Asn Thr Asn Leu Ser Ile Gly Ala Ser Val Glu Val Phe Ser  
115 120 125  
Gly Thr Arg Arg Leu His Asp Leu Lys Gln Gln Lys Tyr Asn Val Glu  
130 135 140  
75 Asp Gly Ile Ala Arg Leu Gln Lys Ala Arg Glu Asp Leu Ser Leu Gln  
145 150 155 160



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5 Ile Ala Ala Leu Tyr Ile Asn Leu Leu Phe Arg Gln Glu Met Thr Arg  
 165 170 175  
 Thr Ala Glu Thr Gln Leu Ala Leu Ile Arg Glu Gln Arg Asn Arg Thr  
 180 185 190  
 Ala Glu Met Val Arg Val Gly Lys Trp Ala Glu Gly Lys Leu Leu Asp  
 195 200 205  
 10 Ile Asn Ala Gln Met Ala Lys Asp Glu Gln Leu Leu Val Gln Tyr Arg  
 210 215 220  
 Ser Glu Glu Glu Leu Ala Arg Leu Asp Leu Gly Gln Ala Leu Glu Leu  
 225 230 235 240  
 Glu His Pro Glu Ser Ile Ala Val Lys Ala Pro Asp Thr Asp Val Leu  
 245 250 255  
 Val Ala Glu Arg Leu Gly Ser Leu Leu Ala Pro Glu Glu Ile Tyr Arg  
 260 265 270  
 15 Thr Ala Leu Gly Leu Lys Pro Ala Leu His Ser Ser Glu Leu Gln Ile  
 275 280 285  
 Ala Ser Ala Arg Glu Gly Leu Ala Ser Ala Arg Ala Tyr Phe Pro  
 290 295 300  
 20 Thr Leu Ser Leu Ser Ala Gly Tyr Ser Asn Gly Tyr Phe Arg Asp Leu  
 305 310 315 320  
 Gly Lys Glu Tyr Ala Ala Ile Asn Pro Ser Phe Ser Glu Gln Trp Lys  
 325 330 335  
 Asn Asn Gly Ser Tyr Ser Ile Gly Leu Ser Leu Asn Ile Pro Ile Phe  
 340 345 350  
 25 Ser Ala Met Gln Thr Gln Asp Arg Val Arg Ser Ser Arg Leu Gln Ile  
 355 360 365  
 Arg Ser Ser Glu Leu Arg Leu Val Glu Glu Lys Lys Ala Leu Tyr Lys  
 370 375 380  
 30 Glu Ile Arg Gln Ala Tyr Ser Asn Ala Val Ala Ala Asp Lys Ala Ile  
 385 390 395 400  
 Ala Ala Ala Glu Asn Ser Lys Ala Ala Thr Leu Lys Ala Tyr Glu Tyr  
 405 410 415  
 Ala Arg Asp Ser Phe Glu Ala Gly Arg Leu Ser Ala Tyr Glu Tyr Ala  
 420 425 430  
 35 Glu Ala Lys Thr Lys Tyr Ala Leu Ser Gln Val Glu Glu Leu Arg Ala  
 435 440 445  
 Lys Tyr Asp Phe Ile Tyr Lys Ala Lys Val Leu Asp Phe Tyr Gln Gly  
 450 455 460  
 40 Lys Asp Phe  
 465

## (2) INFORMATION FOR SEQ ID NO:335

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 451 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 50 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 55 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...451  
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:335

65 Lys Thr Ser Tyr Arg Asn Asn Met Arg Phe Gln His Tyr Leu Ile Cys  
 1 5 10 15  
 Thr Ala Ala Val Ala Ala Leu Ala Ala Asn Pro Leu Thr Gly Gln Ser  
 20 25 30  
 Asn Met Thr Leu Glu Glu Cys Ile Asp Tyr Ala Arg Arg His Ser Ser  
 35 40 45  
 Ala Val Ala Leu Ser Ala Ala Glu Leu Glu Gln Ser Lys Ala Asp Tyr  
 50 55 60  
 70 Leu Gln Ala Val Gly Asn Phe Leu Pro Arg Val Ser Ala Gly Thr Gly  
 65 70 75 80  
 Ala Ser Trp Asn Phe Gly Arg Gly Leu Asp Ala Glu Thr Asn Thr Tyr  
 85 90 95  
 75 Thr Asp Ile Asn Ser Phe Asn Asn Ser Tyr Ser Ile His Ala Thr Met  
 100 105 110

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Thr Leu Phe Asp Gly Leu Gln Ser Val Tyr Arg Leu Arg Met Ala His  
 115 120 125  
 Ala Arg Arg Glu Ala Ser Arg Leu Ser Val Arg Glu Gln Gln Leu  
 130 135 140  
 5 Ala Ala Leu Gly Thr Thr Glu Ala Tyr Tyr Asp Leu Val Tyr Ala Arg  
 145 150 155 160  
 Gln Met Gln Glu Leu Ala Met Gln Lys Tyr Glu Glu Ser Ser Arg Leu  
 165 170 175  
 10 His Arg Gln Thr Ala Arg Met Glu Glu Leu Gly Met Lys Ser Arg Pro  
 180 185 190  
 Asp Val Leu Glu Met Gln Ser Arg Met Ala Gly Asp Arg Leu Ala Leu  
 195 200 205  
 Thr Gln Ala Asp Asn Gln Cys Ile Ile Ala Leu Ile Arg Leu Lys Glu  
 210 215 220  
 15 Lys Met Asn Phe Pro Ile Asp Asp Glu Leu Val Val Asp Asp Met Pro  
 225 230 235 240  
 Ala Asp Ser Leu Ser Ala Asp Met Ala Glu Ser Asp Ser Ala Gly  
 245 250 255  
 20 Val Phe Ala Arg Ala Ala His His Pro Val Leu Leu Arg Ala Lys  
 260 265 270  
 Leu Asp Glu Gln Ala Ala Thr Asp Arg Leu Arg Ala Ala Arg Gly Ala  
 275 280 285  
 Phe Leu Pro Ser Val Ser Val Ser Gly Gly Trp Asn Thr Gly Phe Ser  
 290 295 300  
 25 Arg Phe Leu Asn Gly Ser Asp Tyr Thr Pro Phe Ser Glu Gln Phe Arg  
 305 310 315 320  
 Asn Arg Arg Gly Glu Tyr Val Ser Leu Asn Leu Ser Ile Pro Ile Phe  
 325 330 335  
 Ser Gly Phe Ser Leu Val Ser His Leu Arg Gln Ala Arg Ala Glu Arg  
 340 345 350  
 30 Arg Ala Ala Ile Val Arg Arg Gly Glu Ala Glu Arg Arg Leu Tyr Ser  
 355 360 365  
 Glu Ile Ala Gln Ala Met Ala Asp Arg Asp Ala Leu Ala Ser Tyr  
 370 375 380  
 35 Arg Gln Ala Lys Glu His Thr Asp Ala Met Gln Thr Ala Tyr Glu Ala  
 385 390 395 400  
 Val Leu Gln Arg Tyr Glu Glu Gly Leu Asn Thr Ala Ile Asp Leu Thr  
 405 410 415  
 40 Thr Gln Ala Asn Arg Leu Leu Asp Ala Arg Val Gln Arg Leu Arg Ala  
 420 425 430  
 Ala Met Thr Tyr Arg Leu Lys Cys Lys Leu Ile Ala Tyr Tyr Gly Cys  
 435 440 445  
 Leu Ser Asp  
 450

(2) INFORMATION FOR SEQ ID NO:336

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 962 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...962

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336

65 Ala Ile Phe Val Val Ser Leu Gln Ile Glu Lys Ile Thr Glu Asn Lys  
 1 5 10 15  
 Tyr Asn Ser Asp Lys Ser Met Asn Lys Phe Tyr Lys Ser Leu Leu Gln  
 20 25 30  
 70 Ser Gly Leu Ala Ala Phe Val Ser Met Ala Thr Ala Leu Thr Ala Ser  
 35 40 45  
 Ala Gln Ile Ser Phe Gly Gly Glu Pro Leu Ser Phe Ser Ser Arg Ser  
 50 55 60  
 75 Ala Gly Thr His Ser Phe Asp Asp Ala Met Thr Ile Arg Leu Thr Pro  
 65 70 75 80

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Asp Phe Asn Pro Glu Asp Leu Ile Ala Gln Ser Arg Trp Gln Ser Gln  
85 90 95  
Arg Asp Gly Arg Pro Val Arg Ile Gly Gln Val Ile Pro Val Asp Val  
100 105 110  
5 Asp Phe Ala Ser Lys Ala Ser His Ile Ser Ser Ile Gly Asp Val Asp  
115 120 125  
Val Tyr Arg Leu Gln Phe Lys Leu Glu Gly Ala Lys Ala Ile Thr Leu  
130 135 140  
10 Tyr Tyr Asp Ala Phe Asn Ile Pro Glu Gly Gly Arg Leu Tyr Ile Tyr  
145 150 155  
Thr Pro Asp His Glu Ile Val Leu Gly Ala Tyr Thr Asn Ala Thr His  
165 170 175  
15 Arg Arg Asn Gly Ala Phe Ala Thr Glu Pro Val Pro Gly Ser Glu Leu  
180 185 190  
Ile Met Asp Tyr Glu Val Ser Arg Gly Gly Thr Leu Pro Asp Ile Lys  
195 200 205  
Ile Ser Gly Ala Gly Tyr Ile Phe Asp Lys Val Gly Gly Arg Pro Val  
210 215 220  
20 Thr Asp Asn His Tyr Gly Ile Gly Glu Asp Asp Ser Asp Ser Asp Cys  
225 230 235  
Glu Ile Asn Ile Asn Cys Pro Glu Gly Ala Asp Trp Gln Ala Glu Lys  
245 250 255  
Asn Gly Val Val Gln Met Ile Met Val Lys Gly Gln Tyr Ile Ser Met  
260 265 270  
25 Cys Ser Gly Asn Leu Leu Asn Asn Thr Lys Gly Asp Phe Thr Pro Leu  
275 280 285  
Ile Ile Ser Ala Gly His Cys Ala Ser Ile Thr Thr Asn Phe Gly Val  
290 295 300  
30 Thr Gln Ser Glu Leu Asp Lys Trp Ile Phe Thr Phe His Tyr Glu Lys  
305 310 315  
Arg Gly Cys Ser Asn Gly Thr Leu Ala Ile Phe Arg Gly Asn Ser Ile  
325 330 335  
Ile Gly Ala Ser Met Lys Ala Phe Leu Pro Ile Lys Gly Lys Ser Asp  
340 345 350  
35 Gly Leu Leu Leu Gln Leu Asn Asp Glu Val Pro Leu Arg Tyr Arg Val  
355 360 365  
Tyr Tyr Asn Gly Trp Asp Ser Thr Pro Asp Ile Pro Ser Ser Gly Ala  
370 375 380  
40 Gly Ile His His Pro Ala Gly Asp Ala Met Lys Ile Ser Ile Leu Lys  
385 390 395  
Lys Thr Pro Ala Leu Asn Thr Trp Ile Ser Ser Ser Gly Ser Gly Gly  
405 410 415  
Thr Asp Asp His Phe Tyr Phe Lys Tyr Asp Gln Gly Gly Thr Glu Gly  
420 425 430  
45 Gly Ser Ser Gly Ser Ser Leu Phe Asn Gln Asn Lys His Val Val Gly  
435 440 445  
Thr Leu Thr Gly Gly Ala Gly Asn Cys Gly Gly Thr Glu Phe Tyr Gly  
450 455 460  
50 Arg Leu Asn Ser His Trp Asn Glu Tyr Ala Ser Asp Gly Asn Thr Ser  
465 470 475  
Arg Met Asp Ile Tyr Leu Asp Pro Gln Asn Asn Gly Gln Thr Thr Ile  
485 490 495  
Leu Asn Gly Thr Tyr Arg Asp Gly Tyr Lys Pro Leu Pro Ser Val Pro  
500 505 510  
55 Arg Leu Leu Leu Gln Ser Thr Gly Asp Gln Val Glu Leu Asn Trp Thr  
515 520 525  
Ala Val Pro Ala Asp Gln Tyr Pro Ser Ser Tyr Gln Val Glu Tyr His  
530 535 540  
60 Ile Phe Arg Asn Gly Lys Glu Ile Ala Thr Thr Lys Glu Leu Ser Tyr  
545 550 555  
Ser Asp Ala Ile Asp Glu Ser Ile Ile Gly Ser Gly Ile Ile Arg Tyr  
565 570 575  
Glu Val Ser Ala Arg Phe Ile Tyr Pro Ser Pro Leu Asp Gly Val Glu  
580 585 590  
65 Ser Tyr Lys Asp Thr Asp Lys Thr Ser Ala Asp Leu Ala Ile Gly Asp  
595 600 605  
Ile Gln Thr Lys Leu Lys Pro Asp Val Thr Pro Leu Pro Gly Gly Gly  
610 615 620  
70 Val Ser Leu Ser Trp Lys Val Pro Phe Leu Ser Gln Leu Val Ser Arg  
625 630 635  
Phe Gly Glu Ser Pro Asn Pro Val Phe Lys Thr Phe Glu Val Pro Tyr  
645 650 655  
Val Ser Ala Ala Ala Ala Gln Thr Pro Asn Pro Pro Val Gly Val Val  
660 665 670  
75 Ile Ala Asp Lys Phe Met Ala Gly Thr Tyr Pro Glu Lys Ala Ala Ile



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130 135 140  
 Val Ala Asn Leu Asp Phe Asn Ala Pro Ala Thr Glu Ala Ala Leu Ser  
 145 150 155 160  
 Gln Phe Val Val Glu Lys Ser Ile Glu Val Ser Ser Thr Thr Ala Pro  
 165 170 175  
 Ala Asp Phe Val Met Leu Ala His Gly Asn Lys Gln Ile Asn Met Ala  
 180 185 190  
 Thr Thr Glu Gly Lys Leu Leu Gly Asp Tyr Lys Leu Lys Arg Val Ala  
 195 200 205  
 10 Ala Lys Ile Arg Met Ile Lys Pro Thr Ile Asn Val Gln Gly Tyr Glu  
 210 215 220  
 Val Val Gly Asn Ile Gln Ala Lys Phe Arg Asn Ser Val Thr Lys Gly  
 225 230 235 240  
 15 Phe Leu Thr Thr Glu Ala Gln Glu Ile Pro Ala Ala Ala Ser Tyr Lys  
 245 250 255  
 Thr Ser Glu Tyr Leu Asp Ile Ala Glu Ser Ala Pro Ala Asn Ser Ile  
 260 265 270  
 His Phe Tyr Ser Tyr Tyr Asn Lys Trp Thr Leu Ser Thr Pro Glu Lys  
 275 280 285  
 20 Arg Pro Glu Phe Phe Ile Met Val Lys Phe Lys Lys Thr Gly Gln Pro  
 290 295 300  
 Asp Asn Thr Ala Lys Pro Tyr Tyr Arg Val Pro Leu Glu Ser Gln  
 305 310 315 320  
 25 Asp Asn Gln Val Lys Ser Asn Val Leu Tyr Asn Leu Asn Val Lys Ile  
 325 330 335  
 Glu Ile Leu Gly Ser Leu Gln Glu Pro Glu Ala Val Ser Val Asn Gly  
 340 345 350  
 Thr Leu Ala Ile Glu Glu Trp Ile Leu His Gln Asp Ala Phe Asn Leu  
 355 360 365  
 30 Pro Ala Thr Asn Tyr Leu Ile Val Glu Gln His Glu Ile Phe Met Asn  
 370 375 380  
 Asn Val Asn Thr Tyr Ser Val Lys Tyr Gln Thr Ser Gln Lys Pro Ile  
 385 390 395 400  
 35 Ser Ile Ser Ile Gln Ser Val Thr Phe Ser Tyr Val Ser Ser Asp Gly  
 405 410 415  
 Thr Gln His Asn Asp Leu Val Ala Ser Ser Ser Asp Gln Tyr Pro Thr  
 420 425 430  
 Ile Thr Ser Asp Asn Thr Ser Ile Ile Ile Thr Ser Lys Ile Pro Val  
 435 440 445  
 40 Asn Asn Val Pro Lys Lys Ile Val Phe Glu Val Thr Asn Gly Val Ala  
 450 455 460  
 Gly Leu Lys Glu Thr Val Thr Val Leu Gln Tyr Pro Ala Gln Phe Ile  
 465 470 475 480  
 Val Asn Thr Leu Gly Thr Ala Ser Ala Trp Arg Pro Asp Gly Ser Leu  
 485 490 495  
 45 Ala Pro Gly Leu Asn Asn Lys Ala Ile Tyr His Val Val Val Leu Val  
 500 505 510  
 Pro Pro Glu Asn Leu Phe Glu Asp Gly Thr Gln Thr Ile Ile Gly Tyr  
 515 520 525  
 50 Pro Pro Thr Glu Thr Ile Ser Phe His Lys Lys Glu Asn Asn Thr Tyr  
 530 535 540  
 Pro Ile Val Trp Ser Asp Thr Asn Thr Thr Lys Gln Asp Leu Glu Thr  
 545 550 555 560  
 Ser Arg Met Ile Ser Pro Ser Phe Glu Leu Ala Ser Gln Leu Gly Ala  
 565 570 575  
 55 Thr Leu Pro Met Pro Tyr Leu Glu Tyr Trp Pro Gly Thr Ser Tyr Leu  
 580 585 590  
 Leu Asp Tyr Ser Gly Asn Tyr Asn Asn Lys Arg Tyr Ala Leu Phe Asn  
 595 600 605  
 60 Cys Ala Phe Tyr Trp Glu Lys Arg Lys Val Asn Asn Glu Glu Ile Lys  
 610 615 620  
 Phe Asp Asp Trp Arg Leu Pro Thr Glu Ala Glu Ile Lys Leu Ile Asp  
 625 630 635 640  
 Lys Leu Gln His Asn Glu Gln Ser Ala Val Gln Ala Ile Met Thr Gly  
 645 650 655  
 65 Asn Tyr Tyr Trp Asp Ser Tyr Ser Ala Asn Gly Ser Tyr Lys Met Gln  
 660 665 670  
 Gly Gly Gly Gly Gln Gly Asn Ser Ser Lys Ala Tyr Val Arg Cys Val  
 675 680 685  
 70 Arg Asp Val Lys Lys Pro Ile Arg Asp Lys Lys Ser Gly Lys  
 690 695 700

(2) INFORMATION FOR SEQ ID NO:338

75

(1) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1312 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 10 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...1312  
 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:338

20 Lys Arg Val Asp Ser Tyr Glu Cys Arg Gln Lys Ala Cys Lys Cys Ala  
 1 5 10 15  
 Ile Cys Val Ile Gln Lys Phe Thr Asn Val Lys Leu Asn Asp Met Arg  
 20 25 30  
 Lys Ile Leu Ser Phe Leu Met Met Cys Ser Leu His Leu Gly Leu Gln  
 35 40 45  
 25 Ser Gln Thr Trp His Gly Asp Pro Asp Ser Val Ala Ala Leu Pro Ser  
 50 55 60  
 Ile Gly Ile Gln Glu Ser Ser Cys Thr Arg Ile Thr Phe Glu Val Val  
 65 70 75 80  
 Phe Pro Gly Phe Tyr Ser Val Glu Lys Arg Glu Gly Asn Gln Val Phe  
 85 90 95  
 30 Gln Arg Ile Ser Met Pro Gly Cys Gly Ser Phe Gly Asn Leu Gly Glu  
 100 105 110  
 Ala Glu Leu Pro Val Leu Lys Lys Met Ile Ala Val Pro Glu Phe Ser  
 115 120 125  
 35 Thr Ala Asn Val Ala Val Lys Ile Lys Glu Thr Glu Thr Phe Asp Asn  
 130 135 140  
 Tyr Asn Ile Tyr Pro Asn Pro Thr Tyr Val Val Glu Glu Leu Pro Glu  
 145 150 155 160  
 Gly Gly Thr Tyr Leu Val Glu Ala Phe Ala Ile Asn Asn Asp Tyr Tyr  
 165 170 175  
 40 Ser Gln Asn Val Ser Leu Pro Ser Thr His Tyr Val Tyr Ser Gln Asp  
 180 185 190  
 Gly Tyr Phe Arg Ser Gln Arg Phe Ile Glu Val Thr Leu Tyr Pro Phe  
 195 200 205  
 45 Arg Tyr Asn Pro Val Arg Gln Glu Ile Leu Phe Ala Lys Lys Ile Glu  
 210 215 220  
 Val Thr Ile Thr Phe Asp Asn Pro Gln Pro Pro Leu Gln Lys Asn Thr  
 225 230 235 240  
 Gly Ile Phe Asn Lys Val Ala Ser Ser Ala Phe Ile Asn Tyr Glu Ala  
 245 250 255  
 50 Asp Gly Lys Ser Ala Ile Glu Asn Asp Met Val Phe Ser Arg Gly Thr  
 260 265 270  
 Thr Thr Tyr Ile Ser Gly Asn Val Ala Ser Asn Leu Pro Gln Asn Cys  
 275 280 285  
 55 Asp Tyr Leu Val Ile Tyr Asp Asp Met Phe Asn Val Asn Gln Gln Pro  
 290 295 300  
 His Asp Glu Ile Lys Arg Leu Cys Glu His Arg Ala Phe Tyr Asn Gly  
 305 310 315 320  
 Phe Asp Val Ala Ala Val Ser Ile Lys Asp Val Leu Asn Ser Phe Pro  
 325 330 335  
 60 Ser Asn Ala Thr Ser Tyr Ile Asn Glu Thr Lys Leu Lys Asn Phe Ile  
 340 345 350  
 Arg Ser Val Tyr Asn Gln Ser Asn Ala Lys Arg Thr Leu Asp Gly Lys  
 355 360 365  
 65 Leu Gly Tyr Val Leu Leu Ile Gly Lys Pro Leu Ser Lys Tyr Leu Ala  
 370 375 380  
 Asp Thr Asp Asn Thr Lys Val Pro Thr Ser Phe Ile His Asn Val Ser  
 385 390 395 400  
 Leu Ile Pro Ser His Pro Thr Phe Gly Ser Ile Cys Ala Ser Asp Tyr  
 405 410 415  
 70 Phe Phe Ser Cys Val Ser Pro Leu Asp Thr Val Gly Asp Leu Phe Ile  
 420 425 430  
 Gly Arg Phe Ser Val Thr Asn Ala His Glu Leu His Asn Leu Ile Glu  
 435 440 445  
 75 Lys Thr Ile Asn Lys Glu Ile Ser Tyr Asn Pro Ile Ala His Lys Asn  
 450 455 460

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Ile Leu Tyr Ala Glu Gly Lys Gly Cys Asp Ala Pro Ile Leu Arg Leu  
 465 470 475 480  
 Phe Leu Lys Glu Ile Ala Ser Gly Tyr Thr Val Asn Ser Ile Leu Lys  
 485 490 495  
 5 Ser Asn Gln Val Ser Ala Ile Asp Ser Ile Phe Asp Cys Leu Asn Asn  
 500 505 510  
 Gly Ser His His Phe Tyr Phe Asn Thr His Gly Met Pro Thr Val Trp  
 515 520 525  
 10 Gly Ile Gly Gln Gly Leu Asp Val Asn Thr Leu Thr Ala Arg Leu Asn  
 530 535 540  
 Asn Thr Ser Ser Gln Gly Leu Cys Thr Ser Leu Ser Cys Ser Ser Ala  
 545 550 555 560  
 Val Ala Asp Ser Thr Ile Arg Ser Leu Gly Glu Val Leu Thr Thr Tyr  
 565 570 575  
 15 Ala Pro Asn Lys Gly Phe Ser Ala Phe Leu Gly Gly Ser Arg Ala Thr  
 580 585 590  
 Gln Tyr Ala Val Tyr Leu Glu Gly Pro Cys Pro Pro Ser Glu Phe Tyr  
 595 600 605  
 20 Glu Tyr Leu Pro Tyr Ser Leu Tyr His Asn Leu Ser Thr Val Val Gly  
 610 615 620  
 Glu Met Leu Leu Ser Ser Ile Ile Asn Thr Asn Ser Val Asp Thr Tyr  
 625 630 635 640  
 Ser Lys Phe Asn Phe Asn Leu Leu Gly Asp Pro Ala Leu Asn Ile Met  
 645 650 655  
 25 Ala His Gly Met Glu Val Ser Asn Cys Ile Thr Leu Pro Asn Asn Thr  
 660 665 670  
 Ile Ile Ser Ser Pro Ile Thr Ile Lys Asn Gly Gly Cys Leu Lys Ile  
 675 680 685  
 30 Pro Glu Lys Gly Val Leu His Phe Thr Asn Asn Gly Ser Ile Gln Val  
 690 695 700  
 Met Ser Gly Gly Thr Leu Glu Ile Gly Asn Gln Ala Lys Ile Ser Gly  
 705 710 715 720  
 Glu Thr Gly Ala Asn Pro Thr Phe Ile Thr Val Tyr Gly Asp Gly Leu  
 725 730 735  
 35 Ala Ile Asn Lys Gln Val Glu Ile Asp Asn Ile Asp Arg Leu Asn Leu  
 740 745 750  
 Phe Ser Thr His Ser Val Met Pro Lys Phe His Phe Asp Ser Val Lys  
 755 760 765  
 40 Phe Asn Ser Ala Pro Leu Tyr Thr Thr Asn Cys Ile Val Glu Ile Ser  
 770 775 780  
 Asn Cys Glu Phe Thr Asn Arg Ser Asp Ile Ile Ser Lys Asn Cys Asp  
 785 790 795 800  
 Leu Ser Val Glu Asn Ser Met Phe Ser Ser Gly Ile Thr Val Phe  
 805 810 815  
 45 Lys Pro Met Ala Thr Ser Ser Ile Thr Gly Leu Ser Thr Lys Ala Lys  
 820 825 830  
 Ile Thr Asp Asn Thr Phe Phe Ala Thr Gly Asn Phe Ala Tyr His Ile  
 835 840 845  
 50 Thr Asn Thr Pro Gly Leu Thr Ala Thr Ser Asn Ala Ala Ile Lys Leu  
 850 855 860  
 Asp Asn Ile Pro Glu Tyr Tyr Ile Ser Gly Asn Lys Ile Val Asn Cys  
 865 870 875 880  
 Asp Glu Ala Leu Val Leu Asn Asn Ser Gly Asn Arg Thr Asn Arg Leu  
 885 890 895  
 55 His Asn Ile Thr Arg Asn Val Ile Lys Asn Cys Arg Ile Gly Ser Thr  
 900 905 910  
 Leu Tyr Asn Ser Tyr Gly Ile Tyr Asn Arg Asn Lys Ile Ser Asn Asn  
 915 920 925  
 60 His Ile Gly Val Arg Leu Leu Asn Asn Ser Cys Phe Tyr Phe Asp Asn  
 930 935 940  
 Ala Pro Val Ile Asn Glu Glu Asp Lys Gln Thr Phe Ile Ser Asn Arg  
 945 950 955 960  
 Thr Trp Gln Leu Tyr Ser Ser Asn Gly Thr Phe Pro Leu Asn Phe His  
 965 970 975  
 65 Tyr Asn Ser Leu Gln Gly Gly Asp Thr Asp Thr Trp Ile Tyr Asn Asp  
 980 985 990  
 Thr Tyr Thr Asn Arg Tyr Ile Asp Val Ser Asn Asn His Trp Gly Asn  
 995 1000 1005  
 70 Asn Asp Leu Phe Asp Pro Asn Gln Val Phe Asn Thr Pro Asp Leu Phe  
 1010 1015 1020  
 Ile Trp Ile Pro Phe Trp Asp Gly Leu Pro Asn Gly Arg Ser Gly Asn  
 1025 1030 1035 1040  
 Ser Ser Ala Glu Ala Val Glu Phe Gln Thr Ala Leu Asp Cys Ile Gly  
 1045 1050 1055  
 75 Asn Ser Asp Tyr Leu Ser Ala Lys Val Ala Leu Lys Met Met Val Glu

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1060 1065 1070  
 Thr Tyr Pro Glu Ser Asp Phe Ala Ile Ala Leu Lys Glu Leu Phe  
 1075 1080 1085  
 Arg Ile Glu Lys Met Ser Gly Asn Asp Tyr Glu Gly Leu Lys Asp Tyr  
 1090 1095 1100  
 Phe Arg Ser Asn Pro Thr Ile Ile Ser Ser Gln Asn Leu Phe Pro Thr  
 1105 1110 1115 1120  
 Ala Asp Phe Leu Ser Ala Arg Cys Asp Ile Val Cys Glu Asn Tyr Gln  
 1125 1130 1135  
 10 Ser Ala Ile Asp Trp Tyr Glu Asn Arg Leu Asn Ser Glu Ile Ser Tyr  
 1140 1145 1150  
 Gln Asp Ser Val Phe Ala Val Ile Asp Leu Gly Asp Ile Tyr Trp Asn  
 1155 1160 1165  
 15 Met Gln Leu Asp Ser Leu Arg Gly Thr Gly Ile Asp Leu Asn Ile Leu  
 1170 1175 1180  
 Ser Cys Glu Gln Arg Lys Ser Leu Glu Ser His Gln Asn Val Lys Asn  
 1185 1190 1195 1200  
 Tyr Leu Leu Ser Thr Leu Pro Glu Ser Thr Gly Thr Leu Leu Pro Pro  
 1205 1210 1215  
 20 Leu Glu Cys Asn Lys Ser Ser Leu Asp Lys Ser Lys Ile Ile Ser Ile  
 1220 1225 1230  
 Ser Pro Asn Pro Ala Lys Ala Val Val Thr Ile Ile Tyr Tyr Thr Asp  
 1235 1240 1245  
 Asn Pro Ser Cys Ser Val Ile Lys Ile Tyr Gly Ile Asn Gly Ala Ser  
 1250 1255 1260  
 25 Ala Asp Ile Thr Gly Leu Pro Lys His Leu Ser Glu Gly Tyr Tyr Ser  
 1265 1270 1275 1280  
 Ile Gln Phe Asn Thr Ser Asn Phe Asp Pro Gly Phe Tyr Leu Val Thr  
 1285 1290 1295  
 30 Leu Asn Val Asp Gln Lys Ile Ile Asp Thr Glu Lys Leu Arg Ile Lys  
 1300 1305 1310

(2) INFORMATION FOR SEQ ID NO:339

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 938 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 40 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 45 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...938  
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:339

Ser Glu Asn Tyr Arg Tyr Gly Lys Ile Thr Asn Gln Ile Met Ala Ile  
 1 5 10 15  
 55 Met Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile Leu Leu Ser  
 20 25 30  
 Trp Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser Gly Met Asn  
 35 40 45  
 60 Ala Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile Leu Tyr Glu  
 50 55 60  
 Ser Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu Ile Asp Ala  
 65 70 75 80  
 Asp Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser Phe Ser Val  
 85 90 95  
 65 Pro Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile Arg Ser Gly  
 100 105 110  
 Ile Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile Glu Gly Ala  
 115 120 125  
 70 Lys Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr Asn Pro Glu  
 130 135 140  
 His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile Glu Asp Phe  
 145 150 155 160  
 Val Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr Pro Leu Val  
 165 170 175  
 75 Trp Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys Tyr Ile Ala



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180 185 190  
 Trp Arg His Tyr Lys Val Thr Asp Ser His Thr Glu Phe Leu Lys Leu  
 195 200 205  
 5 Asp Asp Val Thr Val Tyr Arg Ser Ile Glu Gly Pro Glu Pro Ala Thr  
 210 215 220  
 Asp Phe Thr Val Ile Asn Ile Gly Gln Asn Val Gly Arg Leu Thr Trp  
 225 230 235 240  
 Asn Tyr Pro Glu Asp Tyr Gln Pro Glu Gly Lys Gly Asn Glu Glu Leu  
 245 250 255  
 10 Gln Leu Ser Gly Tyr Asn Ile Tyr Ala Asn Gly Thr Leu Leu Ala Gln  
 260 265 270  
 Ile Lys Asp Val Ser Ile Leu Glu Tyr Val Asp Ser Thr Tyr Ser Leu  
 275 280 285  
 15 Arg Asp Asn Pro Leu Gln Val Glu Tyr Cys Val Thr Ala Val Tyr Asp  
 290 295 300  
 Glu Ser Ile Glu Ser Ser Thr Val Cys Gly Thr Leu His Tyr Ala Thr  
 305 310 315 320  
 Asp Ala Ile Leu Tyr Glu Asn Phe Glu Asn Gly Pro Val Pro Asn Gly  
 325 330 335  
 20 Trp Leu Val Ile Asp Ala Asp Gly Asp Gly Phe Ser Trp Gly His Tyr  
 340 345 350  
 Leu Asn Ala Tyr Asp Ala Phe Pro Gly His Asn Gly Gly His Cys Ser  
 355 360 365  
 25 Leu Ser Ala Ser Tyr Val Pro Gly Ile Gly Pro Val Thr Pro Asp Asn  
 370 375 380  
 Tyr Leu Ile Thr Pro Lys Val Glu Gly Ala Lys Arg Val Lys Tyr Trp  
 385 390 395 400  
 Val Ser Thr Gln Asp Ala Asn Trp Ala Ala Glu His Tyr Ala Val Met  
 405 410 415  
 30 Ala Ser Thr Thr Gly Thr Ala Val Gly Asp Phe Val Ile Leu Phe Glu  
 420 425 430  
 Glu Thr Met Thr Ala Lys Pro Thr Gly Ala Trp Tyr Glu Arg Thr Ile  
 435 440 445  
 35 Asn Leu Pro Glu Gly Thr Lys Tyr Ile Ala Trp Arg His Tyr Asn Cys  
 450 455 460  
 Thr Asp Ile Tyr Phe Leu Lys Leu Asp Asp Ile Thr Val Phe Gly Thr  
 465 470 475 480  
 Pro Ala Ser Glu Pro Glu Pro Val Thr Asp Phe Val Val Ser Leu Ile  
 485 490 495  
 40 Glu Asn Asn Lys Gly Arg Leu Lys Trp Asn Tyr Pro Asn Gly Tyr Glu  
 500 505 510  
 Pro Asp Lys Thr Asp Asp Lys Asp Pro Leu Gln Leu Ala Gly Tyr Asn  
 515 520 525  
 45 Ile Tyr Ala Asn Gly Ser Leu Leu Val His Ile Gln Asp Pro Thr Val  
 530 535 540  
 Leu Glu Tyr Ile Asp Glu Thr Tyr Ser Ser Arg Asp Asp Gln Val Glu  
 545 550 555 560  
 Val Glu Tyr Cys Val Thr Ala Val Tyr Asn Asp Asn Ile Glu Ser Gln  
 565 570 575  
 50 Ser Val Cys Asp Lys Leu Ile Tyr Asp Ser Gln Ser Asp Ile Ile Leu  
 580 585 590  
 Tyr Glu Gly Phe Glu Ala Gly Ser Ile Pro Glu Gly Trp Leu Leu Ile  
 595 600 605  
 55 Asp Ala Asp Gly Asp Asn Val Asn Trp Asp Tyr Tyr Pro Trp Thr Met  
 610 615 620  
 Tyr Gly His Asp Ser Glu Lys Cys Ile Ala Ser Pro Ser Tyr Leu Pro  
 625 630 635 640  
 Met Ile Gly Val Leu Thr Pro Asp Asn Tyr Leu Val Thr Pro Arg Leu  
 645 650 655  
 60 Glu Gly Ala Lys Leu Val Lys Tyr Trp Val Ser Ala Gln Asp Ala Val  
 660 665 670  
 Tyr Ser Ala Glu His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala  
 675 680 685  
 65 Val Glu Asp Phe Val Leu Leu Phe Glu Glu Thr Met Thr Ala Lys Ala  
 690 695 700  
 Asn Gly Ala Trp Tyr Glu Arg Thr Ile Thr Leu Pro Ala Gly Thr Lys  
 705 710 715 720  
 Tyr Ile Ala Trp Arg His Tyr Asp Cys Thr Asp Met Phe Phe Leu Leu  
 725 730 735  
 70 Leu Asp Asp Ile Thr Val Tyr Arg Ser Thr Glu Thr Val Pro Glu Pro  
 740 745 750  
 Val Thr Asp Phe Val Val Ser Leu Ile Glu Asn Asn Lys Gly Arg Leu  
 755 760 765  
 75 Lys Trp Asn Tyr Pro Asn Gly Tyr Glu Pro Asp Lys Thr Asp Asp Lys  
 770 775 780

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Lys Pro Leu Gln Leu Thr Gly Tyr Asn Ile Tyr Ala Asn Gly Ser Leu  
 785 790 795 800  
 Leu Val His Ile Gln Asp Pro Thr Val Leu Glu Tyr Ile Asp Glu Thr  
 805 810 815  
 5 Tyr Ser Ser Arg Asp Gly Gln Val Glu Met Glu Tyr Cys Val Thr Ala  
 820 825 830  
 Val Tyr Asn Asp Asn Ile Glu Ser Gln Ser Val Cys Asp Lys Leu Asn  
 835 840 845  
 10 Tyr Thr Ile Thr Ser Leu Asp Asn Ile Gln Ser Asp Thr Ser Leu Lys  
 850 855 860  
 Ile Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu Gly Leu Ser  
 865 870 875 880  
 Arg Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly Ile Cys Ile  
 885 890 895  
 15 Leu Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp Val Ser Arg  
 900 905 910  
 Leu Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly Asn Lys Thr  
 915 920 925  
 20 Thr Thr Glu Lys Val Glu Ile Lys Arg Pro  
 930 935

## (2) INFORMATION FOR SEQ ID NO:340

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 606 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 30 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 35 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...606  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:340

Ile Ile Phe Cys Thr Ile His His Ser Glu Leu Glu Ile Met Asn Ser  
 1 5 10 15  
 45 Ile Met Lys Tyr Gln Leu Tyr Thr Ala Val Ile Met Ala Leu Ser Val  
 20 25 30  
 Ser Ser Val Cys Gly Gln Thr Pro Arg Asn Thr Glu Thr Lys Arg Pro  
 35 40 45  
 Asp Thr Leu Arg Arg Glu Leu Thr Ile Val Asn Asp Gln Thr Val Glu  
 50 55 60  
 Met Glu His Ala Asp Pro Leu Pro Ala Ala Tyr Lys Ala Ile Glu Pro  
 65 70 75 80  
 Arg Leu Lys Pro Phe Arg Pro Glu Tyr Asn Lys Arg Thr Phe Gly Phe  
 85 90 95  
 55 Val Pro Glu Val Ser Ser Ser Gly Arg Asn Asn Leu Pro Asn Ile Leu  
 100 105 110  
 Pro Thr Glu Gly His Met Lys His Arg Gly Tyr Leu Asn Ile Gly Ile  
 115 120 125  
 Gly His Thr Leu Asn Gln Arg Met Asp Ala Gly Tyr Arg Leu Ile Asp  
 130 135 140  
 60 Ala Glu Gln Glu Arg Leu Asn Leu Phe Leu Ser Tyr Arg Gly Met Lys  
 145 150 155 160  
 Ser Ala Phe Asn Thr Gly Asp Phe Asp Gly Asp Arg Lys Asp Arg Arg  
 165 170 175  
 65 Met Met Ala Gly Val Asp Tyr Glu Gln Arg Arg Pro Ser Phe Val Leu  
 180 185 190  
 Ala Thr Gly Leu Tyr Tyr Ser Asn His Tyr Phe Asn Asn Tyr Gly Arg  
 195 200 205  
 Gly Ala Thr Thr Asn Val Gly Ser Ile Pro Gln Leu Ser Thr Pro Val  
 210 215 220  
 70 Thr Pro Gln Met Asp Asn Gly Thr His Asn Val Arg Val Tyr Leu Gly  
 225 230 235 240  
 Ala Lys Asn Asp Val Ile Asp Ala Arg Ile Asp Tyr Arg Phe Phe Arg  
 245 250 255  
 75 Ser Ile Pro Tyr Leu Gly Thr Asp Pro Met Lys Ala Leu Thr Glu His  
 260 265 270

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Thr Pro Glu Leu Asn Val Thr Met Ser Asn Glu Leu Ser Asp Asp Ile  
 275 280 285  
 Lys Leu Gly Val Glu Val Arg Thr Gly Gly Leu Phe Phe Ala Lys Asn  
 290 295 300  
 5 Ser Glu Met Ile Gln Thr Gly Val Leu Ser Glu Thr Asp Arg Asn Leu  
 305 310 315 320  
 Tyr Tyr Val Glu Gly Ala Pro Thr Ile Gly Phe Val Gly Asp Ser Asp  
 325 330 335  
 10 Asn Met Gln Trp Asn Ile Gln Ala Gly Val Gly Ile Ser Ser His Phe  
 340 345 350  
 Gly Ala Lys Gly Arg Leu Phe Phe Thr Pro Lys Leu Asp Ala Ser Leu  
 355 360 365  
 Ser Ile Phe Pro Ser Trp Arg Val Tyr Ala Lys Ala Phe Gly Gly Val  
 370 375 380  
 15 Ile Arg Asn Gly Leu Ala Asp Val Met Gln Glu Glu Met Pro Tyr Leu  
 385 390 395 400  
 Met Pro Asn Thr Ile Val Leu Pro Ser Arg Asn Ala Leu Thr Ala Gln  
 405 410 415  
 20 Leu Gly Val Lys Gly Asn Ile Ala Asp Val Val Arg Met Glu Val Tyr  
 420 425 430  
 Gly Asp Phe Ser Lys Leu Thr Gly Val Pro Phe Tyr Thr Pro Thr Leu  
 435 440 445  
 Pro Leu Tyr Asn Pro Ser Asp Leu Tyr Gln Tyr Asn Val Ser Phe Leu  
 450 455 460  
 25 Pro Ile Tyr Ala Asp Gly Ser Arg Trp Arg Ala Gly Gly Lys Leu Glu  
 465 470 475 480  
 Tyr Ser Tyr Arg Asp Met Leu Arg Phe Leu Val Asp Ala Ser Tyr Gly  
 485 490 495  
 30 Lys Trp Asn Leu Asp Gly Gly Leu Val Ala Ser Met Gln Pro Asp Leu  
 500 505 510  
 Ile Leu Lys Ala Glu Val Gly Val His Pro Ile Ala Pro Leu Asp Val  
 515 520 525  
 Arg Leu Arg Tyr Thr Gln Leu Asn Gly Arg Tyr Arg Tyr Ser Phe Gly  
 530 535 540  
 35 Ser Ala Gly Ser Glu Ala Leu Gly Ile Gly Asn Val His Leu Leu Ser  
 545 550 555 560  
 Ala Asp Val Ser Tyr Lys Leu Lys Lys Asn Leu Ser Leu Tyr Leu Lys  
 565 570 575  
 40 Ile Asp Asn Met Leu Ala Glu Thr Thr Glu Leu Ile Gly Tyr Tyr Pro  
 580 585 590  
 Met Gln Pro Phe His Cys Phe Ala Gly Phe Ser Trp Thr Phe  
 595 600 605  
 (2) INFORMATION FOR SEQ ID NO:341  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 357 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...357  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:341  
 Asn Ser His Ala Thr Val Ser Val Ile Cys Ser Met Met Glu Lys Cys  
 1 5 10 15  
 Ile Phe Ala His Tyr Pro His Asn Leu Val Phe Met Ile Arg Lys His  
 20 25 30  
 Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val Phe Ser Ala Gly Ala  
 35 40 45  
 70 Gln Gln Glu Lys Gln Val Phe His Phe Leu Asn Leu Pro Ala Thr Ala  
 50 55 60  
 Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr Ile Val Asp Asp Asn  
 65 70 75 80  
 75 Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu Gly Tyr Glu Ser Gly  
 85 90 95

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Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met Ser Gly Ser His Met  
 100 105 110  
 Gly Asn Ala Cys Tyr Ala Ser Ser Val Gly Glu Arg Gly Met Trp Gly  
 115 120 125  
 5 Val Gly Met Arg Phe Leu Asn Tyr Gly Ser Met Gln Gly Tyr Asp Gln  
 130 135 140  
 Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser Asp Ile Ala Val Gln  
 145 150 155  
 Gly Phe Tyr Ser His Glu Leu Ser Asn His Phe Arg Gly Gly Val Ser  
 160 165 170 175  
 10 Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr Ser Ser Phe Gly Leu  
 180 185 190  
 Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp Asp Lys Gly Tyr Ser  
 195 200 205  
 15 Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln Leu Lys Gly Tyr Asn  
 210 215 220  
 Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln Leu Gly Phe Ser Arg  
 225 230 235 240  
 Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile Thr Leu Phe Asn Leu  
 245 250 255  
 20 Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg Asp Leu Ser Lys Met  
 260 265 270  
 Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala Glu Phe Thr Pro Ser  
 275 280 285  
 25 Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro Gln Ile Ala Gln Asp  
 290 295 300  
 Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly Leu Ser Ala Gly Val  
 305 310 315 320  
 Gly Phe Thr Ser Gly Val Val Arg Val Gly Val Ser Ala Ala Thr Tyr  
 325 330 335  
 30 His Pro Ala Ala Leu Ser Phe Met Cys Ser Val Gly Ile Arg Leu Asp  
 340 345 350  
 Asp Lys Ser Ile Phe  
 355  
 35

(2) INFORMATION FOR SEQ ID NO:342

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 337 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature  
 (B) LOCATION 1...337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342

Pro Gln Pro Val Gly Leu Lys Glu Ile Thr Ile Lys Pro Met Cys Leu  
 1 5 10 15  
 Glu Pro Ile Ile Ala Pro Ile Ser Ser Glu Leu Leu Glu Gln Glu Leu  
 20 25 30  
 60 Thr Ala Asp Arg Phe Leu Arg Met Thr Asn Lys Ala Gly Asn Glu Ile  
 35 40 45  
 Tyr Val Phe Thr Ala Glu Glu Ala Pro His Cys Met Lys Glu Val Gly  
 50 55 60  
 65 Arg Leu Arg Glu Glu Ala Phe Arg His Tyr Gly Gly Thr Gly Lys  
 65 70 75 80  
 Ala Ile Asp Ile Asp Glu Phe Asp Thr Met Pro Gly Ser Tyr Lys Gln  
 85 90 95  
 Leu Ile Val Trp Asp Pro Gln Asn Lys Ala Ile Leu Gly Gly Tyr Arg  
 100 105 110  
 70 Phe Ile Tyr Gly Arg Asp Val Ala Phe Asp Thr Asp Gly Lys Pro Leu  
 115 120 125  
 Leu Ala Thr Ala Glu Met Phe Arg Phe Ser Asp Ala Phe Leu His Asp  
 130 135 140  
 75 Tyr Leu Pro Tyr Thr Val Glu Leu Gly Arg Ser Phe Val Ser Leu Gln  
 145 150 155 160

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Tyr Gln Ser Thr Arg Met Gly Thr Lys Ala Ile Phe Val Leu Asp Asn  
 165 170 175  
 Leu Trp Asp Gly Ile Gly Ala Leu Thr Val Val Asn Pro Glu Ala Leu  
 180 185 190  
 5 Tyr Phe Tyr Gly Lys Val Thr Met Tyr Lys Asp Tyr Asp Arg Arg Ala  
 195 200 205  
 Arg Asn Leu Ile Leu Tyr Phe Leu Arg Lys His Phe Ser Asp Pro Glu  
 210 215 220  
 10 Gly Leu Val Lys Pro Ile His Pro Leu Pro Ile Glu Ile Ser Ala Glu  
 225 230 235 240  
 Asp Glu Ala Leu Phe Ser Ser Ser Asp Phe Asp Thr Asn Tyr Lys Thr  
 245 250 255  
 Leu Asn Ile Glu Val Arg Lys Leu Gly Ile Asn Ile Pro Pro Leu Val  
 260 265 270  
 15 Ser Ala Tyr Ile Ala Leu Ser Pro Glu Met Arg Val Phe Gly Thr Ala  
 275 280 285  
 Val Asn Glu Ser Phe Gly Glu Val Glu Thr Gly Ile Phe Ile Ala  
 290 295 300  
 20 Val Gly Lys Ile Leu Glu Lys Lys Gln Arg His Ile Glu Ser Phe  
 305 310 315 320  
 Ile Leu Ser Arg Asn Glu Lys Lys Gly Leu Asp Ser Ser Asn Gly Arg  
 325 330 335  
 Ser

25 (2) INFORMATION FOR SEQ ID NO:343  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 566 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30  
 (ii) MOLECULE TYPE: protein  
 35 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 40 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...566  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:343  
 Tyr Asp Gly Ala Arg Leu Val Tyr Thr Leu Phe Arg Asn Arg Asn Asp  
 1 5 10 15  
 Ile His Pro Met Lys Thr Ile Val Arg Tyr Ser Arg Leu Pro Val Ala  
 20 25 30  
 50 Leu Phe Phe Cys Leu Leu Gly Ala Val His Leu Ser Val Glu Ala Gln  
 35 40 45  
 Met Leu Asn Thr Pro Phe Glu Leu Ser Asp Gln Ile Val Leu Ser Pro  
 50 55 60  
 55 Thr Glu Arg Gln Tyr Arg Glu Ile Cys Val Gln Thr Lys Glu Lys Arg  
 65 70 75 80  
 Gly Ala Asp Leu Phe Pro Leu Ser Asp Lys Leu Arg Asp Ser Ala Tyr  
 85 90 95  
 Val Arg Phe Gly Ser Ala Tyr Gly Asp Ile Ala Gly Asp Tyr Leu Pro  
 100 105 110  
 60 Tyr Asn Gly Asn Asn Tyr Ser Ser Leu Ser Leu Glu Ser Gly Gly Arg  
 115 120 125  
 Ile Ser Val Arg Asn Tyr Gly Thr Leu Gln Gly Ser Ala Ser Tyr Ser  
 130 135 140  
 65 Arg Gly Met His Lys Arg Ile Gly Trp Asn Ala Leu Arg Asn Ala Glu  
 145 150 155 160  
 Ala Tyr Tyr Pro Tyr Leu Val Ser Asp Ser Thr Gly Gly Asp Tyr His  
 165 170 175  
 Phe Glu Asp Tyr Arg Leu Ala Gly Tyr Tyr Ser Phe Arg Ala Gly Arg  
 180 185 190  
 70 Leu Pro Leu Gly Ile Gly Phe Ser Tyr Arg Gly Glu Val Ala Tyr Arg  
 195 200 205  
 Leu Thr Asp Pro Arg Thr Thr Asn Thr Thr Gly Ala Leu Glu Leu Ser  
 210 215 220  
 75 Cys Ala Thr Ser Leu Thr Leu Pro Arg Glu Asn Arg Leu Ser Leu Ser  
 225 230 235 240

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Ala Ala Tyr Leu Tyr His Arg Gln His Leu Thr Gln Tyr Asn Trp Arg  
 245 250 255  
 Pro Gly Gln Gln Asp Lys Phe Phe Val Ser Tyr Gly Phe Gly Gln Val  
 260 265 270  
 5 Asp Val Ser Asn Ser Pro Ile Trp Phe Gly Ile Ser Arg Met Asn Tyr  
 275 280 285  
 Val Asn Gly Trp Lys Leu Ser Ser Arg Leu Asp Thr Arg Arg Gly Asp  
 290 295 300  
 10 Ala Ile Gly Leu Asp Tyr Ser Gly Tyr Phe Leu Asp Thr Glu Glu Arg  
 305 310 315 320  
 Ser Ser Ile Asn Leu Phe Ala Leu Leu Tyr Asn Arg Leu Arg Leu Tyr  
 325 330 335  
 Gly Ser Trp His Leu Ser Asp Phe Asp Phe Ser Phe Ser Ala Asp Tyr  
 340 345 350  
 15 Ala Leu Arg Gln Gly Ile Glu Arg Ile Tyr Glu Asp Tyr Lys Pro Asp  
 355 360 365  
 Asp Asn Tyr His Ile Tyr Asp Leu Arg Ile Leu Ala Ile Arg Arg Trp  
 370 375 380  
 20 Tyr Met Leu Asn Glu Phe Ser Ala Gln Ala Gln Ala Ser Tyr Arg Ile  
 385 390 395 400  
 Arg Thr Asp Arg Gly Cys Ala Leu Arg Val Ser Ala Gly Ser Asp Phe  
 405 410 415  
 Tyr Gly Tyr Asp Glu Thr Tyr Arg Lys His Gly His His Thr Met Ser  
 420 425 430  
 25 Gly Met Leu Arg Pro Phe Ala Gly Ile Ala Tyr Asp His Ala Gly Ser  
 435 440 445  
 Lys Leu Asp Phe Gly Leu Ser Leu Ser Ala Ala Tyr Arg Met Val Leu  
 450 455 460  
 30 Thr His Ser Tyr Lys Ile Arg Thr Ile Gln Lys Glu Gln Leu Asp Tyr  
 465 470 475 480  
 Gln Leu Ala Tyr Leu Pro Tyr Ala Tyr Arg Asn Arg Glu Gly Val Glu  
 485 490 495  
 Val Arg Ser Ser Leu Tyr Val Ser Ile Pro Met Gln Asn Thr His Arg  
 500 505 510  
 35 Leu Met Thr Glu Leu Arg Leu Tyr Gly Asp Leu Met Lys Arg Lys Asp  
 515 520 525  
 Gly Ile Ala Tyr Gly Lys Thr Pro Gly Val Ile Ser His Ile Leu Ser  
 530 535 540  
 40 Asp Pro Gln Ala Glu Arg Thr Ser Gly His Thr Ile Gly Ala Ile Cys  
 545 550 555 560  
 Asn Ile Ser Tyr Leu Phe  
 565

(2) INFORMATION FOR SEQ ID NO:344

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 819 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344

Arg Thr Asn Val Phe Leu Ser Leu Ser His Lys Ile Gly Arg Arg Gly  
 1 5 10 15  
 Ala Ser Cys Ser Asn Arg Asn Ala Trp Met Ala Glu Asn Lys Pro Ser  
 20 25 30  
 Ser Pro Glu Pro Asp Asn Thr Gly Val Gly Asn Ser Pro Ser Asp Tyr  
 35 40 45  
 70 Leu His Gly Glu Ala Ile Ile Pro Pro Leu Ser Ser Leu Ser Asn Phe  
 50 55 60  
 Asn Asp Lys Arg Phe Met Lys Lys Leu His Met Ile Ala Ala Leu Ala  
 65 70 75 80  
 75 Val Leu Pro Phe Cys Leu Thr Ala Gln Ala Pro Val Ser Asn Ser Glu  
 85 90 95

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Ile Asp Ser Leu Ser Asn Val Gln Leu Gln Thr Val Gln Val Val Ala  
 100 105 110  
 Thr Arg Ala Thr Ala Lys Thr Pro Val Ala Tyr Thr Asn Val Arg Lys  
 115 120 125  
 5 Ala Glu Leu Ser Lys Ser Asn Tyr Gly Arg Asp Ile Pro Tyr Leu Leu  
 130 135 140  
 Met Leu Thr Pro Ser Val Val Ala Thr Ser Asp Ala Gly Thr Gly Ile  
 145 150 155 160  
 10 Gly Tyr Ser Gly Phe Arg Val Arg Gly Thr Asp Ala Asn Arg Ile Asn  
 165 170 175  
 Ile Thr Thr Asn Gly Val Pro Leu Asn Asp Ser Glu Ser Gln Ser Val  
 180 185 190  
 Phe Trp Val Asn Met Pro Asp Phe Ala Ser Ser Ile Glu Asp Leu Gln  
 195 200 205  
 15 Val Gln Arg Gly Val Gly Thr Ser Thr Asn Gly Ala Gly Ala Phe Gly  
 210 215 220  
 Ala Ser Val Asn Met Arg Thr Asp Asn Leu Gly Leu Ala Pro Tyr Gly  
 225 230 235 240  
 20 Arg Val Asp Leu Ser Gly Gly Ser Phe Gly Thr Phe Arg Arg Ser Val  
 245 250 255  
 Lys Leu Gly Ser Gly Arg Ile Gly Arg His Trp Ala Val Asp Ala Arg  
 260 265 270  
 Leu Ser Lys Ile Gly Ser Asp Gly Tyr Val Asp Arg Gly Ser Val Asp  
 275 280 285  
 25 Leu Lys Ser Tyr Phe Ala Gln Val Gly Tyr Phe Gly Ser Asn Thr Ala  
 290 295 300  
 Leu Arg Phe Ile Thr Phe Gly Gly Lys Glu Val Thr Gly Ile Ala Trp  
 305 310 315 320  
 30 Asn Gly Leu Ser Lys Glu Asp Glu Ala Lys Tyr Gly Arg Arg Tyr Asn  
 325 330 335  
 Ser Ala Gly Leu Met Tyr Val Asp Ala Gln Gly Val Pro His Tyr Tyr  
 340 345 350  
 His Asn Thr Asp Asn Tyr Glu Gln Arg His Tyr His Ala Ile Met Thr  
 355 360 365  
 35 His Ser Phe Ser Pro Ser Val Ile Leu Asn Leu Thr Ala His Tyr Thr  
 370 375 380  
 Ala Gly Tyr Gly Tyr Thr Asp Glu Tyr Arg Thr Gly Arg Lys Leu Lys  
 385 390 395 400  
 40 Glu Tyr Ala Leu Gln Pro Tyr Val Glu Asn Ser Val Thr Val Lys Lys  
 405 410 415  
 Thr Asp Leu Ile Arg Gln Lys Tyr Leu Asp Asn Asp Phe Gly Gly Leu  
 420 425 430  
 Ile Gly Ser Leu Asn Trp His Thr Gly Ala Trp Asp Leu Gln Phe Gly  
 435 440 445  
 45 Ala Ser Gly Asn Ile Tyr Lys Gly Asp His Phe Gly Arg Ile Thr Tyr  
 450 455 460  
 Ile Lys Lys Tyr Asn Gln Pro Leu Ala Pro Asp Phe Glu Tyr Tyr Arg  
 465 470 475 480  
 50 Asn Arg Ala Asp Lys Arg Glu Gly Ala Ala Phe Ala Lys Ala Asn Trp  
 485 490 495  
 Gln Ile Thr Pro Glu Leu Asn Met Tyr Ala Asp Leu Gln Tyr Arg Thr  
 500 505 510  
 Ile Gly Tyr Thr Ile Asn Gly Ile Thr Asp Glu Tyr Asp Glu Val Gln  
 515 520 525  
 55 Gly Ser Met Gln His Ile Asp Leu Asp Lys Thr Phe Arg Phe Leu Asn  
 530 535 540  
 Pro Lys Ala Gly Leu Thr Tyr Ser Phe Asp Asp Ala His Thr Ala Tyr  
 545 550 555 560  
 60 Ala Ser Val Ala Val Ala His Arg Glu Pro Asn Arg Thr Asn Tyr Thr  
 565 570 575  
 Glu Ala Gly Ile Gly Gln Tyr Pro Thr Pro Glu Arg Leu Ile Asp Tyr  
 580 585 590  
 Glu Leu Gly Tyr Arg Tyr Ala Ser Pro Leu Leu Ser Ala Gly Val Gly  
 595 600 605  
 65 Leu Tyr Tyr Met Gln Tyr Lys Asp Gln Leu Val Leu Asp Gly Arg Leu  
 610 615 620  
 Ser Asp Val Gly Gln Met Leu Thr Ser Asn Val Pro Asp Ser Tyr Arg  
 625 630 635 640  
 70 Met Gly Leu Glu Leu Thr Leu Gly Trp Gln Ile Leu Pro Arg Leu Leu  
 645 650 655  
 Arg Trp Asp Ala Ser Phe Thr Met Ser Arg Asn Lys Ile Asp Arg Tyr  
 660 665 670  
 Val Gln Tyr Thr Ser Val Tyr Asp Ala Asp Tyr Asn Trp Leu Glu Leu  
 675 680 685  
 75 Lys Glu Glu Thr Leu Glu Ser Thr Asp Ile Ala Tyr Ser Pro Asn Val

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        690              695              700
Ile Ala Gly Ser Met Leu Thr Leu Ser His Ala Gly Phe Glu Met Ala
705              710              715              720
Trp Thr Ser Arg Phe Val Ser Lys Gln Tyr Leu Asp Asn Thr Gln Arg
5   Ser Asp Arg Met Leu Ser Ser Tyr Trp Val Asn Asp Leu Arg Leu Gly
        725              730              735
Tyr Val Leu Pro Val His Phe Val Lys Arg Val Ala Leu Gly Val Gln
        740              745              750
10  Leu Asn Asn Leu Phe Asn Leu Met Tyr Ala Ser Asn Ala Tyr Ile Tyr
        755              760              765
Asp Ala Gly Tyr Val Gln Ala Ser Gly Glu Leu Ser Ala Tyr Ala Asp
785              790              795              800
Leu Arg Tyr Tyr Pro Gln Ala Gly Phe Asn Ala Leu Gly Ser Leu Thr
15  Ile Asp Phe
        805              810              815

```

- (2) INFORMATION FOR SEQ ID NO:345
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 532 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Porphyromonas gingivalis*
- (ix) FEATURE:
- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...532
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:345

```

Tyr Arg Arg Ser Gly Arg Val Cys Pro Arg Ile Leu Arg Asn Lys Arg
40 1      5      10      15
Ser Tyr Ala Asp Thr Arg Leu Gln Pro Arg Arg Ala Val Arg Leu Arg
        20      25      30
Ala Gly Thr Arg Thr Lys Met Lys Arg Arg Phe Leu Ser Leu Leu Leu
        35      40      45
45 Leu Tyr Ile Leu Ser Ser Ile Ser Leu Ser Ala Gln Arg Phe Pro Met
        50      55      60
Val Gln Gly Ile Glu Leu Asp Thr Asp Ser Leu Phe Ser Leu Pro Lys
65      70      75      80
Arg Pro Trp Arg Ala Ile Gly Lys Thr Ile Gly Val Asn Leu Ala Val
50      85      90      95
Trp Gly Phe Asp His Phe Ile Met Asn Glu Asp Phe Ala Asp Ile Ser
        100      105      110
Trp Gln Thr Ile Lys Ser Asn Phe Gln Thr Gly Phe Gly Trp Asp Asn
        115      120      125
55 Asp Lys Phe Val Thr Asn Leu Phe Ala His Pro Tyr His Gly Ser Leu
        130      135      140
Tyr Phe Asn Ala Ala Arg Ser Asn Gly Leu Ser Phe Arg His Ser Ala
145      150      155      160
Pro Phe Ala Phe Phe Gly Ser Leu Met Trp Glu Leu Leu Met Glu Asn
60      165      170      175
Glu Pro Pro Ser Ile Asn Asp Leu Cys Ala Thr Thr Ile Gly Gly Ile
        180      185      190
Ala Leu Gly Glu Met Gly His Arg Leu Ser Asp Leu Leu Ile Asp Asn
195      200      205
65 Arg Thr Thr Gly Trp Glu Arg Met Gly Arg Glu Val Ala Ile Ala Leu
        210      215      220
Ile Asn Pro Met Arg Phe Leu Asn Arg Leu Thr Ala Gly Glu Val Thr
225      230      235      240
Ser Val Gly Ser Arg Ser Gly Gln Ile Phe Gln Ser Val Pro Ile Asn
70      245      250      255
Ile Val Val Asp Ala Gly Phe Arg Phe Leu Ala Asp Lys Arg His Ala
        260      265      270
Arg Thr Gly Ala Thr Ala Leu Thr Leu Asn Leu Arg Phe Asp Tyr Gly
275      280      285
75 Asp Pro Phe Arg Ser Glu Thr Phe Ser Pro Tyr Asp Phe Phe Gln Phe

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290  
 Lys Ala Gly Leu Ser Phe Ser Glu Ser Gln Pro Leu Leu Ser Gln Ile  
 305  
 Asn Leu Ile Gly Ile Leu Ser Gly Cys Gln Leu Leu Ala His Glu Arg  
 320  
 Thr Val Leu Val Gly Gly Leu Phe Gln His Phe Asp Tyr Tyr Asn Ser  
 335  
 Glu Lys Arg Ile Ser Lys Asn Ser Glu Glu Val Leu Val Thr Pro Tyr  
 350  
 10 Arg Ile Ser Gln Val Ala Ala Leu Gly Gly Leu Ile Phe Gln His  
 365  
 His Gly Lys Phe Arg Arg Arg Pro Leu Glu Leu Tyr Ala Glu Thr Tyr  
 380  
 Leu Asn Val Val Pro Met Gly Ala Ser Leu Ser Asp His Tyr Asn Val  
 395  
 15 Asp Asn Arg Asp Tyr Asn Leu Gly Ser Gly Leu Ser Gly Lys Leu Tyr  
 410  
 Leu Gly Ala Thr Tyr Asn Asp Leu Trp Ser Trp Leu Leu Gly Val Glu  
 425  
 20 Ser Tyr Arg Leu Tyr Thr Trp Ile Gly Tyr Glu Glu Pro His Gln Lys  
 440  
 Asn Thr Asp Val Ser Ser Phe Met Val Gln Gly Asp Glu Ser Lys Ala  
 455  
 25 Arg Leu Leu Val Thr Ser Ser Glu Phe Ala Phe His Pro Gly Pro Trp  
 470  
 His Val Ala Ile Val Ala Arg Arg Phe Ile Arg Lys Thr Ala Tyr Gln  
 485  
 Phe Tyr Pro Asn Val Ser Phe Asp Thr Gly Asp Ile Gln Leu Arg Val  
 500  
 30 Gly Phe His Phe  
 515  
 530  
 (2) INFORMATION FOR SEQ ID NO:346  
 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 300 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 40 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 45 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...300  
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:346  
 Lys Arg Arg Lys Lys Gln Met Lys Arg Leu Ile Val Phe Leu Ala Met  
 1 5 10 15  
 Gly Gly Leu Leu Phe Thr Leu Ala Asn Ala Gln Glu Ala Asn Thr Ala  
 20 25 30  
 Ser Asp Thr Pro Lys Lys Asp Trp Thr Ile Lys Gly Val Thr Gly Leu  
 35 40 45  
 Asn Ala Ser Gln Thr Ser Leu Thr Asn Trp Ala Ala Gly Gly Glu Asn  
 50 55 60  
 Thr Val Ala Gly Asn Leu Tyr Leu Asn Ile Asp Ala Asn Tyr Leu Lys  
 65 70 75 80  
 Asp Lys Trp Ser Trp Asp Asn Gly Leu Arg Thr Asp Phe Gly Leu Thr  
 85 90 95  
 Tyr Thr Thr Ala Asn Lys Trp Asn Lys Ser Val Asp Lys Ile Glu Leu  
 100 105 110  
 Phe Thr Lys Ala Gly Tyr Glu Ile Gly Lys His Trp Tyr Gly Ser Ala  
 115 120 125  
 Leu Phe Thr Phe Leu Ser Gln Tyr Ala Lys Gly Tyr Glu Lys Pro Ser  
 130 135 140  
 Asp His Leu Thr Gly Val Lys His Ile Ser Asn Phe Phe Ala Pro Ala  
 145 150 155 160  
 Tyr Leu Thr Leu Gly Ile Gly Ala Asp Tyr Lys Pro Asn Glu Lys Phe  
 165 170 175  
 75 Ser Leu Tyr Leu Ser Pro Thr Thr Gly Lys Leu Thr Val Val Ala Asp

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180 185 190  
 Asp Tyr Leu Ser Ser Leu Gly Ala Phe Gly Val Lys Val Gly Glu Lys  
 195 200 205  
 Thr Met Phe Glu Leu Gly Ala Leu Val Val Gly Ser Ala Asn Ile Asn  
 210 215 220  
 Leu Met Glu Asn Val Asn Leu Ile Thr Lys Ala Ser Phe Phe Ser Ala  
 225 230 235 240  
 Tyr Thr His Asp Phe Gly Asn Ile Asp Ile Asn Trp Glu Ala Met Leu  
 245 250 255  
 10 Ala Met Lys Ile Asn Lys Phe Leu Thr Ala Thr Ile Ala Thr Asn Leu  
 260 265 270  
 Ile Tyr Asp Asp Asp Val Lys Ile Asn Asp Gly Pro Lys Ile Gln Phe  
 275 280 285  
 15 Lys Glu Val Val Gly Val Gly Val Ala Tyr Thr Phe  
 290 295 300

## (2) INFORMATION FOR SEQ ID NO:347

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 221 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 25 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 30 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...221  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:347

Thr Arg Glu Ser Val Leu His Cys Arg Thr Lys Leu Lys Lys Glu Arg  
 1 5 10 15  
 40 Lys Met Lys Lys Met Ile Leu Ala Ala Thr Met Leu Leu Ala Thr Ile  
 20 25 30  
 Gly Phe Ala Asn Ala Gln Ser Arg Pro Ala Leu Arg Leu Asp Ala Asn  
 35 40 45  
 Phe Val Gly Ser Asn Leu Met Gln Lys Val Ala Asn Thr Ser Val Asn  
 50 55 60  
 45 Asn Lys Met Ile Val Gly Leu Arg Val Gly Ala Ala Glu Phe Ala  
 65 70 75 80  
 Leu Ser Asn Asp Gly Phe Tyr Leu Ala Pro Gly Leu Ala Tyr Thr Met  
 85 90 95  
 50 Arg Gly Ala Lys Met Glu Ser Leu Ser Glu Thr Thr Thr Arg Leu His  
 100 105 110  
 Tyr Leu Gln Ile Pro Val Asn Ala Gly Met Arg Phe Ser Phe Ala Asp  
 115 120 125  
 Asn Met Ala Ile Ser Leu Glu Ala Gly Pro Tyr Phe Ala Tyr Gly Val  
 130 135 140  
 55 Ala Gly Thr Ile Lys Thr Lys Val Ala Gly Val Thr Ala Ser Val Asp  
 145 150 155 160  
 Ala Phe Gly Asp Asn Gly Tyr Asn Arg Phe Asp Leu Gly Leu Gly Leu  
 165 170 175  
 60 Ser Ala Ala Leu Ser Tyr Asp Arg Tyr Tyr Val Gln Ile Gly Tyr Glu  
 180 185 190  
 His Gly Leu Leu Asn Met Leu Lys Asp Ala Pro Asp Lys Thr Ser Leu  
 195 200 205  
 Arg Asn His Asp Phe Phe Val Gly Leu Gly Val Arg Phe  
 210 215 220

## (2) INFORMATION FOR SEQ ID NO:348

- 70 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 248 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 75 (iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

5 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...240

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:348

```

1   Ile Lys Arg Ile Glu Met Lys Arg Ile Phe Thr Val Ala Leu Val Leu
    1           5           10           15
Leu Ala Ser Val Thr Met Ala Ile Gly Gln Ser Arg Pro Ala Leu Arg
    20           25           30
15 Val Asp Ala Asn Phe Val Gly Ser Asn Gln Ser Met Lys Arg Asp Gly
    35           40           45
Tyr Val Trp Asp Thr Lys Met Asn Val Gly Leu Arg Val Gly Ala Ala
    50           55           60
20 Ala Glu Phe Met Ile Gly Ser Arg Gly Phe Tyr Leu Ala Pro Gly Leu
    65           70           75           80
Asn Tyr Thr Met Lys Gly Ser Lys Thr Glu Trp Asp Ile Pro Glu Met
    85           90           95
Val Pro Gly Thr Tyr Ile Thr Met Val Ser Thr Arg Leu His Tyr Leu
    100          105          110
25 Gln Leu Pro Ile Asn Ala Gly Met Arg Phe Asp Leu Met Asn Asp Met
    115          120          125
Ala Val Ser Ile Glu Ala Gly Pro Phe Leu Ala Tyr Gly Ile Tyr Gly
    130          135          140
30 Thr Tyr Arg Gln Lys Leu Glu Gly Trp Lys Pro Asn Asn Tyr Ser Thr
    145          150          155          160
Glu Phe Phe Gly Pro Thr Leu Gly Gly Pro Thr Asn Ile Arg Trp Asp
    165          170          175
Ile Gly Ala Asn Ile Ile Ala Ala Phe His Tyr Lys Arg Tyr Tyr Ile
    180          185          190
35 Gln Ile Gly Tyr Glu His Gly Phe Val Asp Ile Val Ser Gly Gly Gly
    195          200          205
Ser Asp Ile Pro Arg Leu Asn Asp Asn Arg Gln Ser Ser Ser Thr Thr
    210          215          220
40 Ala Leu Arg Glu Lys Gly Asn Asn Glu Tyr Ala Tyr Asn Arg Asp Phe
    225          230          235          240
Phe Val Gly Ile Gly Tyr Arg Phe
    245

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45 (2) INFORMATION FOR SEQ ID NO:349

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 211 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

55 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...211

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:349

```

65 Lys Arg Lys Ser Met Lys Arg Met Leu Leu Leu Val Val Leu Leu
    1           5           10           15
Tyr Gly Ile Ala Gly Arg Leu Ala Ala Gln Asp Val Ile Arg Pro Trp
    20           25           30
Ser Leu Gln Val Gly Ala Gly Tyr Ser Asp Thr Glu Asn Ile Pro Gly
    35           40           45
70 Gly Phe Thr Tyr Gly Phe Tyr Leu Gly Lys Arg Met Gly Ser Phe Leu
    50           55           60
Glu Val Gly Leu Ser Met Tyr Asn Ser Thr Arg Gln Thr Ala Asn Asn
    65           70           75           80
Ala Asp Ser Phe Ala Ser Asn Glu Gly Asp Gly Ser Phe Gln Val Asn
    85           90           95

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Met Ser Ser Pro Asn Glu Lys Trp Ser Phe Phe Asp Ala Gly Ser Ala  
 100 105 110  
 Asn Cys Tyr Met Ile Val Val Gly Val Asn Pro Leu His Leu Phe Trp  
 115 120 125  
 5 Gln Asn Ser Arg His Asn Leu Phe Leu Ala Val Gln Ala Gly Leu Ser  
 130 135 140  
 Asn Lys His Asn Ile His Phe Ile Tyr Gly Asp Lys Gly Ala Lys Val  
 145 150 155 160  
 10 Ser Ile Tyr Thr Asn Ser Asn Thr Tyr Ile Gly Tyr Gly Ala Arg Val  
 165 170 175  
 Ala Tyr Glu Tyr Gln Ile His Lys Asn Val Gly Ala Gly Ala Ala Val  
 180 185 190  
 Met Tyr Asp His Gly Asn Lys Met Leu Thr Ala Met Ala Thr Leu Ser  
 195 200 205  
 15 Thr His Phe  
 210

(2) INFORMATION FOR SEQ ID NO:350

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 953 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...953
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:350

Ile Arg Met Arg Val Ser Asp Leu Cys Ser Arg Leu Ser Trp Leu Leu  
 1 5 10 15  
 40 Pro Val Ile Leu Val Gly Leu Leu Cys Ala Thr Leu Val Ala Ala Glu  
 20 25 30  
 Arg Pro Met Ala Gly Ala Val Gly Leu His His Arg Arg His Ala Ala  
 35 40 45  
 45 Leu Ser Asp Ser Thr Ala Lys Asp Thr Val Pro Leu Ala Lys Pro Ile  
 50 55 60  
 Pro Asp Ser Ala Phe Arg Asp Ser Leu Pro Ala Asp Ser Thr Gly Ser  
 65 70 75 80  
 Met Arg Gln Asp Ser Val Tyr Asp Asp Glu Phe Glu Leu Glu Asp Ile  
 85 90 95  
 50 Val Glu Tyr Glu Ala Ala Asp Ser Ile Val Leu Leu Gly Gln Asn Arg  
 100 105 110  
 Ala Tyr Leu Phe Gly Lys Ser Tyr Val Ser Tyr Gln Lys Ser Arg Leu  
 115 120 125  
 55 Glu Ala Asn Phe Met Tyr Leu Asn Thr Asp Ser Ser Thr Val Tyr Thr  
 130 135 140  
 Arg Tyr Val Leu Asp Thr Ala Gly Tyr Pro Met Ala Phe Pro Val Phe  
 145 150 155 160  
 Lys Asp Gly Glu Gln Ser Phe Glu Ala Lys Asn Phe Thr Tyr Asn Phe  
 165 170 175  
 60 Arg Thr Glu Lys Gly Ile Ile Ser Gly Val Ile Thr Gln Gln Gly Glu  
 180 185 190  
 Gly Tyr Leu Thr Ala Gly Lys Thr Lys Lys Met Pro Asp Asn Ile Met  
 195 200 205  
 65 Phe Met Gln Gly Gly Arg Tyr Thr Thr Cys Asp Asn His Asp His Pro  
 210 215 220  
 His Phe Tyr Ile Asn Leu Ser Lys Ala Lys Val His Pro Glu Lys Asp  
 225 230 235 240  
 Ile Val Thr Gly Pro Val Asn Leu Val Ile Ala Asp Met Pro Leu Pro  
 245 250 255  
 70 Ile Gly Leu Pro Phe Gly Tyr Phe Pro Phe Ser Asn Lys Tyr Ser Ser  
 260 265 270  
 Gly Ile Leu Met Pro Thr Tyr Gly Glu Asp Asn Arg Tyr Gly Phe Tyr  
 275 280 285  
 75 Leu Arg Asn Gly Gly Tyr Tyr Phe Ala Phe Ser Asp Tyr Ile Asp Leu  
 290 295 300

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Ala Leu Arg Gly Glu Ile Phe Ser Lys Gly Ser Trp Gly Ile Ser Ala  
 305 310 315 320  
 Gln Ser Lys Tyr Lys Arg Tyr Lys Tyr Asn Gly Ser Phe Glu Ala  
 325 330 335  
 5 Asn Tyr Leu Val Ser Lys Ser Gly Asp Lys Tyr Val Pro Gly Asp Tyr  
 340 345 350  
 Ser Lys Thr Thr Ser Leu Asn Ile Arg Trp Thr His Ser Gln Asp Pro  
 355 360 365  
 10 Lys Ala Asn Pro Leu Gln Thr Leu Ser Ala Asn Val Asn Phe Ala Thr  
 370 375 380  
 Gly Ser Tyr Phe Gln Asn Ser Leu Asn Thr Thr Tyr Asp Val Asn Ala  
 385 390 395 400  
 Arg Thr Ala Thr Thr Arg Ser Ser Ala Val Ser Tyr Ser Arg Lys Phe  
 405 410 415  
 15 Pro Gly Thr Pro Phe Ser Ile Thr Gly Ser Met Asp Ile Ser Gln Asn  
 420 425 430  
 Met Arg Asp Thr Thr Val Ser Leu Thr Leu Pro Asn Leu Ser Ile Asn  
 435 440 445  
 20 Met Ser Thr Arg Tyr Pro Phe Lys Arg Lys Thr Arg Val Gly Pro Glu  
 450 455 460  
 Arg Trp Tyr Glu Lys Leu Ser Val Gly Tyr Ser Gly Gln Leu Arg Asn  
 465 470 475 480  
 Ser Ile Leu Thr Lys Glu Lys Asp Leu Leu Gln Ser Asn Leu Val Arg  
 485 490 495  
 25 Asp Trp Lys Asn Gly Met Arg His Ser Val Pro Ile Ser Leu Thr Val  
 500 505 510  
 Pro Leu Leu Asp Tyr Ile Asn Leu Thr Met Gly Val Asn Tyr Asn Glu  
 515 520 525  
 30 Trp Trp Tyr Thr Lys Gly Ile Arg Lys Ser Trp Asn Glu Asp Lys Lys  
 530 535 540  
 Thr Phe Leu Pro Ser Asp Thr Thr Tyr Lys Phe Arg Arg Leu Tyr Asp  
 545 550 555 560  
 Tyr Ser Leu Ser Ala Gly Leu Ser Thr Thr Leu Tyr Gly Met Phe Lys  
 565 570 575  
 35 Pro Trp Lys Pro Phe Ser Phe Gly Gly Asn Leu Ile Met Ile Arg His  
 580 585 590  
 Arg Phe Thr Pro Thr Val Ser Phe Ser Tyr Met Pro Asp Phe Thr Lys  
 595 600 605  
 40 Arg Arg Tyr Gly Phe Trp Glu Leu Leu Glu His Thr Asp Gln Asn Gly  
 610 615 620  
 Lys Leu His Thr Leu Leu Tyr Ser Pro Tyr Phe Glu Gln Ile Phe Gly  
 625 630 635 640  
 Ala Pro Ser Met Gly Asn Ala Gly Ser Val Asn Phe Ser Phe Asp Asn  
 645 650 655  
 45 Asn Leu Glu Ala Lys Ile Lys Ser Lys Ser Asp Ser Thr Gly Ile Lys  
 660 665 670  
 Lys Ile Ser Leu Ile Asp Gln Phe Thr Trp Ser Thr Ser Tyr Asn Met  
 675 680 685  
 50 Phe Ala Asp Ser Ile Arg Trp Ser Asn Ile Ser Ala Ser Leu Ala Leu  
 690 695 700  
 Arg Leu Ser Lys Ser Phe Thr Leu Arg Leu Ser Gly Leu Phe Asp Pro  
 705 710 715 720  
 Tyr Leu Thr Lys Tyr Tyr Glu Gly Glu Asp Gly Lys Ile Ile Pro Tyr  
 725 730 735  
 55 Lys Ser Asn Asp Leu Arg Ile Phe Asn Gly Lys Gly Leu Ala Arg Leu  
 740 745 750  
 Ile Ser Thr Gly Thr Ser Phe Ser Tyr Thr Leu Asn Lys Glu Ser Leu  
 755 760 765  
 60 Ser Gly Leu Ile Ala Leu Phe Ser Gly Lys Lys Glu Arg Arg Asp Glu  
 770 775 780  
 Lys Lys Asn Thr Gly Ala Thr Pro His Glu Gly Asp Asp Ala Ala Asp  
 785 790 795 800  
 Ile Leu Glu Gly Gly Arg Pro Gln Asn Glu Ser Gly Gly Ser Leu Leu  
 805 810 815  
 65 Glu Arg Asn Arg Gln Gly Gly Ala Val Asp Gln Asp Gly Tyr Phe Ala  
 820 825 830  
 Tyr Ser Ile Pro Trp Ser Leu Ser Phe Asp Tyr Ser Trp Asn Ile Ala  
 835 840 845  
 70 Thr Asp Tyr Asn Arg Tyr Asn Val Asn Lys Met Glu His Tyr Tyr Arg  
 850 855 860  
 Val Thr Gln Asn Leu Ser Phe Arg Gly Asn Ile Gln Pro Thr Pro Asn  
 865 870 875 880  
 Trp Ser Phe Gly Phe Asn Ala Asn Tyr Asn Phe Asp Leu Lys Lys Ile  
 885 890 895  
 75 Thr Ser Leu Thr Cys Asn Val Thr Arg Asp Met His Cys Trp Ala Ile

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5 Ser Ala Ser Phe Ile Pro Ile Gly Ala Tyr Lys Ser Tyr Asn Phe Val  
 900 905 910  
 915 920 925  
 10 Ile Ser Val Lys Ser Ser Leu Leu Gln Asp Leu Lys Tyr Gln Gln Ser  
 930 935 940  
 15 Asn Arg Pro Ile Thr Asn Thr Trp Tyr  
 945 950

10 (2) INFORMATION FOR SEQ ID NO:351  
 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1251 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 20 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 25 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1251  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:351

30 Lys Trp Lys Leu Ala Cys Ala Phe Asp Cys Ala Cys Cys Phe Asp Pro  
 1 5 10 15  
 Phe Val Val Thr Asn Glu Val Ile Ile Met Met Lys Arg Tyr Thr Ile  
 20 25 30  
 35 Ile Leu Ala Val Phe Leu Leu Phe Cys Thr Val Phe Thr Phe Gln Ile  
 35 40 45  
 Lys Ala Arg Pro Tyr Glu Arg Phe Ala Asp Val Glu Lys Pro Trp Ile  
 50 55 60  
 Gln Lys His Ser Met Asp Ser Lys Leu Val Pro Ala Asn Lys Gly Asn  
 65 70 75 80  
 40 Leu Ile Gln Ala Glu Ile Val Tyr Gln Ser Val Ser Glu His Ser Asp  
 85 90 95  
 Leu Val Ile Ser Pro Val Asn Glu Ile Arg Pro Ala Asn Arg Phe Pro  
 100 105 110  
 Ser His Arg Lys Ser Phe Phe Ala Glu Asn Leu Arg Ala Ser Pro Pro  
 115 120 125  
 45 Val Val Pro Val Ala Val Asp Lys Tyr Ala Val Pro Val Ala Asn Pro  
 130 135 140  
 Met Asp Pro Glu Asn Pro Asn Ala Trp Asp Val Thr Leu Lys Ile Thr  
 145 150 155 160  
 50 Thr Lys Ala Val Thr Val Pro Val Asp Val Val Met Val Ile Asp Gln  
 165 170 175  
 Ser Ser Ser Met Gly Gly Gln Asn Ile Ala Arg Leu Lys Ser Ala Ile  
 180 185 190  
 Ala Ser Gly Gln Arg Phe Val Lys Lys Met Leu Pro Lys Gly Thr Ala  
 195 200 205  
 55 Thr Glu Gly Val Arg Ile Ala Leu Val Ser Tyr Asp His Glu Pro His  
 210 215 220  
 Arg Leu Ser Asp Phe Thr Lys Asp Thr Ala Phe Leu Cys Gln Lys Ile  
 225 230 235 240  
 60 Arg Ala Leu Thr Pro Ile Trp Gly Thr His Thr Gln Gly Gly Leu Lys  
 245 250 255  
 Met Ala Arg Asn Ile Met Ala Thr Ser Thr Ala Val Asp Lys His Ile  
 260 265 270  
 Ile Leu Met Ser Asp Gly Leu Ala Thr Glu Gln Tyr Pro Val Lys Asn  
 275 280 285  
 65 Val Thr Thr Ala Asp Phe Ile Gly Lys Thr Gly Asn Ala Asn Asp Pro  
 290 295 300  
 Ile Asp Leu Val Ile Gln Gly Ala Ile Asn Phe Pro Thr Asn Tyr Val  
 305 310 315 320  
 70 Ser Asn Asn Pro Ser Thr Pro Leu Thr Pro Asn Tyr Pro Thr His Ser  
 325 330 335  
 Ser Lys Val Gly Arg Arg Asn Leu Pro Glu Ser Lys Phe Asp Tyr Ser  
 340 345 350  
 Asn Leu Ser Ala Arg Ile Thr Phe Asp Gly Val Ala Gly Ala Leu Val  
 355 360 365  
 75 Tyr Glu Pro Arg Phe Pro His Pro Tyr Tyr Tyr Tyr Phe Pro Cys Asn

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	370		375		380
	Ala Ala Ile Asn Glu	Ala Gln Phe Ala Lys Asn Ser Gly Tyr Thr Ile			
	385	390	395	400	
5	His Thr Ile Gly Tyr Asp Leu Gly Asp Phe Ala Leu Ala Asn Asn Ser				
	405	410	415		
	Leu Lys Leu Thr Ala Thr Asp Glu Asn His Phe Phe Thr Ala Thr Pro				
	420	425	430		
	Ala Asn Leu Ala Ala Ala Phe Asp Asn Ile Ala Gln Thr Ile Asn Ile				
10	Gly Ile Gln Arg Gly Glu Val Thr Asp Phe Val Ala Pro Gly Phe Ile				
	435	440	445		
	Val Lys Asn Leu Thr Gln Ser Gly Asp Val Thr His Leu Leu Asn Val				
	450	455	460		
	Ser Asn Gly Thr Val His Tyr Asp Val Ser Thr Lys Lys Leu Thr Trp				
15	Thr Thr Gly Thr Ile Leu Ser Ser Ser Glu Ala Thr Ile Thr Tyr Arg				
	465	470	475		
	Ile Tyr Ala Asp Leu Asp Tyr Ile Gln Asn Asn Asp Ile Pro Val Asn				
	480	485	490		
20	Thr Thr Ser Ala Ile Gly Pro Asp Leu Gly Gly Phe Asp Thr Asn Thr				
	495	500	505		
	Glu Ala Lys Leu Thr Tyr Thr Asn Ser Asn Gly Glu Pro Asn Gln Gln				
	510	515	520		
25	Leu Ile Phe Pro Arg Pro Thr Val Lys Leu Gly Tyr Gly Val Ile Lys				
	525	530	535		
	Arg His Tyr Val Leu Val Asn Lys Asp Gly Gln Pro Ile Gln Ala Asn				
	540	545	550		
	Gly Thr Val Val Ser Ser Leu Ser Glu Ala His Val Leu Gln Ser Gln				
30	Asp Phe Phe Leu Pro Ser Gly Gly Gly His Ile Val Pro Lys Trp Ile				
	555	560	565		
	Lys Leu Asp Lys Thr Thr Glu Ala Leu Gln Tyr Tyr Ser Val Pro Pro				
	570	575	580		
35	Thr Asn Thr Val Ile Thr Thr Ala Asp Gly Lys Arg Tyr Arg Phe Val				
	585	590	595		
	Glu Val Pro Gly Ser Thr Pro Asn Pro Gly Gln Ile Gly Ile Ser Trp				
	600	605	610		
40	Lys Lys Pro Ala Gly Asn Ala Tyr Phe Ala Tyr Lys Leu Leu Asn Tyr				
	615	620	625		
	Trp Met Gly Gly Thr Thr Asp Gln Gln Ser Glu Trp Asp Val Thr Ser				
	630	635	640		
	Asn Trp Thr Gly Ala Gln Val Pro Leu Thr Gly Glu Asp Val Glu Phe				
45	Ala Thr Thr Glu Asn Phe Gly Ser Pro Ala Val Ala Asp Leu His Val				
	645	650	655		
	Pro Thr Thr Asn Pro Lys Ile Ile Gly Asn Leu Ile Asn Asn Ser Asp				
	660	665	670		
	Lys Asp Leu Val Val Thr Thr Ser Ser Gln Leu Thr Ile Asn Gly Val				
50	Val Glu Asp Asn Asn Pro Asn Val Gly Thr Ile Val Val Lys Ser Ser				
	675	680	685		
	Lys Asp Asn Pro Thr Gly Thr Leu Leu Phe Ala Asn Pro Gly Tyr Asn				
	690	695	700		
55	Gln Asn Val Gly Gly Thr Val Glu Phe Tyr Asn Gln Gly Tyr Asp Cys				
	705	710	715		
	Ala Asp Cys Gly Met Tyr Arg Arg Ser Trp Gln Tyr Phe Gly Ile Pro				
	720	725	730		
	Val Asn Glu Ser Gly Phe Pro Ile Asn Asp Val Gly Gly Asn Glu Thr				
60	Val Asn Gln Trp Val Glu Pro Phe Asn Gly Asp Lys Trp Arg Pro Ala				
	735	740	745		
	Pro Tyr Ala Pro Asp Thr Glu Leu Gln Lys Phe Lys Gly Tyr Gln Ile				
	750	755	760		
65	Thr Asn Asp Val Gln Ala Gln Pro Thr Gly Val Tyr Ser Phe Lys Gly				
	765	770	775		
	Met Ile Cys Val Cys Asp Ala Phe Leu Asn Leu Thr Arg Thr Ser Gly				
	780	785	790		
	Val Asn Tyr Ser Gly Ala Asn Leu Ile Gly Asn Ser Tyr Thr Gly Ala				
70	Ile Asp Ile Lys Gln Gly Ile Val Phe Pro Pro Glu Val Glu Gln Thr				
	795	800	805		
	Val Tyr Leu Phe Asn Thr Gly Thr Arg Asp Gln Trp Arg Lys Leu Asn				
	810	815	820		
75	Gly Ser Thr Val Ser Gly Tyr Arg Ala Gly Gln Tyr Leu Ser Val Pro				
	825	830	835		

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Lys Asn Thr Ala Gly Gln Asp Asn Leu Pro Asp Arg Ile Pro Ser Met  
 980 985 990  
 His Ser Phe Leu Val Lys Met Gln Asn Gly Ala Ser Cys Thr Leu Unk  
 995 1000 1005  
 5 Ile Leu Tyr Asp Lys Leu Leu Lys Asn Thr Thr Val Asn Asn Gly Asn  
 1010 1015 1020  
 Gly Thr Gln Ile Thr Trp Arg Ser Gly Asn Ser Gly Ser Ala Asn Met  
 1025 1030 1035 1040  
 10 Pro Ser Leu Val Met Asp Val Leu Gly Asn Glu Ser Ala Asp Arg Leu  
 1045 1050 1055  
 Trp Ile Phe Thr Asp Gly Gly Leu Ser Phe Gly Phe Asp Asn Gly Trp  
 1060 1065 1070  
 Asp Gly Arg Lys Leu Thr Glu Lys Gly Leu Ser Gln Leu Tyr, Ala Met  
 1075 1080 1085  
 15 Ser Asp Ile Gly Asn Asp Lys Phe Gln Val Ala Gly Val Pro Glu Leu  
 1090 1095 1100  
 Asn Asn Leu Leu Ile Gly Phe Asp Ala Asp Lys Asp Gly Gln Tyr Thr  
 1105 1110 1115 1120  
 20 Leu Glu Phe Ala Leu Ser Asp His Phe Ala Lys Gly Ala Val Tyr Leu  
 1125 1130 1135  
 His Asp Leu Gln Ser Gly Ala Lys His Arg Ile Thr Asn Ser Thr Ser  
 1140 1145 1150  
 Tyr Ser Phe Asp Ala Lys Arg Gly Asp Ser Gly Ala Arg Phe Arg Leu  
 1155 1160 1165  
 25 Ser Tyr Gly Cys Asp Glu Asn Val Asp Asp Ser His Val Val Ser Thr  
 1170 1175 1180  
 Asn Gly Arg Glu Ile Ile Ile Leu Asn Gln Asp Ala Leu Asp Cys Thr  
 1185 1190 1195 1200  
 30 Val Thr Leu Phe Thr Ile Glu Gly Lys Leu Leu Arg Arg Leu Lys Val  
 1205 1210 1215  
 Leu Ala Gly His Arg Glu Val Met Lys Val Gln Thr Gly Gly Ala Tyr  
 1220 1225 1230  
 Ile Val His Leu Gln Asn Ala Phe Thr Asn Asp Val His Lys Val Leu  
 1235 1240 1245  
 35 Val Glu Tyr  
 1250

## (2) INFORMATION FOR SEQ ID NO:352

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 426 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 50 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...426  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:352

Thr Met Glu Val Lys Lys Asn Thr Val Val Leu Arg Leu Leu Ile Trp  
 1 5 10 15  
 60 Phe Val Ala Ile Leu Leu Phe His Ser Ser Arg Leu Trp Gly Gln Glu  
 20 25 30  
 Gly Glu Gly Ser Ala Arg Tyr Arg Phe Lys Gly Phe Val Asp Thr Tyr  
 35 40 45  
 65 His Ala Val Arg Ser Ser Ser Pro Phe Asp Phe Met Ser Ser Arg Thr  
 50 55 60  
 Arg Val Arg Gly Glu Leu Glu Arg Ser Phe Gly Asn Ser Lys Val Ala  
 65 70 75 80  
 Val Ser Val Asn Ala Thr Tyr Asn Ala Leu Leu Lys Asp Glu Thr Gly  
 85 90 95  
 70 Leu Arg Leu Arg Glu Ala Phe Phe Glu His Gln Glu Glu His Trp Gly  
 100 105 110  
 Leu Arg Leu Gly Arg Gln Ile Val Ile Trp Gly Ala Ala Asp Gly Val  
 115 120 125  
 75 Arg Ile Thr Asp Leu Ile Ser Pro Met Asp Met Thr Glu Phe Leu Ala  
 130 135 140



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Gln Asp Tyr Asp Asp Ile Arg Met Pro Val Asn Ala Leu Arg Phe Ser  
 145 150 155 160  
 Val Phe Asn Glu Ser Met Lys Val Glu Val Val Leu Pro Val Phe  
 165 170 175  
 5 Glu Gly Tyr Arg Leu Pro Val Asp Pro Arg Asn Pro Trp Asn Ile Phe  
 180 185 190  
 Ser Leu Ser Pro Ile Ala Gln Gly Met Asn Ile Val Trp Lys Glu Glu  
 195 200 205  
 10 Ala Gly Lys Pro Ala Phe Lys Val Ala Asn Ile Glu Tyr Gly Ala Arg  
 210 215 220  
 Trp Ser Thr Thr Leu Ser Gly Ile Asp Phe Ala Leu Ala Ala Leu His  
 225 230 235 240  
 Thr Trp Asn Lys Met Pro Val Ile Glu Val Gln Gly Ile Val Pro Thr  
 245 250 255  
 15 Glu Ile Ile Val Ser Pro Arg Tyr Tyr Arg Met Gly Phe Val Gly Gly  
 260 265 270  
 Asp Leu Ser Val Pro Val Gly Gln Phe Val Phe Arg Gly Glu Ala Ala  
 275 280 285  
 20 Phe Asn Ile Asp Lys His Phe Thr Tyr Lys Ser His Ala Glu Gln Glu  
 290 295 300  
 Gly Phe Gln Thr Ile Asn Trp Leu Ala Gly Ala Asp Trp Tyr Ala Pro  
 305 310 315 320  
 Gly Glu Trp Met Ile Ser Gly Gln Phe Ser Met Glu Ser Ile Phe Arg  
 325 330 335  
 25 Tyr Arg Asp Phe Ile Ser Gln Arg Gln His Ser Thr Leu Ile Thr Leu  
 340 345 350  
 Asn Val Ser Lys Lys Phe Phe Gly Ser Thr Leu Gln Leu Ser Asp Phe  
 355 360 365  
 30 Thr Tyr Tyr Asp Leu Thr Gly Lys Gly Trp Phe Ser Arg Phe Ala Ala  
 370 375 380  
 Asp Tyr Ala Leu Asn Asp Gln Ile His Leu Met Ala Gly Tyr Asp Trp  
 385 390 395 400  
 Phe Ser Ser Lys Gly Ser Gly Ile Phe Asp Arg Tyr Lys Asp Asn Ser  
 405 410 415  
 35 Glu Leu Trp Phe Lys Ala Arg Tyr Ser Phe  
 420 425

(2) INFORMATION FOR SEQ ID NO:353

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 464 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 50 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...464  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:353

Tyr Gly Lys Arg Arg Lys Leu Gly Thr Ser Val Arg Pro Ser Val Leu  
 1 5 10 15  
 60 Thr Gln Ile Arg Phe Ile Leu Asp Leu His Leu Ile Thr Asp Phe Phe  
 20 25 30  
 Glu Gly Leu Arg Val Asn Pro Ile Gly Ala Ala Ala Ile Val Ala Phe  
 35 40 45  
 65 Ile Ile Asp Leu Leu Leu Leu Cys Cys Ser Ala Phe Met Ser Ser Cys  
 50 55 60  
 Glu Val Ala Tyr Phe Ser Leu Lys Pro Ile Asp Leu Gln Asn Ile Arg  
 65 70 75 80  
 Glu Arg Asn His Ser Ser Asp Ile Ala Leu Ser Asn Leu Leu Asp Asn  
 85 90 95  
 70 Ser Asn Gln Leu Leu Ala Thr Ile Leu Ile Gly Asn Asn Val Ile Asn  
 100 105 110  
 Val Ala Ile Val Ile Leu Ser Asn Tyr Ala Ile Glu Gln Thr Phe Val  
 115 120 125  
 75 Phe Ser Ser Pro Ile Ile Gly Phe Leu Ile Gln Thr Ile Leu Leu Thr  
 130 135 140

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    Thr Val Leu Leu Leu Phe Gly Glu Ile Leu Pro Lys Val Tyr Ala Arg
    145      150      155      160
    Lys Asn Pro Leu Gln Tyr Ser Arg Phe Ser Ala Ala Met Ser Val
    165      170      175
5   Ile Tyr Lys Ile Leu Ser Pro Phe Ser Lys Leu Leu Val Lys Ser Thr
    180      185      190
    Gly Ile Val Thr Arg Gly Ile Ser Lys Lys Lys Tyr Asp Met Ser Val
    195      200      205
10  Asp Glu Leu Ser Lys Ala Val Ala Leu Thr Thr Thr Glu Gly Glu Pro
    210      215      220
    Glu Glu Lys Glu Met Ile Asn Glu Ile Ile Lys Phe Tyr Asn Lys Thr
    225      230      235      240
    Ala Cys Glu Ile Met Val Pro Arg Ile Asp Ile Val Asp Val Asp Leu
    245      250      255
15  Ser Trp Pro Phe Arg Lys Met Leu Asp Phe Val Val Ser Ser Gly Tyr
    260      265      270
    Ser Arg Leu Pro Val Ser Glu Gly Ser Glu Asp Asn Ile Lys Gly Val
    275      280      285
20  Ile Tyr Ile Lys Asp Leu Ile Pro His Met Asp Lys Gly Asp Glu Phe
    290      295      300
    Asp Trp His Pro Leu Ile Arg Lys Ala Tyr Phe Val Pro Glu Asn Lys
    305      310      315      320
    Arg Ile Asp Asp Leu Leu Glu Glu Phe Arg Ala Asn Lys Val His Val
    325      330      335
25  Ser Ile Val Val Asp Glu Phe Gly Gly Thr Cys Gly Leu Ile Thr Met
    340      345      350
    Glu Asp Ile Leu Glu Glu Ile Val Gly Glu Ile Thr Asp Glu Tyr Asp
    355      360      365
30  Glu Glu Glu Leu Pro Phe Lys Val Leu Gly Asp Gly Ser Tyr Leu Phe
    370      375      380
    Glu Gly Lys Thr Ser Leu Ser Asp Val Arg His Tyr Leu Asp Leu Pro
    385      390      395      400
    Glu Asn Ala Phe Gly Glu Leu Gly Asp Glu Val Asp Thr Leu Ser Gly
    405      410      415
35  Leu Phe Leu Glu Ile Lys Gln Glu Leu Pro His Val Gly Asp Thr Ala
    420      425      430
    Val Tyr Glu Pro Phe Arg Phe Gln Val Thr Gln Met Asp Lys Arg Arg
    435      440      445
40  Ile Ile Glu Ile Lys Ile Phe Pro Phe Glu Arg Thr Trp Glu Val Glu
    450      455      460

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(2) INFORMATION FOR SEQ ID NO:354

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 266 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...266
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:354

```

    Ile Ile Tyr Arg Ser Thr Met Lys Leu Leu Leu Tyr Leu Leu Leu Val
    1      5      10      15
    Leu Ser Thr Leu Ser Pro Met Tyr Ser Gln Met Leu Phe Ser Glu Asn
    20      25      30
65  Leu Thr Met Asn Ile Asp Ser Thr Lys Thr Ile Gln Gly Thr Ile Leu
    35      40      45
    Pro Val Leu Asp Phe Lys Thr Glu Lys Glu Asn Val Phe Thr Phe Lys
    50      55      60
70  Asn Thr Ala Asn Leu Asn Leu Leu Ile Lys His Gly Gln Val Ile Asn
    65      70      75      80
    Leu Ile Asn Lys Leu Glu Phe Ser Thr Tyr Gly Asn Lys Val Thr Val
    85      90      95
75  Ser Gly Gly Tyr Val His Thr Glu Tyr Arg Tyr Leu Leu His His Val
    100      105      110

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Phe Glu Val Tyr Pro Tyr Val Glu Ser Gln Trp Ala Glu Ser Arg Gly  
 115 120 125  
 Met Lys Tyr Lys Val Ser Thr Gly Leu Gln Ser Arg Tyr Arg Leu Val  
 130 135 140  
 5 Asn Ser Asp Asn Cys Leu Met Phe Ala Thr Leu Gly Val Phe Phe Glu  
 145 150 155 160  
 Phe Glu Lys Trp Glu Gln Pro Ala Thr Ser Leu Phe Ala Gly Thr Tyr  
 165 170 175  
 10 Ala Tyr Ser Arg Ser Ile Lys Ser His Leu Ser Ile Ser Phe Arg His  
 180 185 190  
 Arg Leu Gly Glu His Trp Glu Phe Thr Thr Thr Ala Ile His Gln Gly  
 195 200 205  
 Lys Pro Asp Ser Tyr Phe Lys Lys Ala Arg Phe Gly Gly Ala Ile Asp  
 210 215 220  
 15 Leu Lys Tyr His Ile Thr Pro Thr Ile Gly Ile Arg Gly Ala Tyr Arg  
 225 230 235 240  
 Ile Ile Tyr Asp Thr Ala Pro Ile Val Pro Val Arg Lys Asp Tyr Asn  
 245 250 255  
 20 Thr Val Asp Val Gly Ile Asp Ile Ser Phe  
 260 265

(2) INFORMATION FOR SEQ ID NO:355

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 907 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 35 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...907  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:355

Thr Ile Cys Val Ala Phe Leu Ser Ala Pro Val Ala Ala Leu Arg Glu  
 1 5 10 15  
 45 Ser Pro Pro Met Gly Ala Glu Arg Lys Thr Pro Ser Leu Leu Pro Leu  
 20 25 30  
 Leu Phe Glu His Ser Asp Lys Gly Lys Gly Phe Asp Tyr Arg Leu Phe  
 35 40 45  
 Thr Ser Asn Lys Leu Lys Val Phe Ala Thr Gly Asn Ser Arg Tyr Ile  
 50 55 60  
 His Asn Lys Pro Thr Ile Ile Gln Ala Met Lys Arg Ile Val Leu Ser  
 65 70 75 80  
 Ser Phe Leu Phe Val Leu Ser Ile Leu Ser Leu Met Ala Gln Asn Asn  
 85 90 95  
 55 Thr Leu Asp Val His Ile Ser Gly Thr Ile Lys Asp Ala Ser Ser Gly  
 100 105 110  
 Glu Pro Val Pro Tyr Ala Thr Val Ser Ile Arg Leu Thr Gly Ala Asp  
 115 120 125  
 Thr Thr Gln Val Phe Arg Gln Val Thr Asp Gly Asn Gly Tyr Phe Val  
 130 135 140  
 60 Ile Gly Leu Pro Ala Ala Pro Ser Tyr His Leu Thr Ala Ser Phe Val  
 145 150 155 160  
 Gly Met Lys Thr His Thr Met Gln Ile Ser Arg Gly Asn Gly Gln His  
 165 170 175  
 65 Asp Ile Lys Ser Ile Asp Ile Ser Leu Glu Ser Glu Asp Lys Gln Leu  
 180 185 190  
 Ser Thr Val Thr Val Ser Ala Ala Arg Pro Leu Val Lys Met Glu Ile  
 195 200 205  
 Asp Arg Leu Ser Tyr Asn Met Lys Asp Asp Pro Ala Ala Lys Thr Asn  
 210 215 220  
 70 Asn Leu Leu Glu Met Leu Arg Asn Val Pro Leu Val Thr Val Asp Gly  
 225 230 235 240  
 Gln Gly Asn Ile Gln Val Lys Gly Ser Ser Asn Phe Lys Ile His Leu  
 245 250 255  
 75 Asn Gly Arg Pro Ser Thr Met Val Ser Ser Asn Pro Lys Glu Val Phe  
 260 265 270

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Arg Ser Ile Pro Ala His Thr Ile Lys Arg Val Glu Val Ile Thr Asp  
 275 280 285  
 Pro Gly Val Lys Tyr Asp Ala Glu Gly Thr Ser Ala Ile Leu Asp Ile  
 290 295 300  
 5 Val Thr Glu Glu Gly Lys Lys Leu Glu Gly Tyr Ser Gly Ser Ile Thr  
 305 310 315 320  
 Ala Ser Val Ser Asn Asn Pro Thr Ala Asn Gly Ser Ile Phe Leu Thr  
 325 330 335  
 10 Ala Lys Ser Gly Lys Val Gly Leu Thr Thr Asn Tyr Asn Tyr Tyr Gly  
 340 345 350  
 Gly Lys Asn Lys Gly Ser Arg Tyr Phe Thr Glu Arg Thr Thr Ser Met  
 355 360 365  
 Leu Gln Thr Ile Glu Glu Gly Lys Gly Gln Glu Thr Phe Gly Gly His  
 370 375 380  
 15 Phe Gly Asn Ala Leu Leu Ser Phe Glu Ile Asp Ser Leu Asn Leu Phe  
 385 390 395 400  
 Thr Val Gly Gly Asn Val Arg Leu Trp Glu Met Thr Thr Asp Arg Asn  
 405 410 415  
 20 Ser Val Glu Lys Ser Phe Ala Gly Ser Asn Leu Met Ser Tyr Ile Asp  
 420 425 430  
 Arg Lys Leu Lys Thr Gln Met Asp Ala Gly Ser Tyr Glu Leu Asn Ala  
 435 440 445  
 Asp Tyr Gln His Ser Thr Arg Leu Pro Gly Glu Leu Leu Thr Val Ser  
 450 455 460  
 25 Tyr Arg Phe Thr His Asn Pro Asn Asn Ser Glu Thr Phe Ile Asp Gln  
 465 470 475 480  
 Trp Lys Arg Asp Pro Leu Asn Thr Ala Asn Thr Ile Gln Tyr Ala Gly  
 485 490 495  
 30 Gln His Ser Lys Ser Asp Ala Gly Met Asp Glu His Thr Ala Gln Val  
 500 505 510  
 Asp Tyr Thr Arg Pro Leu Gly Gln Ala His Ser Leu Glu Ala Gly Leu  
 515 520 525  
 Lys Tyr Ile Tyr Arg His Ala Thr Ser Asp Pro Leu Tyr Glu Ile Arg  
 530 535 540  
 35 Pro Ser Glu Asp Ala Pro Trp Gln Pro Gly Ser Leu Tyr Ala Gln Asn  
 545 550 555 560  
 Pro Ser Asn Gly Lys Phe Arg His Asp Gln Tyr Ile Gly Ala Ala Tyr  
 565 570 575  
 40 Ala Gly Tyr Asn Tyr Arg Lys Asp Gln Tyr Ser Leu Gln Thr Gly Leu  
 580 585 590  
 Arg Val Glu Ser Ser Arg Leu Lys Ala Leu Phe Pro Glu Asn Ala Ala  
 595 600 605  
 Ala Asp Phe Ser His Asn Ser Phe Asp Trp Val Pro Gln Leu Thr Leu  
 610 615 620  
 45 Gly Tyr Thr Pro Ser Pro Met Lys Gln Leu Lys Leu Ala Tyr Asn Phe  
 625 630 635 640  
 Arg Ile Gln Arg Pro Ala Ile Gly Gln Leu Asn Pro Tyr Arg Leu Gln  
 645 650 655  
 50 Thr Asn Asp Tyr Gln Val Gln Tyr Gly Asn Pro Asp Leu Lys Ser Glu  
 660 665 670  
 Lys Arg His His Val Gly Leu Ser Tyr Asn Gln Tyr Gly Ala Lys Val  
 675 680 685  
 Met Leu Thr Ala Ser Leu Asp Tyr Asp Phe Cys Asn Asn Ala Ile Gln  
 690 695 700  
 55 Asn Tyr Thr Phe Ser Asp Pro Ala Asn Pro Asn Leu Phe His Gln Thr  
 705 710 715 720  
 Tyr Gly Asn Ile Gly Arg Glu His Ser Phe Ser Leu Asn Thr Tyr Ala  
 725 730 735  
 60 Met Tyr Thr Pro Ala Val Trp Val Arg Ile Met Leu Asn Gly Asn Ile  
 740 745 750  
 Asp Arg Thr Phe Gln Lys Ser Glu Ala Leu Gly Ile Asp Val Asn Ser  
 755 760 765  
 Trp Ser Gly Met Val Tyr Ser Gly Leu Met Phe Thr Leu Pro Lys Asp  
 770 775 780  
 65 Trp Thr Val Asn Leu Phe Gly Gly Tyr Tyr His Gly Gly Arg Ser Tyr  
 785 790 795 800  
 Gln Thr Lys Tyr Asp Gly Asn Val Phe Asn Asn Ile Gly Ile Ala Lys  
 805 810 815  
 70 Gln Leu Phe Asp Lys Lys Leu Arg Val Ser Leu Ser Ala Asn Ile  
 820 825 830  
 His Ala Lys Tyr Ser Thr Trp Lys Ser Arg Thr Ile Gly Asn Gly Phe  
 835 840 845  
 Thr Ile Tyr Ser Glu Asn Ala Gly Ile Gln Arg Ser Val Ser Leu Ser  
 850 855 860  
 75 Leu Thr Tyr Ser Phe Gly Lys Met Asn Thr Gln Val Arg Lys Val Glu

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865 870 875 880  
 Arg Thr Ile Val Asn Asp Asp Leu Lys Gln Thr Ser Ser Gln Gly Gln  
 885 890 895  
 Gln Gly Gly Gly Gln Gly Asn Pro Thr Gly Asn  
 900 905

5

(2) INFORMATION FOR SEQ ID NO:356

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 450 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

20 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...450

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:356

Trp Cys Gln Ser Asp Pro Ile Pro His Cys His Ala Val Tyr Arg Asn  
 1 5 10 15  
 Ala Gln Gly His Gln Gln Gly Arg Ser Asp Gln Asp Arg Leu Pro Pro  
 20 25 30  
 Val Arg Gly Tyr Arg Tyr Ala Arg Cys Leu Gly Arg Tyr Glu Gly Phe  
 35 40 45  
 Gly Glu Arg Met Arg Leu Ser Ala Ile Leu Ile Ala Leu Ile Val Met  
 50 55 60  
 Leu Pro Ala Val Leu Ser Gly Gln His Tyr Tyr Ser Met Ala Gly Glu  
 65 70 75 80  
 Arg Leu Glu Thr Asp Ser Ile Arg Pro Asn Glu Leu Ser Ala Ser Ile  
 85 90 95  
 Arg Ser Ala Leu Phe Phe Arg Asn Asn Glu Tyr Asn Ala Arg Ser Val  
 100 105 110  
 Lys Gly Tyr Thr Leu Pro Gly Ala Arg Val Ser Ala Phe Ala Ser Tyr  
 115 120 125  
 Ser Leu Pro Ala Ala His Gly Val Lys Leu Ser Leu Gly Val Ser Thr  
 130 135 140  
 Leu Asn Tyr Trp Gly Ala Ser Arg Tyr Pro Ala Gly Ile Ala Tyr Ser  
 145 150 155 160  
 Asp Leu Pro Tyr Trp Thr Asp Tyr Asn Asp Tyr Val Arg Leu Arg Ile  
 165 170 175  
 Leu Pro Tyr Val Gln Ala Met Leu Lys Pro Thr Ala Thr Thr Ala Leu  
 180 185 190  
 Met Leu Gly Asn Ile Ala Gly Gly Thr Ala His Gly Leu Ile Glu Pro  
 195 200 205  
 Ile Tyr Asn Pro Glu Leu Asp Leu Thr Ala Asp Pro Glu Ala Gly Val  
 210 215 220  
 Gln Phe Arg Gly Asp Trp Thr Arg Phe Arg Met Asp Val Trp Val Asn  
 225 230 235 240  
 Trp Met Ser Met Ile Phe Lys Asn Asp Asn His Gln Glu Ser Phe Val  
 245 250 255  
 Phe Gly Leu Ser Thr Thr Ser Lys Leu Leu Ser Gly Glu Gly Lys Trp  
 260 265 270  
 Arg Leu Glu Leu Pro Leu Gln Ala Ile Ala Thr His Arg Gly Gly Glu  
 275 280 285  
 Tyr Asn Trp Ala Gln Gln Asp Thr Val His Thr Trp Val Asn Gly Ala  
 290 295 300  
 Val Gly Leu Lys Leu Ser Tyr Arg Pro Arg Thr Asp Lys Pro Met Gln  
 305 310 315 320  
 Ile Trp Gly Ser Ala Tyr Gly Val Ala Ala Leu Ser Ser Gly Gly Tyr  
 325 330 335  
 Phe Pro Tyr Glu Arg Gly Trp Gly Gly Tyr Leu Ser Leu Gly Met Asp  
 340 345 350  
 Leu Glu His Phe Ala Phe Arg Thr Asp Tyr Trp Tyr Gly Arg His Tyr  
 355 360 365  
 Val Ser Pro Phe Ala Ala Pro Phe Ala Asn Ser Leu Thr Tyr Asp Lys  
 370 375 380  
 Gln Pro Leu Thr Asn Gly Trp Gly Asp Tyr Ile Arg Leu Tyr Ala Asp

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385                      390                      395                      400  
 Tyr Ser Trp Arg Met Ala Arg Ser Val Ser Leu Ala Ala Val Ala Arg  
                                  405                      410                      415  
 5 Val Trp Phe Gln Pro Ser Asp Arg Phe Ala Met Ser His Ala Leu Glu  
                                  420                      425                      430  
 Leu Thr Met Arg Ile Asp Pro Lys Phe Pro Ile Ala Phe Leu Lys Gly  
                                  435                      440                      445  
 Asn His  
 450

10 (2) INFORMATION FOR SEQ ID NO:357

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 447 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

20 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

25 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...447

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:357

Pro Phe Ser Pro Pro Trp Val Cys Ala Gly Ala Ala Ser Ser Val Arg  
 1                      5                      10                      15  
 Thr Arg Pro Cys Ser Thr Val Ser Ser Thr Ala Ala Ser Ser His Arg  
 20                      25                      30  
 35 Arg Ser Glu His Met Arg Ser Ala Asp Ser Ser Pro Ala Tyr Ser Pro  
                                  35                      40                      45  
 Ile Gly Ser Leu Ser Ser Ser His Ser Phe Asp Ser Ile Pro Asp Gln  
 50                      55                      60  
 Arg Met Asn Lys Ser Leu Leu Ser Leu Ala Cys Leu Ile Leu Cys Gly  
 40 65                      70                      75                      80  
 Met Pro Ala Ile Ala Gln Gln Thr Gly Pro Ala Glu Arg Ser Gly Glu  
                                  85                      90                      95  
 Pro Ser Leu Ala Glu Arg Val Phe Gly Leu Glu Gln Lys Gln Lys Lys  
 100                      105                      110  
 45 Leu Lys Val Tyr Leu Gly Ile Gln Ser Phe Tyr Asp Gln Pro Leu Val  
                                  115                      120                      125  
 Asp Asp Glu Ser His Ile Gly His Phe Lys Val Gln Glu Leu Arg Met  
 130                      135                      140  
 50 Ser Ala His Gly Glu Leu Asn Arg His Leu Ser Phe Asp Trp Arg Gln  
 145                      150                      155                      160  
 Arg Leu Asn Arg Ala Ala Asp Gly Thr Ser Phe Ala Asp Asn Leu Ser  
                                  165                      170                      175  
 Asn Ala Ile Asp Ile Ala Gly Val Asp Trp His Pro Asn Asp Lys Val  
 180                      185                      190  
 55 Ser Phe Phe Phe Gly Arg Gln Tyr Ala Arg Phe Gly Gly Ile Glu Tyr  
                                  195                      200                      205  
 Asp Met Asn Pro Val Glu Ile Tyr Gln Tyr Ser Asp Leu Val Asp Tyr  
 210                      215                      220  
 60 Met Thr Cys Tyr Thr Ser Gly Val Asn Phe Ala Trp Asn Phe His Pro  
 225                      230                      235                      240  
 Glu Gln Gln Leu Gln Leu Gln Val Leu Asn Ala Tyr Asn Asn Arg Phe  
                                  245                      250                      255  
 Ala Asp Arg Tyr His Val Thr Pro Asp Val Ala Thr Ala Thr Ser Tyr  
 260                      265                      270  
 65 Pro Leu Leu Tyr Ser Ala Gln Trp Asn Gly Thr Leu Leu Gly Gly Ala  
                                  275                      280                      285  
 Leu His Met Arg Tyr Ala Val Ser Met Ala His Gln Ala Gln Glu Arg  
 290                      295                      300  
 70 Asn Met Trp Tyr Phe Thr Ala Gly Asn Leu Phe Asn Pro Gly Lys Arg  
 305                      310                      315                      320  
 Ile Asn Gly Tyr Leu Asp Leu Thr Tyr Ser Ile Glu Gly Leu Asp Asp  
                                  325                      330                      335  
 Lys Gly Ile Met Thr Ala Arg Tyr Gly Lys Gly Lys Thr Leu Thr Asp  
 340                      345                      350  
 75 Val Lys Tyr Tyr Ala Leu Val Ser Lys Trp Asn Phe Arg Ile Phe Asp

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355                      360                      365  
 Gln Val Asn Leu Phe Leu Lys Gly Met Tyr Glu Asn Gly Tyr Ala Pro  
 370                      375                      380  
 5    Ala Gln Tyr Gly Glu Ser Ser His Thr Arg His Ser Tyr Gly Tyr Met  
 385                      390                      395                      400  
 Gly Gly Val Glu Tyr Tyr Pro Thr Glu Thr Asn Phe Arg Leu Phe Val  
 405                      410                      415  
 Thr Tyr Ile Gly Arg His Tyr Arg Tyr Ser Ala Thr Glu Thr Glu Ser  
 420                      425                      430  
 10   Thr Asn Ala Leu Arg Ala Gly Leu Ile Tyr Gln Ile Pro Phe Leu  
 435                      440                      445

(2) INFORMATION FOR SEQ ID NO:358

- 15    (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 227 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear  
 20    (ii) MOLECULE TYPE: protein  
       (iii) HYPOTHETICAL: YES  
 25    (vi) ORIGINAL SOURCE:  
       (A) ORGANISM: Porphyromonas gingivalis  
       (ix) FEATURE:  
           (A) NAME/KEY: misc feature  
           (B) LOCATION 1...227  
 30    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:358

Tyr Lys Gln Ala Ile Met Lys His Leu Phe Lys Ser Thr Leu Val Leu  
 1                      5                      10                      15  
 35    Leu Cys Ala Leu Ser Phe Ser Gly Thr Tyr Thr Phe Ala Gln Glu Asn  
                     20                      25                      30  
 Asn Thr Glu Lys Ser Arg Phe Asp Phe Ser Val Arg Leu Gly Gln Gly  
                     35                      40                      45  
 40    Tyr Ile Ala Gly Ser Thr Thr Asn Leu Met Tyr Gly Tyr Thr Ser Ala  
                     50                      55                      60  
 Asn Asp Arg Leu Leu Ser Gly Ala Ile Tyr Leu Gly Leu Thr Pro Ser  
                     65                      70                      75                      80  
 Lys Lys Glu Asn Ala Thr Gly Val Ala Phe Arg Phe Leu Ser Pro Ser  
                     85                      90                      95  
 45    Pro Gly Tyr Tyr Val Asp Ile Ser Gly Lys Glu Asn Thr Leu Asn Tyr  
                     100                      105                      110  
 Ala Phe Tyr Val Val Gly Ala Tyr Asn Arg Ile Ala Ile Pro Ile Arg  
                     115                      120                      125  
 50    Pro Ile Lys Asn Phe Asn Phe Ile Phe Ser Thr Glu Val Gly Met Ala  
                     130                      135                      140  
 Trp Met Ser Arg His Glu Gln Ile Tyr Asn Ser Thr Ser Gln Thr Trp  
                     145                      150                      155                      160  
 Asp Lys Gln Arg Lys Ser Arg Ser Gly Leu Asp Phe Gly Leu Gly Met  
                     165                      170                      175  
 55    His Leu Gln Unk His Ile Asn Lys Thr Val Tyr Phe Met Ala Gly Thr  
                     180                      185                      190  
 Asp Leu Thr Ser Cys Met Phe Gly Lys Arg Ile Asn Asp Tyr Gln Gln  
                     195                      200                      205  
 60    Lys Asp Arg Thr Phe Ile Ala Leu Ile Asp Asn Ser Ile Gly Ile Gly  
                     210                      215                      220  
 Leu Asn Leu  
 225

(2) INFORMATION FOR SEQ ID NO:359

- 65    (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 406 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear  
 70    (ii) MOLECULE TYPE: protein  
       (iii) HYPOTHETICAL: YES  
 75    (vi) ORIGINAL SOURCE:

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(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1...406

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359

10 Ile Phe Ile Asp Pro Asp Lys Asn Thr Lys Gln Asn Glu Arg Asn Met  
 1 5 10 15  
 Ile Ile Lys Lys Met Leu Lys Asn Lys Leu Ala Pro Leu Ala Ile Leu  
 20 25 30  
 Phe Leu Phe Ala Pro Lys Ala Met Lys Ala Gln Glu Gln Leu Asn Val  
 35 40 45  
 15 Val His Thr Ser Val Pro Ser Leu Asn Ile Ser Pro Asp Ala Arg Ala  
 50 55 60  
 Ala Gly Met Gly Asp Ile Gly Val Ala Thr Thr Pro Asp Ala Tyr Ser  
 65 70 75 80  
 20 Gln Tyr Trp Asn Pro Ser Lys Tyr Ala Phe Met Asp Thr Lys Ala Gly  
 85 90 95  
 Ile Ser Phe Ser Tyr Thr Pro Trp Leu Ser Lys Leu Val Asn Asp Ile  
 100 105 110  
 Ala Leu Met Gln Met Thr Gly Phe Tyr Lys Leu Gly Thr Asp Glu Asn  
 115 120 125  
 25 Gln Ala Ile Ser Ala Ser Leu Arg Tyr Phe Thr Leu Gly Lys Leu Glu  
 130 135 140  
 Thr Phe Asp Glu Leu Gly Glu Ser Met Gly Glu Ala His Pro Asn Glu  
 145 150 155 160  
 Phe Ala Val Asp Leu Gly Tyr Ser Arg Gln Leu Ser Glu Asn Phe Ser  
 165 170 175  
 30 Met Ala Val Ala Leu Arg Tyr Ile Arg Ser Asp Gln Ser Thr His Asn  
 180 185 190  
 Thr Gly Glu Asn Gln Ala Gly Asn Ala Phe Ala Ala Asp Ile Ala Gly  
 195 200 205  
 35 Tyr Leu Gln Lys Tyr Val Leu Leu Gly Asn Ala Glu Ser Leu Trp Ser  
 210 215 220  
 Leu Gly Phe Asn Val Lys Asn Ile Gly Thr Lys Ile Ser Tyr Asp Gly  
 225 230 235 240  
 Gly Val Thr Ser Phe Phe Ile Pro Thr Ser Leu Asn Leu Gly Thr Gly  
 245 250 255  
 40 Leu Leu Tyr Pro Ile Asp Asp Tyr Asn Ser Ile Asn Phe Asn Leu Glu  
 260 265 270  
 Leu Ser Lys Leu Leu Val Pro Thr Pro Ile Met Asp Gln Asn Asp  
 275 280 285  
 45 Gln Ala Gly Tyr Glu Ala Ala Leu Lys Lys Tyr Gln Glu Thr Ser Ser  
 290 295 300  
 Ile Ser Gly Ile Phe Ser Ser Phe Gly Asp Ala Pro Gly Gly Leu Lys  
 305 310 315 320  
 Glu Glu Phe Arg Glu Ile Thr Trp Gly Leu Gly Ala Glu Tyr Ser Tyr  
 325 330 335  
 50 Asp Asp Lys Phe Phe Val Arg Ala Gly Tyr Ser Tyr Leu His Pro Thr  
 340 345 350  
 Lys Gly Asn Leu Gln Tyr Phe Thr Ala Gly Ala Gly Phe Lys Met Asn  
 355 360 365  
 55 Ile Phe Arg Ile Asp Ala Ser Tyr Leu Leu Ser Thr Ile Gln Ser Asn  
 370 375 380  
 Pro Leu Asp Gln Thr Leu Arg Phe Thr Leu Ala Phe Asp Met Asp Gly  
 385 390 395 400  
 60 Leu Arg Asn Leu Phe His  
 405

(2) INFORMATION FOR SEQ ID NO:360

65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 452 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

70 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

75 (A) ORGANISM: Porphyromonas gingivalis

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## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...452

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:360

```

Leu Ile Ile Glu Lys Glu Met Lys Thr Thr Val Gln Gln Ile Ile Leu
1      5      10      15
Cys Leu Ala Leu Met Met Ser Gly Val Leu Gly Gly Asn Ala Gln Ser
10     20     25     30
Phe Trp Glu Glu Ile Ala Pro Pro Phe Ile Ser Asn Glu Pro Asn Val
35     40     45
Lys Tyr Ile Ile Pro Asn Met Gly Ile Asp Ser Lys Gly Thr Ile Tyr
50     55     60
Val Thr Val Thr Lys Arg Ile Gln Gln Gly Ala Asn Tyr Thr Ser Glu
15     65     70     75     80
Gln Leu Gly Met Tyr Tyr Arg Pro Leu Gly Asp Asn Glu Gln Trp Trp
85     90     95
Lys His Asp Pro Tyr Phe Asp Asp Lys Ile Val Ala Asp Ile Gln Thr
20     100    105    110
Asp Ala Tyr Gly Arg Val Tyr Val Cys Thr Thr Ser Ser Arg Asp Gln
115    120    125
Glu Tyr Gln Leu Tyr Ile Asn Glu Gln Asn Glu Trp Arg Cys Ile Phe
130    135    140
25 Lys Thr Ser Val Ser Thr Tyr Glu His Gly Met Ala Val Phe Arg Ser
145    150    155    160
Ser Thr Gly Val Thr Tyr Ile Gly Thr Arg His His Ile Phe Ala Ser
165    170    175
30 Gly Val Asn Asp Phe Glu Phe Asn Thr Ile Tyr Glu Asp Ser Thr Pro
180    185    190
Met Ser Cys Arg Phe Ala Glu Ala Thr Asn Ser Gly Thr Ile Tyr Leu
195    200    205
Ala Leu Met His Glu Thr Thr Met Ser Thr Thr Ile Leu Thr Tyr Gln
210    215    220
35 Asn Gly Glu Phe Val Asp Ile Ser Glu Ser Glu Leu Ser Asn Ser Ile
225    230    235    240
Ile Ala Ser Met Cys Ser Asn Lys Glu Gly Asp Ile Ile Ala Leu Val
245    250    255
40 Thr Ser Tyr Thr Gly Phe Met Ser Gly Thr Leu Ala Ile Arg Lys Ala
260    265    270
Asp Glu Gly Lys Trp Gln Leu Val Gly Gly Asp Ile Gln Asn Ala Ile
275    280    285
Val Gln Asn Ile Cys Met Met Asp Asp Asn Lys Ile Ala Cys Glu Val
290    295    300
45 Phe Gly Thr Pro Asn Gly Val Asp Gly Arg Thr Arg Val Cys Val Ser
305    310    315    320
Asp Ala Ser Val Phe Asp Phe Glu Trp Tyr Glu Asp Glu Ile Tyr Gly
325    330    335
50 Gly Leu Ile Phe Asp Thr Phe Phe Tyr Ser Pro Trp Asp Lys Leu Leu
340    345    350
Tyr Ala Lys Phe Gly Gly Ile Met Leu Arg Ser Lys Glu Ser Phe Ile
355    360    365
Thr Ser Phe Ile Ser Pro Thr Val Val Gln Gly Val Asp Val Tyr Thr
370    375    380
55 Leu Ala Gly Lys Ile Arg Ile Glu Ser Glu Thr Pro Val Ser Glu Val
385    390    395    400
Leu Leu Phe Asp Leu Ala Gly Arg Met Val Leu Arg Gln Thr Ile Asp
405    410    415
60 Asn Lys Ile Tyr Ser Asp Ile Asp Thr Asn Gly Leu Lys Arg Ser Gly
420    425    430
Ile Tyr Val Val Ser Val Arg Leu Ser Ser Gly Gln Val Phe Ser His
435    440    445
Lys Val Gln Val
450

```

65

## (2) INFORMATION FOR SEQ ID NO:361

## (i) SEQUENCE CHARACTERISTICS:

```

70 (A) LENGTH: 331 amino acids
    (B) TYPE: amino acid
    (D) TOPOLOGY: linear

```

## (ii) MOLECULE TYPE: protein

75

## (iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

5 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...331

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:361

Gly Leu Tyr Gly Met Ser Val Val Pro Ile Ile Ile Tyr Leu Cys Gly  
1 5 10 15  
Ile Ser Asn Tyr Ala Arg Leu Met Ile Ile Arg Cys Leu Ile Arg Arg  
20 25 30  
15 Pro Arg Thr Val Leu Phe Gly Leu Ile Phe Val Val Gly Leu Phe Ser  
35 40 45  
Ala Met Ala Gln Glu Lys Lys Asp Ser Leu Ser Thr Val Gln Pro Val  
50 55 60  
20 Pro Asn Ser Ser Met Val Glu Gln Thr Pro Leu Leu Ser Ile Asp His  
65 70 75 80  
Pro Val Leu Pro Ala Ser Phe Gln Asn Thr Arg Thr Leu Lys Arg Phe  
85 90 95  
Arg Asp Lys His Leu Ser Asp Ala Leu Leu Asn Gly Leu Lys Pro His  
100 105 110  
25 Arg Ser Ser Leu Gln Leu Asn Glu Leu Asn Phe Ala Ala Glu Arg  
115 120 125  
Arg Asp Phe Val Ser Pro Leu Leu Gln Thr Arg His Ala Ala Gly Val  
130 135 140  
30 Leu Ser Trp Arg Pro Thr Asp Arg Met His Phe Tyr Thr Ser Gly Asn  
145 150 155 160  
Ile Gly Leu Gly His Asp Leu Leu Thr Gly Val Arg Lys Asp Phe Gly  
165 170 175  
Trp Asn Ala Gly Ala Asp Phe Leu Leu Ser Gln Asn Leu Thr Ala His  
180 185 190  
35 Val Gln Gly Gly Trp Gln Gln Asn Phe Gly Phe Ile Pro Met Thr Ala  
195 200 205  
Val Asn Gly Gln Leu Arg Trp Gln Ala Thr Glu Arg Leu Ser Phe Thr  
210 215 220  
40 Thr Gly Ile Asp Tyr Arg Gln Val Gln Trp Asn Ala Phe Asp Asn Arg  
225 230 235 240  
Thr Phe Ser Leu Lys Gly Ser Ala Arg Tyr Glu Val Met Asp Asn Val  
245 250 255  
Phe Val Asn Gly Phe Gly Ser Tyr Pro Leu Tyr Ser Ser Thr Arg Ser  
260 265 270  
45 Gly Leu Asn Met Ala Val Pro Met His Gly Phe Gly Pro Gln Tyr Gly  
275 280 285  
Gly Ser Leu Glu Leu Lys Val Ser Glu Arg Phe Gly Phe Ala Val Gly  
290 295 300  
50 Met Glu Arg Glu Tyr Asn Ile Trp Thr Arg Arg Trp Glu Thr His Tyr  
305 310 315 320  
Phe Ala Tyr Pro Val Phe Tyr Gly Asp Lys Lys  
325 330

55 (2) INFORMATION FOR SEQ ID NO:362

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 329 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

65 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

70 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362

75 Glu Thr Asn Ser Trp Val Ser Ser Asp Cys Asn Ser Thr Thr Met Lys  
1 5 10 15

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Thr Asn Arg Arg Tyr Ala Phe Val Leu Pro Leu Leu Leu Leu Thr Gly  
 20 25 30  
 Leu Leu Ala Trp Gly Gln Asp Ser Ser His Gly Ser Asn Thr Ala Phe  
 35 40 45  
 5 Ala Thr Asp Ser Ser Ser Arg Glu Leu Pro Thr Glu Gln Ser Ala Tyr  
 50 55 60  
 Arg Ile His Ser Ala Tyr Met Val Gly Gly Gly Ser Ile Thr Arg  
 65 70 75 80  
 10 Asp Thr Tyr Leu Ser Pro Leu Arg Tyr Gly Gly Trp Thr Leu Asn Leu  
 85 90 95  
 Leu Gly Glu Lys Thr Phe Pro Leu Lys Ala Ser Asp Ser Arg Trp Met  
 100 105 110  
 Ile Arg Thr Gly His Glu Leu Asp Phe Ala Leu Met Asp Asn Pro Ala  
 115 120 125  
 15 Asn Asn Ala His Phe Tyr Ser Leu Leu Tyr Asn Gly Ser Ala Ala Ala  
 130 135 140  
 Leu Tyr Arg Leu Gly Ala Lys His Leu Arg Ala Ala Trp Met Asp Asn  
 145 150 155 160  
 20 Leu Arg Leu Ala Phe Gly Pro Gly Leu Glu Ile Gly Leu Gly Gly Ile  
 165 170 175  
 Tyr Ser Thr Arg Asn Gly Asn Asn Pro Ala Thr Leu Lys Leu Tyr Thr  
 180 185 190  
 Asn Ala Ile Ala Gln Ala Ser Ile Gly Tyr Tyr Val Pro Ser Glu Thr  
 195 200 205  
 25 Phe Pro Leu Tyr Phe Arg Leu Leu Ser Gln Ile Asn Leu Phe Gly Ile  
 210 215 220  
 Ala Tyr Gly Asn Gly Phe Gly Glu Ser Tyr Tyr Glu Asn Phe Leu Leu  
 225 230 235 240  
 30 Asn Asn Gly Ile Ala Gly Ser Leu His Phe Thr Tyr Pro Gly Lys Phe  
 245 250 255  
 Thr Arg Phe Thr Thr Leu Ile Thr Ala Asp Ile Pro Ile Arg Asn Phe  
 260 265 270  
 Cys Thr Leu Arg Val Gly Tyr Arg Tyr Ser His Leu Gly Ser Ser Leu  
 275 280 285  
 35 Asn Ala Leu Asp Thr Arg Ile His Ser His Thr Ala Phe Ile Gly Phe  
 290 295 300  
 Val Thr Glu Phe Tyr Arg Phe Arg Gly Arg Lys Ala Met Asn Thr Gly  
 305 310 315 320  
 40 Arg Arg Thr Ser Leu Tyr Tyr His Asp  
 325

(2) INFORMATION FOR SEQ ID NO:363

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 319 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
  
 50 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 55 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...319  
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:363

Phe Thr Ser Gly Thr Ile Phe Val Arg Ile Ala Ile Ser Gly Arg Val  
 1 5 10 15  
 65 Val Cys Arg Glu Val Glu Asp Asn Gly Arg Arg Glu Ala Val Arg His  
 20 25 30  
 Asp Gly Met Val Val Thr Leu Leu Val Ile Val Gly Ile Val Val Val  
 35 40 45  
 Val Arg Tyr Ser Leu Arg Val His Val His Lys Thr Gly Thr Val Val  
 50 55 60  
 70 Ser Ala Ala Ile Phe Gly Phe Ile Leu Leu Gly Lys Thr Val Pro Cys  
 65 70 75 80  
 Asp Thr Arg Asn Phe Phe Ser Ser Glu Ser Asp Glu Pro Glu Ser Arg  
 85 90 95  
 75 Val Ala Thr Glu Ile Ala His Leu Cys Glu Ile Gly Phe Gln Ile His  
 100 105 110

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Ala Ser Ser Ile His Val Ala Val Arg Thr Asp Phe Gly Gln Ala Gly  
 115 120 125  
 Ile His Cys Pro Met Ala Thr Asp Ala Ser Ala Thr Glu Phe Asp Arg  
 130 135 140  
 5 Ser Ala Glu Cys Ala Glu Arg Thr Ser Ala Gln Ile Asp Thr Ala Ile  
 145 150 155 160  
 Arg Ser Gln Ser Gln Ile Ile Arg Thr His Ile Asp Thr Cys Pro Lys  
 165 170 175  
 10 Ser Ser Gly Thr Ile Gly Gly Ser Thr His Thr Ser Leu His Leu Lys  
 180 185 190  
 Val Phe Asp Gly Arg Gly Glu Val Gly His Ile His Pro Lys Asp Gly  
 195 200 205  
 Leu Arg Phe Gly Val Val Glu Gly Tyr Ser Ile Gly Ser Tyr Val Asp  
 210 215 220  
 15 Ala Ile Gly Ile Gly Ala Thr His Ala Lys Ala Gly Ile Ser Asp Thr  
 225 230 235 240  
 Arg Thr Gly Ile Ala Gly Gly Tyr His Gly Gly Ser Gln His Gln Gln  
 245 250 255  
 20 Ile Gly Asp Val Thr Thr Ile Ile Gly Leu Gly Lys Phe Gly Leu Ala  
 260 265 270  
 Asn Val Gly Val Ser Asp Arg Gly Phe Arg Arg Gly Ala Ser Ser Tyr  
 275 280 285  
 Asp Leu Tyr Gly Leu Glu Leu His Ile Ala Lys Thr Ile Tyr Leu Ala  
 290 295 300  
 25 Val Gly Asp Gly Cys Leu Cys Arg Gln Ala Glu Arg Gln Asp Gly  
 305 310 315

(2) INFORMATION FOR SEQ ID NO:364

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 614 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 40 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...614
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:364

Pro Tyr Asn Val Gln Ser Ile Ser Asn Lys Thr Ile Lys Lys Gln Met  
 1 5 10 15  
 50 Glu Asn Leu Lys Asn Ile Gln Pro Arg Glu Asp Phe Asn Trp Glu Glu  
 20 25 30  
 Phe Glu Ala Gly Gly Val His Ala Ala Val Ser Arg Gln Glu Gln Glu  
 35 40 45  
 55 Ala Ala Tyr Asp Lys Thr Leu Asn Thr Ile Lys Glu Lys Glu Val Val  
 50 55 60  
 Met Gly Arg Val Thr Ala Ile Asn Lys Arg Glu Val Val Ile Asn Val  
 65 70 75 80  
 Gly Tyr Lys Ser Glu Gly Val Val Pro Ala Thr Glu Phe Arg Tyr Asn  
 85 90 95  
 60 Pro Glu Leu Lys Val Gly Asp Glu Val Glu Val Tyr Ile Glu Asn Gln  
 100 105 110  
 Glu Asp Lys Lys Gly Gln Leu Val Leu Ser His Arg Lys Gly Arg Ala  
 115 120 125  
 65 Ala Arg Ser Trp Glu Arg Val Asn Glu Ala Leu Glu Lys Asp Glu Ile  
 130 135 140  
 Val Lys Gly Tyr Val Lys Cys Arg Thr Lys Gly Gly Met Ile Val Asp  
 145 150 155 160  
 Val Phe Gly Ile Glu Ala Phe Leu Pro Gly Ser Gln Ile Asp Val Arg  
 165 170 175  
 70 Pro Ile Arg Asp Tyr Asp Ala Phe Val Glu Lys Thr Met Glu Phe Lys  
 180 185 190  
 Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val Val Ser His Lys  
 195 200 205  
 75 Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys Glu Ile Ile Gly  
 210 215 220

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Lys Leu Glu Lys Gly Gln Val Leu Glu Gly Ile Val Lys Asn Ile Thr  
 225 230 235 240  
 Ser Tyr Gly Val Phe Ile Asp Leu Gly Gly Val Asp Gly Leu Ile His  
 245 250 255  
 5 Ile Thr Asp Leu Ser Trp Gly Arg Val Ala His Pro Glu Glu Ile Val  
 260 265 270  
 Gln Leu Asp Gln Lys Ile Asn Val Val Ile Leu Asp Phe Asp Glu Asp  
 275 280 285  
 10 Arg Lys Arg Ile Ala Leu Gly Leu Lys Gln Leu Met Pro His Pro Trp  
 290 295 300  
 Asp Ala Leu Asp Ser Glu Leu Lys Val Gly Asp Lys Val Lys Gly Lys  
 305 310 315 320  
 Val Val Val Met Ala Asp Tyr Gly Ala Phe Val Glu Ile Ala Gln Gly  
 325 330 335  
 15 Val Glu Gly Leu Ile His Val Ser Glu Met Ser Trp Thr Gln His Leu  
 340 345 350  
 Arg Ser Ala Gln Asp Phe Leu His Val Gly Asp Glu Val Glu Ala Val  
 355 360 365  
 20 Ile Leu Thr Leu Asp Arg Glu Glu Arg Lys Met Ser Leu Gly Leu Lys  
 370 375 380  
 Gln Leu Lys Pro Asp Pro Trp Ala Asp Ile Glu Thr Arg Phe Pro Val  
 385 390 395 400  
 Gly Ser Arg His His Ala Arg Val Arg Asn Phe Thr Asn Phe Gly Val  
 405 410 415  
 25 Phe Val Glu Ile Glu Glu Gly Val Asp Gly Leu Ile His Ile Ser Asp  
 420 425 430  
 Leu Ser Trp Thr Lys Lys Ile Lys His Pro Ser Glu Phe Thr Glu Val  
 435 440 445  
 30 Gly Ala Asp Ile Glu Val Gln Val Ile Glu Ile Asp Lys Glu Asn Arg  
 450 455 460  
 Arg Leu Ser Leu Gly His Lys Gln Leu Glu Glu Asn Pro Trp Asp Val  
 465 470 475 480  
 Phe Glu Thr Val Phe Thr Val Gly Ser Ile His Glu Gly Thr Val Ile  
 485 490 495  
 35 Glu Val Met Asp Lys Gly Ala Val Val Ser Leu Pro Tyr Gly Val Glu  
 500 505 510  
 Gly Phe Ala Thr Pro Lys His Met Val Lys Glu Asp Gly Ser Gln Ala  
 515 520 525  
 40 Val Leu Glu Glu Lys Leu Pro Phe Lys Val Ile Glu Phe Asn Lys Asp  
 530 535 540  
 Ala Lys Arg Ile Ile Val Ser His Ser Arg Val Phe Glu Asp Glu Gln  
 545 550 555 560  
 Lys Met Ala Gln Arg Glu Ala Asn Ala Glu Arg Lys Ala Glu Ala Lys  
 565 570 575  
 45 Ala Ala Gln Lys Glu Ala Ala Ala Glu Ala Ala Asn Pro Ala Gln Ala  
 580 585 590  
 Val Glu Lys Ala Thr Leu Gly Asp Leu Gly Glu Leu Ala Ala Leu Lys  
 595 600 605  
 50 Glu Lys Leu Ser Glu Asn  
 610

## (2) INFORMATION FOR SEQ ID NO:365

- 55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 243 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 60 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Porphyromonas gingivalis*  
 65 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...243  
 70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:365

Ser Thr Ile Met Lys Lys Ala Ile Leu Ser Gly Ala Ala Leu Leu Leu  
 1 5 10 15  
 Gly Leu Cys Ala Asn Ala Gln Asn Val Gln Leu His Tyr Asp Phe Gly  
 20 25 30

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His Ser Ile Tyr Asp Glu Leu Asp Gly Arg Pro Lys Leu Thr Thr Thr  
 35 40 45  
 Val Glu Asn Phe Thr Pro Asp Lys Trp Gly Ser Thr Phe Phe Phe Ile  
 50 55 60  
 5 Asp Met Asp Tyr Thr Gly Lys Gly Ile Gln Ser Ala Tyr Trp Glu Ile  
 65 70 75 80  
 Ser Arg Glu Leu Lys Phe Trp Gln Ala Pro Val Ser Ile His Leu Glu  
 85 90 95  
 10 Tyr Asn Gly Gly Leu Ser Thr Ser Phe Thr Phe Gly His Asp Ala Leu  
 100 105 110  
 Ile Gly Ala Thr Tyr Thr Tyr Asn Asn Pro Ser Phe Thr Arg Gly Phe  
 115 120 125  
 Thr Ile Thr Pro Met Tyr Lys His Leu Gly Ala His Asp Phe His Thr  
 130 135 140  
 15 Tyr Gln Ile Thr Gly Thr Trp Tyr Met His Phe Leu Asp Gly Leu Leu  
 145 150 155 160  
 Thr Phe Asn Gly Phe Leu Asp Leu Trp Gly Phe Pro Gln Glu Asn Pro  
 165 170 175  
 20 Ile Gly Gly Pro Val Leu Lys Glu Gly Asp Lys Phe Val Phe Leu Ser  
 180 185 190  
 Glu Pro Gln Phe Trp Ile Asn Leu Asn Arg Ile Lys Gly Ile Asp Lys  
 195 200 205  
 Asp Phe Asn Leu Ser Ile Gly Thr Glu Met Glu Ile Ser Arg Asn Phe  
 210 215 220  
 25 Ala Arg Met Asp Lys Phe Ser Cys Ile Pro Thr Leu Ala Val Lys Trp  
 225 230 235 240  
 Thr Phe Asn

30 (2) INFORMATION FOR SEQ ID NO:366  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 235 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 35  
 (ii) MOLECULE TYPE: protein  
 40 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 45 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...235  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:366  
 50 Met Lys Thr Ile Ser Lys Asn His Ala Ala Arg Ile Cys Ala Ala Ile  
 1 5 10 15  
 Ala Leu Phe Ala Val Cys Asn Gly Arg Ile Ala Ala Gln Asp Phe Leu  
 20 25 30  
 55 Tyr Glu Ile Gly Gly Gly Phe Gly Ala Ala Gln Tyr Phe Gly Asp Ala  
 35 40 45  
 Asn Arg Gly Leu Phe Gly Ser Ser Gly Val Gly Leu Glu Leu Val Gly  
 50 55 60  
 Arg Tyr Asn Tyr Asn Phe Arg Trp Ala Phe Ser Thr Met Leu Asp Trp  
 65 70 75 80  
 60 Arg Thr Leu Arg Gly Asp Thr Asp Lys Ser Gly Asn Val Phe Pro Asp  
 85 90 95  
 Phe Ala Gln Ala Asp Phe Lys Val Gly Leu Thr Gln Leu His Val Arg  
 100 105 110  
 65 Ser Glu Phe Asn Phe Leu Pro Tyr Ser Asp Gly Tyr Lys Tyr Leu Gly  
 115 120 125  
 Thr Ala Arg Leu Ser Pro Tyr Val Ala Ala Gly Leu Ser Leu Gly Phe  
 130 135 140  
 Ala Ser Gly Ala Lys Gly Ser Ala Phe Ala Pro Gly Ile Thr Ala Gly  
 145 150 155 160  
 70 Met Gly Val Lys Tyr Lys Leu Lys Pro Arg Ile Asn Val Gly Ile Glu  
 165 170 175  
 Tyr Ser Phe Thr Gly Leu Leu Thr Asp Ala Leu Asp Ala Leu Thr Asp  
 180 185 190  
 75 Lys Ser Val Trp Leu Glu Asp Pro Tyr Lys Ile Asn Asp Ser Trp Val  
 195 200 205

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Lys Asn Lys Asp Ala Thr Gly Ala Leu Val Leu Arg Ile Thr Tyr Asp  
 210 215 220  
 Phe Gly Leu Arg Lys Thr Phe Cys Asn Lys Gln  
 225 230 235

5

(2) INFORMATION FOR SEQ ID NO:367

(1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 436 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

15

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

20

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...436

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367

Asn Ile Met Tyr Lys Asp Tyr Lys Gly Leu Tyr Ala Ser Leu Arg Trp  
 1 5 10 15  
 Tyr Ala Leu Ile Ile Gly Leu Leu Phe Ala Ala Asp Gly Ile Gln Ala  
 20 25 30  
 Gln Asn Asn Asn Phe Thr Glu Ser Pro Tyr Thr Arg Phe Gly Leu Gly  
 35 40 45  
 Arg Leu Gly Glu Arg Thr Thr Ile Ser Gly His Ser Met Gly Gly Leu  
 50 55 60  
 Gly Val Gly Leu Arg Gln Gly Thr Tyr Val Asn Ala Val Asn Pro Ala  
 65 70 75 80  
 Ser Tyr Ser Ala Val Asp Ser Met Thr Phe Ile Phe Asp Phe Gly Ala  
 85 90 95  
 Ser Thr Gly Ile Thr Trp Tyr Ala Glu Asn Gly Lys Lys Asp Asn Arg  
 100 105 110  
 Lys Met Gly Asn Ile Glu Tyr Phe Ala Met Leu Phe Pro Ile Ser Lys  
 115 120 125  
 Ser Ile Ala Met Ser Ala Gly Val Leu Pro Tyr Ser Ala Ser Gly Tyr  
 130 135 140  
 Gln Phe Gly Ser Val Asp Gln Val Glu Gly Gly Ser Val Gln Tyr Thr  
 145 150 155 160  
 Arg Lys Tyr Leu Gly Thr Gly Asn Leu Asn Asp Leu Tyr Val Gly Ile  
 165 170 175  
 Gly Ala Thr Pro Phe Lys Asn Phe Ser Ile Gly Ala Asn Ala Ser Ser  
 180 185 190  
 Leu Phe Gly Arg Phe Thr His Ser Arg Gln Val Ile Phe Ser Thr Glu  
 195 200 205  
 Ala Pro Tyr Asn Pro Val His Leu Ser Thr Leu Tyr Leu Lys Ala Ala  
 210 215 220  
 Lys Phe Asp Phe Gly Met Gln Tyr His Leu Leu Lys Ser Asp Arg  
 225 230 235 240  
 Ser Leu Val Ile Gly Ala Val Tyr Ser Pro Arg Val Lys Met His Ser  
 245 250 255  
 Glu Leu Thr Gln Ile Lys Asn Gln Val Gln Asn Gly Val Val Val Glu  
 260 265 270  
 Ser Glu Thr Gln Glu Tyr Ile Lys Gly Met Asp Tyr Tyr Thr Leu Pro  
 275 280 285  
 His Thr Leu Gly Ile Gly Phe Ser Tyr Glu Lys Lys Asp Lys Leu Leu  
 290 295 300  
 Leu Gly Ala Asp Val Gln Tyr Ser Lys Trp Lys Gly Glu Lys Phe Tyr  
 305 310 315 320  
 Lys Ser Asp Cys Lys Phe Gln Asp Arg Ile Arg Val Ser Leu Gly Gly  
 325 330 335  
 Glu Ile Ile Pro Asp Ile Asn Ala Val Gly Met Trp Pro Lys Val Arg  
 340 345 350  
 Tyr Arg Phe Gly Leu His Gly Glu Asn Ser Tyr Leu Lys Val Pro Thr  
 355 360 365  
 Lys Gly Gly Val Tyr Gln Gly Tyr His Ile Val Gly Ala Val Phe Gly  
 370 375 380  
 Ile Gly Ile Pro Leu Asn Asp Arg Arg Ser Phe Val Asn Val Ser Leu  
 385 390 395 400

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Glu Tyr Asp Arg Leu Ile Pro Lys Glu Gly Met Ile Lys Glu Asn Ala  
 405 410 415  
 Leu Lys Leu Thr Phe Gly Leu Thr Phe Asn Glu Ser Trp Phe Lys Lys  
 420 425 430  
 5 Leu Lys Leu Asn  
 435

(2) INFORMATION FOR SEQ ID NO:368

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 945 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES
- 20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...945
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:368

Asn Thr Ile Ser Glu Asn Gly Asn Asp Ser Thr Tyr Phe Ser Phe Gln  
 1 5 10 15  
 30 Thr Phe Leu Met Arg Ser Ile Tyr Gln Leu Leu Ser Ile Leu Leu  
 20 25 30  
 Ala Ser Leu Gly Phe Val Gly Leu Glu Ala Gln Gln Ala Gly Val Ala  
 35 40 45  
 35 Gly Arg Val Leu Asp Glu Gly Asn Pro Met Ile Gln Ala Asn Val  
 50 55 60  
 Gln Leu Val Gln Ser Thr Gly Gln Val Ala Val Ala Ala Gly Ala Thr  
 65 70 75 80  
 Asn Glu Lys Gly Leu Phe Ser Leu Lys Thr Ser Gln Glu Gly Asp Tyr  
 85 90 95  
 40 Ile Leu Arg Val Ser Tyr Val Gly Tyr Thr Thr His Asp Glu Lys Ile  
 100 105 110  
 Ser Leu Arg Asn Gly Gln Thr Ile Thr Leu Lys Asp Ile Ser Met Asn  
 115 120 125  
 45 Glu Asp Ala Arg Leu Leu Gln Ser Val Thr Val Gln Ala Lys Ala Ala  
 130 135 140  
 Glu Val Val Val Arg Asn Asp Thr Leu Glu Phe Asn Ala Gly Ser Tyr  
 145 150 155 160  
 Thr Val Ala Gln Gly Ala Ser Ile Glu Glu Leu Ile Lys Lys Leu Pro  
 165 170 175  
 50 Gly Ala Glu Ile Gly Ser Asp Gly Lys Ile Thr Ile Asn Gly Lys Asp  
 180 185 190  
 Ile Ser Lys Ile Leu Val Asp Gly Lys Glu Phe Phe Ser Lys Asp Pro  
 195 200 205  
 55 Gln Val Ala Ile Lys Asn Leu Pro Ala Asp Met Val Asn Lys Val Gln  
 210 215 220  
 Val Leu Asn Lys Leu Ser Glu Leu Ser Arg Met Ser Gly Phe Asp Asp  
 225 230 235 240  
 Gly Glu Glu Glu Thr Val Ile Asn Leu Thr Val Lys Pro Glu Lys Lys  
 245 250 255  
 60 Lys Gly Leu Phe Gly Thr Leu Gln Ala Gly Tyr Gly Thr Asp Gln Arg  
 260 265 270  
 Tyr Met Ala Gly Gly Asn Val Asn Arg Phe Asp Gly Asn Lys Gln Trp  
 275 280 285  
 65 Thr Leu Ile Gly Ser Ala Asn Asn Thr Asn Asn Met Gly Phe Ser Glu  
 290 295 300  
 Met Asp Ser Glu Met Gly Ser Met Thr Phe Phe Ser Pro Gln Gly Gly  
 305 310 315 320  
 Gly Arg Arg Gly Phe Gly Asn Ser Gly Gly Val Thr Ser Ser Ser Met  
 325 330 335  
 70 Leu Gly Gly Asn Phe Ser Val Glu Phe Ser Ser Ala Leu Asn Thr Gly  
 340 345 350  
 Gly Asp Ala Arg Tyr Gly Tyr Asn Asp Lys Ala Ile Glu Thr Thr Lys  
 355 360 365  
 75 Arg Val Glu Asn Ile Leu Ala Glu Gly Asn Thr Tyr Met Asp Glu Asn  
 370 375 380

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 412 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

10 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...412

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:369

20 Gly Glu Tyr Pro Ala Asn Ser Asn Asp Lys Lys Glu Met Val Met Lys  
 1 5 10 15  
 Leu Ile Lys Arg Ser Leu Leu Leu Gly Ala Val Leu Leu Ile Thr  
 20 25 30  
 Leu Pro Ala Tyr Ser Gln Asn Asp Asp Ile Phe Glu Asp Asp Ile Tyr  
 35 40 45  
 25 Thr Ser Arg Lys Glu Ile Arg Lys Gln Asn Gln Val Lys Asp Trp Gln  
 50 55 60  
 Asn Gln Glu Asp Gly Tyr Gly Asp Asp Thr Glu Tyr Thr Val Ala Ser  
 65 70 75 80  
 30 Asp Arg Asp Ile Asp Ala Tyr Asn Arg Arg Asp Gly Gln Ser Tyr Asp  
 85 90 95  
 Gly Lys Lys Leu Ser Lys Asp Lys Lys Arg Asp Ser Thr Arg Ser Ser  
 100 105 110  
 Val Pro Gly Arg Tyr Ser Arg Arg Leu Ala Arg Phe Tyr Lys Pro Asn  
 115 120 125  
 35 Thr Ile Val Ile Ser Gly Ala Asp Asn Val Tyr Val Thr Asp Asp Gly  
 130 135 140  
 Glu Tyr Phe Val Tyr Gly Asp Glu Tyr Tyr Asp Asp Ala Ser Ser Val  
 145 150 155 160  
 40 Asn Ile Tyr Ile Asn Ser Pro Trp Cys Asp Pro Phe Pro Tyr Thr Ser  
 165 170 175  
 Trp Tyr Pro Ser Phe Ser Gly Trp Tyr Asn Tyr Thr Trp Asn Tyr Pro  
 180 185 190  
 Trp Phe Tyr Tyr Gly Ser His Ile Gly Trp Gly Gly Tyr Tyr Pro Gly  
 195 200 205  
 45 Tyr Asn Trp Tyr Trp Ser Tyr Tyr Asp Pro Phe Tyr Asn Pro Tyr  
 210 215 220  
 Gly Ile Gly Met Gly Trp Gly Tyr Pro Tyr Gly Trp Gly Ser Tyr Tyr  
 225 230 235 240  
 Gly Trp Gly Gly Tyr Pro Gly Val Ile His His Tyr His Tyr Pro  
 245 250 255  
 50 Lys Lys Thr Tyr Ser Asn Gly Gln His Ser Gly Ala Tyr Tyr Ser Tyr  
 260 265 270  
 Gly Arg Pro Asn Arg Ile Lys Gly Gly Thr Ser Gly Ala Lys Leu Gly  
 275 280 285  
 55 Thr Gly Arg Tyr Asp Arg Ile Gln Asn Ser Ser Ser Gln Lys Asn Lys  
 290 295 300  
 Phe Gly Leu Gln Ser Asn Lys Pro Asn Asn Asn Leu Gln Asn Val Lys  
 305 310 315 320  
 Ser Gly Arg Thr Gly Arg Ala Asn Arg Asp Arg Asn Ile Glu Thr Val  
 325 330 335  
 60 Thr Pro Asn Asn Gly Gln Lys Gln Asn Arg Pro Val Phe Gln Gln Asn  
 340 345 350  
 Gln Ser Gly Asn Asp Arg Pro Thr Gly Arg Asn Ile Arg Ser Glu Arg  
 355 360 365  
 65 Gln Gly Glu Asn Asn Asp Arg Thr Phe Ser Thr Pro Ser Arg Ser Asn  
 370 375 380  
 Ser Asn Gly Gly Phe Ser Thr Pro Ser Arg Ser Ser Ser Gly Ser Met  
 385 390 395 400  
 70 Ser Gly Gly Gly Gly Arg Ser Gly Arg Gly Arg Asn  
 405 410

(2) INFORMATION FOR SEQ ID NO:370

75 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 601 amino acids

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(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370

Ser Asn Ser Ser Ser His Lys Trp Leu Ile Tyr Tyr His Ile Glu Lys  
1 5 10 15  
Thr Lys Ser Ile Met Ile Arg Lys Leu Ile Leu Leu Ala Leu Met  
20 25 30  
Pro Val Ala Ser Val Ala Phe Ala Val Pro Thr Asp Ser Thr Glu Ser  
35 40 45  
Lys Asp Asn Arg Ile Leu Thr Ser Met Gln Ser Ser Ser Leu Asn Arg  
50 55 60  
Asp Asp Ala Pro Asp Lys Trp Gln Pro Met His Ala Asn Phe Ser Ile  
65 70 75 80  
Gln Ser Asp Met Leu Leu Ser Thr Ala Gln Lys Ser Lys Asn Thr Trp  
85 90 95  
Phe Gly Asn Ser Tyr Ile Met Gly Ile Ile Lys Asn Asn Tyr Leu Glu  
100 105 110  
Phe Gly Ala Arg Phe Glu Asp Leu Tyr Lys Pro Leu Pro Gly His Glu  
115 120 125  
Pro Glu Met Gly Arg Gly Val Pro His Met Tyr Val Lys Gly Ser Tyr  
130 135 140  
His Trp Ala Glu Leu Thr Met Gly Asp Phe Tyr Asp Gln Phe Gly Ser  
145 150 155 160  
Gly Met Val Phe Arg Thr Tyr Glu Glu Arg Asn Leu Gly Ile Asp Asn  
165 170 175  
Ala Val Arg Gly Gly Arg Ile Val Leu Thr Pro Phe Asp Gly Val Arg  
180 185 190  
Val Lys Gly Ile Ala Gly Gln Gln Arg Asn Tyr Phe Asp Arg Thr Gly  
195 200 205  
Lys Val Phe Asn Ser Gly Arg Gly Tyr Leu Leu Gly Ser Asp Leu Glu  
210 215 220  
Leu Asn Val Glu Arg Trp Ser Ser Ala Met Arg Asp Asn Asp Tyr His  
225 230 235 240  
Leu Ala Ile Gly Gly Ser Phe Val Ser Lys His Glu Ala Asp Glu Asp  
245 250 255  
Ile Phe Val Gly Val Gly Glu Asp Arg Lys Arg Leu Asn Leu Pro Leu  
260 265 270  
Asn Val Pro Ile Met Gly Leu Arg Thr Asn Phe Gln Lys Gly Gly Leu  
275 280 285  
Ala Leu Tyr Ala Glu Tyr Gly Tyr Lys Tyr Asn Asp Pro Ser Ala Asp  
290 295 300  
Asn Asp Tyr Ile Tyr His Asp Gly Gln Ala Ala Leu Leu Ser Ala Ser  
305 310 315 320  
Tyr Ser Lys Lys Gly Met Ser Ile Leu Leu Gln Ala Lys Arg Cys Glu  
325 330 335  
Asn Phe Ala Phe Arg Ser Lys Arg Ser Ala Gln Leu Thr Pro Leu Met  
340 345 350  
Ile Asn Tyr Met Pro Ala Phe Thr Gln Ala His Thr Tyr Thr Leu Ala  
355 360 365  
Ala Ile Tyr Pro Tyr Ala Thr Gln Pro Gln Gly Glu Trp Ala Phe Gln  
370 375 380  
Gly Glu Leu Arg Tyr Asn Phe Ala Arg Arg Thr Ala Leu Gly Gly Arg  
385 390 395 400  
Tyr Gly Thr Gly Leu Arg Ile Asn Val Ser His Val Arg Gly Leu Asp  
405 410 415  
Lys Lys Met Leu Lys Glu Asn Pro Asp Glu Leu Ile Gly Thr Asp Gly  
420 425 430  
Tyr Thr Val Ser Phe Phe Gly Met Gly Asp Leu Tyr Tyr Ser Asp Ile  
435 440 445  
Asp Val Glu Ile Thr Lys Lys Val Ser Pro Gly Phe Asn Phe Thr Leu  
450 455 460  
75 Thr Tyr Leu Asn Gln Ile Tyr Asn Asn Lys Val Leu His Gly Ala Ala

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465                      470                      475                      480  
 Gly Glu Lys Pro Glu Lys Ile Tyr Ala Asn Ile Phe Val Tyr Asp Gly  
                                  485                      490                      495  
 5    Lys Tyr Lys Leu Ser Asn Lys Val Ala Leu Arg Thr Glu Leu Gln Tyr  
                                  500                      505                      510  
 Leu His Thr Lys Gln Asp Gln Gly Asp Trp Ile Tyr Gly Met Ala Glu  
                                  515                      520                      525  
 Leu Ser Ile Leu Pro Ser Leu Met Leu Ser Leu Ser Glu Gln Tyr Asn  
                                  530                      535                      540  
 10    Ile Gly Glu Thr Lys Lys His Tyr Val Met Gly Ser Val Thr Tyr Thr  
                                  545                      550                      555                      560  
 His Gly Ala His Arg Val Ala Phe Ser Ala Gly Lys Thr Arg Ala Gly  
                                  565                      570                      575  
 15    Met Asn Cys Ser Gly Gly Val Cys Arg Val Val Pro Glu Thr Gln Gly  
                                  580                      585                      590  
 Phe Tyr Leu Ser Tyr Ser Thr Asn Leu  
                                  595                      600

(2) INFORMATION FOR SEQ ID NO:371

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371

40    Arg Gly Ser Ser Ser Gly Ile Ser Ala Arg Gly Arg Asp Met Arg Ser  
                                  5                      10                      15  
 Leu Phe Leu Ser Ala Leu Arg Ser Ser Ser Leu His Gly Ser Glu Arg  
                                  20                      25                      30  
 Arg Ser Arg Ile Ser Ser Ser Val Val Met Ser Ile Arg Gln Lys Ile  
                                  35                      40                      45  
 45    Arg Leu Phe His Leu Ser Val Cys Ala Gln Thr His Asp His Leu Ile  
                                  50                      55                      60  
 Glu Ile His Leu Val Cys Ile Glu Phe Gly Ala Ile Asp Thr Asp Glu  
                                  65                      70                      75                      80  
 50    Phe Arg Leu Ser Ser His Ala Tyr Thr Thr Ser Pro Thr His Thr Gly  
                                  85                      90                      95  
 Ala Ile His His Asn Cys Ile Glu Arg Ser Tyr Gly Arg Tyr Leu Val  
                                  100                      105                      110  
 Thr Phe Gly Gln Glu Arg Asn Glu Leu His His His Ser Arg Pro Asp  
                                  115                      120                      125  
 55    Arg Asn Ala Glu Val Tyr Arg Phe Pro Phe Asp Asn Ala Phe His Ser  
                                  130                      135                      140  
 Ile Arg Tyr Glu Ala Phe Arg Pro Ile Arg Pro Ile Val Cys His Asp  
                                  145                      150                      155                      160  
 60    Asp His Phe Ile Ala Ile Gly Ser His Leu Phe Phe Lys Asp Asn Gln  
                                  165                      170                      175  
 Ile Phe Ser Ser Gly Ser Gln Tyr Asp Asn Tyr Thr Val Ala Cys Phe  
                                  180                      185                      190  
 Val Glu Ser Leu His Asp Arg Glu Gln Arg Ser His Thr His Thr Ala  
                                  195                      200                      205  
 65    Ser Gly Thr Asn His Cys Ala Asp Leu Phe Asp Met Arg Thr Leu Ser  
                                  210                      215                      220  
 Gln Arg Thr Tyr His Ile Arg Asp Ile Val Ala Asp Phe Glu Phe Gly  
                                  225                      230                      235                      240  
 70    Gln Phe Leu Gly Arg Phe Ala His Gly Leu Asn His  
                                  245                      250

(2) INFORMATION FOR SEQ ID NO:372

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 790 amino acids

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(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372

Leu Leu Phe Ser Ser Pro Leu Pro Arg Met Asp Arg Pro Lys Pro Ser  
1 5 10 15  
Tyr Ile Val Arg Ile Ala Ala Ile Leu Cys Leu Phe Val Gly Arg Pro  
20 20 25 30  
Leu Phe Ala Gln Ser Tyr Val Asp Tyr Val Asp Pro Leu Ile Gly Thr  
35 40 45  
Leu Ser Ser Phe Glu Leu Ser Ala Gly Asn Thr Tyr Pro Val Ile Gly  
50 55 60  
Leu Pro Trp Gly Met Asn Ser Trp Thr Pro Met Thr Gly Val Pro Gly  
65 70 75 80  
Asp Gly Trp Gln Tyr Thr Tyr Ser Ala His Lys Ile Arg Gly Phe Lys  
85 90 95  
Gln Thr His Gln Pro Ser Pro Trp Ile Asn Asp Tyr Gly Gln Phe Ser  
100 105 110  
Leu Leu Pro Leu Thr Ala Pro Gln Lys Pro Ser Ser Asn Asp Ser Ile  
115 120 125  
Ala Leu Thr Lys Trp Cys Lys Gln Leu Phe Ser Asp Glu Gln Thr Ser  
130 135 140  
Trp Phe Ser His Lys Ala Glu Thr Ala Thr Pro Tyr Tyr Tyr Ser Val  
145 150 155 160  
Tyr Leu Ala Asp Tyr Asp Thr Arg Val Glu Met Ala Pro Thr Glu Arg  
165 170 175  
Ala Ala Ile Phe Arg Ile Arg Tyr Ser Gly Asn Thr Glu Ser Gly Ser  
180 185 190  
Gly Arg Trp Leu Arg Leu Asp Ala Phe Thr Gly Gly Ser Glu Ile Ser  
195 200 205  
Ile Val Asp Pro His Thr Val Val Gly Ile Ser Arg Lys Asn Ser Gly  
210 215 220  
Gly Val Pro Ala Asn Phe Ala Cys Tyr Phe Ile Leu Gln Ser Asp Thr  
225 230 235 240  
Pro Met Ala Asp Val Leu Leu Glu Thr Asp Thr Gly Lys Ser Asp Glu  
245 250 255  
Gly Thr Arg Ala Trp Ala Ala Cys Arg Phe Asp Ser Gln Glu Val Thr  
260 265 270  
Val Arg Val Ala Ser Ser Phe Ile Ser Val Glu Gln Ala Glu Arg Asn  
275 280 285  
Leu Ala Glu Val Lys Gly Gln Ser Phe Asp Arg Ile Arg Leu Ala Gly  
290 295 300  
Arg Glu Ala Trp Asn Lys Val Leu Gly Arg Ile His Val Glu Gly Gly  
305 310 315 320  
Thr Lys Asp Glu Arg Thr Thr Phe Tyr Ser Ala Leu Tyr Arg Cys Leu  
325 330 335  
Leu Phe Pro Arg Arg Phe Tyr Glu Glu Asp Ala Ser Gly Asn Phe Val  
340 345 350  
His Tyr Ser Pro Tyr Asn Gly Glu Val Leu Pro Gly Tyr Leu Tyr Thr  
355 360 365  
Asp Thr Gly Phe Trp Asp Thr Phe Arg Ala Leu Phe Pro Leu Leu Asn  
370 375 380  
Leu Leu Tyr Pro Asp Glu Asn Ile Lys Ile Gln Glu Gly Leu Leu Asn  
385 390 395 400  
Val Tyr Arg Glu Ser Gly Phe Phe Pro Glu Trp Ala Ser Pro Gly His  
405 410 415  
Arg Asp Cys Met Ile Gly Asn Asn Ser Ala Ser Val Leu Ala Asp Ala  
420 425 430  
Tyr Leu Lys Gly Val Arg Val Glu Asp Thr Arg Thr Leu Met Asn Gly  
435 440 445  
Leu Leu His Ala Thr Lys Ala Val His Pro Lys Ile Ser Ser Thr Gly  
450 455 460  
Arg Lys Gly Trp Glu Trp Tyr Asn Ser Leu Gly Tyr Val Pro Ala Asp



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100 105 110  
 Ala Gln Met Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala Asn  
 115 120 125  
 Leu Gln Gly Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln Glu  
 130 135 140  
 Asn Thr Ile Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile Asn  
 145 150 155 160  
 Thr Tyr Thr Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg Phe  
 165 170 175  
 10 Ala Asn Ile Leu Arg Thr Thr Gly Lys Val Leu Glu Glu Arg Asp Ile  
 180 185 190  
 Phe Lys Ile Asp Tyr Ala Glu Arg Leu Ser Ala Leu Ile Ile Gly Gln  
 195 200 205  
 15 Leu Val His Asp Phe Gly Lys Thr Thr Pro Ala Glu Leu Asp Ala Ile  
 210 215 220  
 Gly Phe Phe Asn Ala Glu Ile Gln Pro Asn Gly Asn Phe Met Ile  
 225 230 235 240  
 Asp Asp Lys Gly Leu Thr Tyr Cys Phe Asn Glu Tyr Gln Ile Ala Ala  
 245 250 255  
 20 Tyr Ala Arg Gly Ala Val Tyr Val Arg Leu Gly Tyr Asp Val Leu Ala  
 260 265 270  
 Pro Leu Leu Arg Asp Asp Ser Pro Leu Lys Arg Tyr Leu Pro  
 275 280 285  
 25 (2) INFORMATION FOR SEQ ID NO:374  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 378 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30  
 (ii) MOLECULE TYPE: protein  
 35 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 40 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...378  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:374  
 45 Gly Ile Ile Ser Val Leu Ser His Val Val Asp Arg Pro Gln Trp Gly  
 1 5 10 15  
 Ala Ser Pro Glu Ala Ala Gly Thr His Ser Val Tyr Ser Ile Leu His  
 20 25 30  
 50 Pro Ser Ala Gly Ile Ile Arg Ile Arg Ser Met Gly Ile Ile Ser Ala  
 35 40 45  
 Cys Arg Ile Ala Ile Leu Ala Gly Lys His Pro Arg Ser Gly Leu Ser  
 50 55 60  
 Arg Ala Asn Val Gly Ile Leu Ser Tyr Asn Pro Glu Asn Thr Pro Glu  
 65 70 75 80  
 55 Lys Lys Arg Lys Leu Gln Glu Lys Asn Val Phe Leu Gln Ile Arg Leu  
 85 90 95  
 Arg Gln Ser Phe Asn Asn Leu Ile Pro Ser Leu Pro Phe Arg Ile Asp  
 100 105 110  
 60 Asn Thr Lys Lys Ile Thr Glu Met Lys Lys Thr Thr Leu Thr Gly Ser  
 115 120 125  
 Ile Cys Ala Leu Leu Leu Phe Leu Gly Leu Ser Ala Asn Ala Gln Ser  
 130 135 140  
 Lys Leu Lys Ile Lys Ser Ile Glu Ala Ala Thr Thr Phe Ser Ser Ala  
 145 150 155 160  
 65 Thr Ala Gly Asn Gly Phe Gly Gly Asn Ile Phe Gly Met Asp Met Ser  
 165 170 175  
 Ile Arg Met Arg Val His His Ser Ile Leu Pro Glu Gly Leu Asp Phe  
 180 185 190  
 70 Ser Val Gly Ile His Glu Arg Arg Ala His Trp Glu Glu Ala Gly Ser  
 195 200 205  
 Pro Lys Leu Met Tyr Thr Asn Val Pro Ser Ile Ile Gly Ile Val Glu  
 210 215 220  
 Lys Val Ile Val Phe Glu Asp Ala Glu Asp Phe Phe Asp Lys Lys Ala  
 225 230 235 240  
 75 Leu Gly Arg Phe Leu Ile Ser Leu Gly Ile Ser Tyr Thr Lys His Leu

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245 250 255  
 Gly Ala Tyr Trp Gly Trp Thr Asn Asp Ala His Ile Leu Phe Ser Pro  
 260 265 270  
 5 Ile Pro Lys Ser Lys Val His Tyr Asp Thr Tyr Thr Arg Ala Gly Ser  
 275 280 285  
 Asp Leu Val Leu Gln Ser Glu Asp Val Ala Thr Val Ser Asn Gly Phe  
 290 295 300  
 Ser Pro Gly Ile Gly Leu Lys Ser Ser Ile Trp Trp Lys Met Pro Ile  
 305 310 315 320  
 10 Lys Ser Lys Tyr Asp Phe Arg Leu Gly Phe Ser Leu Gly Tyr Glu Tyr  
 325 330 335  
 Leu Asn Leu Leu Tyr Pro Tyr Arg Asn Phe Lys Leu Asp Gly Asn Lys  
 340 345 350  
 15 Pro Leu Ser Ala Leu Ser Pro Arg Met Asn His Ile Gly His Val Gly  
 355 360 365  
 Phe Asn Phe Thr Val Gly Leu Trp Thr Asn  
 370 375  
 (2) INFORMATION FOR SEQ ID NO:375  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1269 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1269  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:375  
 Val Lys Cys Met Gly Lys Tyr Lys Arg Ala Lys Tyr Arg Tyr Trp Leu  
 1 5 10 15  
 Phe Pro Phe Cys Ser Asp Tyr Tyr Thr Phe Glu Gly Val Thr Phe Leu  
 20 25 30  
 Cys Ala Ser Asp Asp Met Thr Thr Lys Lys Pro Gln Ala Ile Leu Asp  
 35 40 45  
 45 Leu Glu Lys Ala Tyr Asn Ile Glu Ile Pro Asp Leu Ser Ser Gln Glu  
 50 55 60  
 Gly Ile Ser Trp Ser Val Asn Arg Tyr Phe Lys Gln Asp Ser Ser Gly  
 65 70 75 80  
 50 Ala Val Val Glu Leu Cys Leu Arg Glu Cys Gln Ile Glu Ser Met Thr  
 85 90 95  
 55 Trp Leu Ile Asp Phe Pro Ala Leu Lys Lys Leu Asp Leu Ser Tyr Asn  
 100 105 110  
 Gln Ile Ser Lys Leu Glu Gly Leu Arg Leu Thr Ser Leu Thr Lys  
 115 120 125  
 55 Leu Arg Leu Arg Ser Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Ser  
 130 135 140  
 Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys  
 145 150 155 160  
 60 Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu  
 165 170 175  
 Asp Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu  
 180 185 190  
 Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly Leu  
 195 200 205  
 65 Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile  
 210 215 220  
 Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg  
 225 230 235 240  
 70 Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr  
 245 250 255  
 Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu  
 260 265 270  
 Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn  
 275 280 285  
 75 Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Ser Ser Leu Thr Lys

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290 295 300  
 Leu Arg Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg  
 305 310 315 320  
 5 Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys  
 325 330 335  
 Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu  
 340 345 350  
 Asp Asn Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu  
 355 360 365  
 10 Thr Lys Leu Arg Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu  
 370 375 380  
 Asp Ser Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile  
 385 390 395 400  
 15 Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr  
 405 410 415  
 Leu Leu Asp Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Gly Leu Ala  
 420 425 430  
 Ser Leu Thr Arg Leu Ser Leu Arg Arg Asn Gln Ile Ser Lys Leu Glu  
 435 440 445  
 20 Gly Leu Asp Arg Leu Lys Val Leu Arg Lys Leu Asp Val Ser Gly Asn  
 450 455 460  
 Asp Ile Gln Ser Ile Asp Asp Ile Lys Leu Leu Ala Pro Ile Leu Glu  
 465 470 475 480  
 25 Gln Thr Leu Glu Lys Leu Arg Ile His Asp Asn Pro Phe Val Ala Ser  
 485 490 495  
 Ser Gly Leu Ile Leu Ser Pro Tyr Asp Asn His Leu Pro Glu Ile Lys  
 500 505 510  
 Ala Leu Leu Glu Lys Glu Lys Glu Lys Gln Lys Lys Thr Ser Val Glu  
 515 520 525  
 30 Tyr His Pro Phe Cys Lys Val Met Leu Leu Gly Asn His Ser Ser Gly  
 530 535 540  
 Lys Thr Thr Phe Leu Ser Gln Tyr Asp Thr Asn Tyr Thr Tyr Gln Lys  
 545 550 555 560  
 35 Asn Thr His Val Leu Ser Ile His Arg Ser Asn Asn Pro Asn Ala Ile  
 565 570 575  
 Phe Tyr Asp Phe Gly Gly Gln Asp Tyr Tyr His Gly Ile Tyr Gln Ala  
 580 585 590  
 Phe Phe Thr Thr Gln Ser Leu Tyr Leu Leu Phe Trp Asp Ala Lys Lys  
 595 600 605  
 40 Asp Arg Asn Phe Val Ser Val Asp Asp Lys Glu Tyr Gln Thr Leu Asn  
 610 615 620  
 Phe Asn Arg Pro Tyr Trp Leu Gly Gln Ile Ala Tyr Ala Cys Asn Arg  
 625 630 635 640  
 45 Cys Met Ser Val Gly Gly Asn Pro Asp Gly Lys Asp Thr Pro Gln Thr  
 645 650 655  
 Thr Asp Asp Thr Ile Ile Ile Gln Thr His Ala Asp Glu Thr Gly Ala  
 660 665 670  
 Lys Gln Gln Thr Leu Gly Cys Ala Ala Glu Asn Gly Val Leu Glu Glu  
 675 680 685  
 50 Ile Tyr Val Ser Leu Glu Pro Lys Ala Asn Ser Ala Val His Ala Leu  
 690 695 700  
 Asn Tyr Leu Asn Glu Arg Val Arg Glu Val Val Ala Ser Arg Ser Lys  
 705 710 715 720  
 55 Ser Ile Gln Ile Thr Glu Lys Asp Lys Gly Leu Tyr Glu Ala Leu Pro  
 725 730 735  
 Thr Ile Ala Gly Asp Asn Lys His Ile Pro Ile Ser Leu Glu Ala Leu  
 740 745 750  
 Ala Ala Gln Leu Asn Lys Gly Arg Ala Glu Asn Asp Leu Tyr Thr Ile  
 755 760 765  
 60 Glu Tyr Leu Gln Thr Glu Leu Asn Gln Leu Ser Leu Arg Gly Glu Val  
 770 775 780  
 Leu Tyr Tyr Arg Glu Asn Glu Lys Leu Asn Asn Tyr Val Trp Leu Asp  
 785 790 795 800  
 65 Pro Ala Ala Phe Val Gln Met Ile His Gly Glu Ile Leu Gln Lys Asp  
 805 810 815  
 Asn Ile Asn Arg Gly Thr Val Pro Lys Asp Ile Phe Glu Cys Lys Leu  
 820 825 830  
 His Asn Leu Ser Ser Gly Ser Ile Phe Glu Glu Asp Gly Gln Asn Gly  
 835 840 845  
 70 Asn Met Ile Leu Gln Leu Leu Leu Glu Glu Leu Ile Val Tyr Glu Asp  
 850 855 860  
 Lys Asp Cys Tyr Val Ile Pro Gly Tyr Leu Pro Leu His Ser Asp Asp  
 865 870 875 880  
 75 Glu Ala Tyr Lys Trp Leu Thr Leu Gly Phe Glu Arg Pro Asn Phe Val  
 885 890 895

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Leu Lys Phe Glu Arg Phe Ile Pro Phe Gly Leu Ile Asn Gln Ile Ile  
 900 905 910  
 Ala Tyr Tyr Gly Arg Glu Glu Gly Ala Leu Lys Arg Tyr Trp Arg Asp  
 915 920 925  
 5 Gln Val Ile Phe Thr Ala Gly Arg Glu Met Asp Arg Gln Thr Leu Glu  
 930 935 940  
 Gln Glu Glu Glu Lys Glu Gly Leu Pro Lys Thr Asn Ala Glu Asp Tyr  
 945 950 955 960  
 10 Gln Ile Trp Ile Lys Leu Asp Phe Thr Asp Leu Ala Ile Ser Val Phe  
 965 970 975  
 Ile Lys Glu Gln Arg Lys Thr Ser Ala Lys Asp Met Gln Arg Lys Glu  
 980 985 990  
 Ala Thr Ile Leu Ser Asp Met Leu Asp Met Tyr Trp Asn Asn Ile Pro  
 995 1000 1005  
 15 Pro Arg Glu Gln Ile Gly Asp Lys Asp Thr Glu Gln Thr Arg Ser Thr  
 1010 1015 1020  
 Ile Arg Glu Thr Asn Arg Lys Lys Arg Pro Ile Gln Asp Leu Tyr Leu  
 1025 1030 1035 1040  
 20 Ser Cys Ala Gln Ala Asp Lys Asp Leu Thr Glu Ser His Tyr Ile His  
 1045 1050 1055  
 Leu Gly Thr Leu Asp Asp Glu Ser Lys Thr Thr Ala Arg Ile Ala Ala  
 1060 1065 1070  
 Tyr Pro Leu Lys Asn Gly Val Ile Asp Lys Glu Arg Val Arg Glu Val  
 1075 1080 1085  
 25 Ser Thr Arg Pro Tyr Lys His Leu Ser Val Asn Lys Asn Leu Ala Thr  
 1090 1095 1100  
 Ala Lys Gln Ile Phe Ile Ser Tyr Ser Lys Glu Asp Gln Thr Glu Leu  
 1105 1110 1115 1120  
 30 Glu Thr Cys Leu Gln Phe Phe Lys Pro Leu Glu Lys Asn Gly Gln Ile  
 1125 1130 1135  
 Glu Ile Tyr Tyr Asp Lys Leu Thr Lys Phe Glu Thr Pro Ile His Pro  
 1140 1145 1150  
 Glu Ile Arg Lys Arg Ile Val Glu Ala Asp Cys Ile Ile Ala Leu Ile  
 1155 1160 1165  
 35 Ser Gln Arg Tyr Leu Ala Thr Asp Tyr Ile Leu Asp His Glu Leu Pro  
 1170 1175 1180  
 Val Phe Arg Glu Tyr Asn Lys Thr Ile Val Pro Ile Leu Ile Lys Pro  
 1185 1190 1195 1200  
 40 Cys Thr Phe Glu Asp Asp Glu Phe Leu Arg Glu Lys Tyr Phe Ala Gln  
 1205 1210 1215  
 Lys Ala Gln Ile Ile Asn Leu Gly Lys Glu Gly Lys Thr Ile Lys Ala  
 1220 1225 1230  
 Tyr Asp Ser Ile Thr Ala Ser Ala His Arg Asp Glu Asn Trp Val Ala  
 1235 1240 1245  
 45 Val Val Arg Glu Phe Lys Glu Lys Ile Leu Arg Ile Thr Lys Gln Glu  
 1250 1255 1260  
 Val Asn Thr Asp Glu  
 1265  
 50 (2) INFORMATION FOR SEQ ID NO:376  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 231 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 55 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 60 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...231  
 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:376  
 70 Lys Phe Met Met Lys Lys Ala Phe Val Phe Val Leu Leu Val Cys Leu  
 1 5 10 15  
 Phe Ser Ser Phe Ser Ser Ser Ala Gln Thr Thr Thr Asn Ser Ser Arg  
 20 25 30  
 75 Ser Tyr Phe Thr Gly Arg Ile Glu Lys Val Ser Leu Asn Leu Gly Val  
 35 40 45

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Pro Pro Val Ser Thr Glu Val Trp Gly Met Thr His Asp Ala Asn Gly  
 50 55 60  
 Leu Pro Phe Glu Ile Pro Ile Ser Phe Ser Arg Phe Asn Ser Gln Gly  
 65 70 75 80  
 5 Asp Ile Ala Thr Thr Tyr Tyr Ile Ala Asn Ser Glu Ala Thr Leu Asn  
 85 90 95  
 Glu Trp Cys Asp Tyr Ala His Pro Gly Gly Ile Val Arg Val Glu Gly  
 100 105 110  
 10 Arg Phe Trp Lys Met Thr Tyr Asn Ile Pro Thr Tyr Asn Ala Val Cys  
 115 120 125  
 Thr Arg Ile Thr Phe Glu Asn Gln Glu Ile Glu Gly Thr Ile Val Leu  
 130 135 140  
 Ile Pro Lys Pro Lys Val Ser Leu Pro His Val Ser Glu Ser Val Pro  
 145 150 155 160  
 15 Cys Ile Arg Thr Glu Ala Gly Arg Glu Phe Ile Leu Cys Glu Glu Asp  
 165 170 175  
 Asp Thr Phe Val Ser His Asp Gly Asn Glu Val Thr Ile Gly Gly Lys  
 180 185 190  
 20 Pro Phe Leu Leu Asn Thr Asn Val Lys Ile Val Gly Asp Val Ser Gln  
 195 200 205  
 Lys Tyr Ala Val Gly Val Gly Glu Ile Arg Phe Leu Gln Ile Cys Ala  
 210 215 220  
 Gln Thr Val Ser Gln Gln Lys  
 225 230  
 25 (2) INFORMATION FOR SEQ ID NO:377  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 563 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30 (ii) MOLECULE TYPE: protein  
 35 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 40 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...563  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:377  
 45 Ser Leu Ile Asn Asn Ser Arg Asp Trp Arg Ala Pro Val Arg Leu Ser  
 1 5 10 15  
 Leu Lys Lys Lys Thr Lys Thr Met Lys Thr Lys Val Leu Arg Lys Phe  
 20 25 30  
 50 Val Val Ala Ala Phe Ala Val Ala Thr Leu Cys Pro Leu Ala Gln Ala  
 35 40 45  
 Gln Thr Met Gly Gly Asp Asp Val Lys Val Val Gln Tyr Asn Gln Glu  
 50 55 60  
 55 Lys Leu Val Gln Thr Arg Met Ser Val Ala Asp Asn Gly Trp Ile Tyr  
 65 70 75 80  
 Val Met Thr His Ser Gly Tyr Asp Thr Gly Asn Ser Asn Val Lys Ile  
 85 90 95  
 Phe Arg Ser Lys Asp Gln Gly Ala Thr Tyr Gln Lys Leu Arg Asp Trp  
 100 105 110  
 60 Asp Pro Ser Asp Asp Tyr Gln Phe Gln Asp Phe Asp Ile Val Val Thr  
 115 120 125  
 Gly Lys Asn Glu Ser Asp Ile Lys Ile Trp Ser Val Glu Leu Met Asn  
 130 135 140  
 65 Lys Pro Gly Gly Tyr Lys Ser Arg Val Ala Val Phe Ser Arg Asp Ala  
 145 150 155 160  
 Asn Ala Gln Asn Ala Lys Leu Val Tyr Lys Glu Asp Phe Ser Asn Val  
 165 170 175  
 Gln Leu Tyr Asp Val Asp Ile Ala Ser Asn Tyr Arg Ser Pro Ser Ser  
 180 185 190  
 70 Leu Asn Asn Gly Gly Asn Pro Phe Ala Leu Ala Phe Ala Tyr Thr Gly  
 195 200 205  
 Phe Asn Asn Thr His Lys Ile Ser Phe Val Asp Tyr Val Phe Ser Leu  
 210 215 220  
 75 Asn Gly Gly Gln Asn Phe Asn Lys Asn Leu Leu Phe Ser Gln Asp Gly  
 225 230 235 240

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Glu Lys Lys Ile Asp Lys Val Asp Leu Ser Leu Gly Ser Thr Ser Glu  
 245 250 255  
 Ser Met Gly His Asn Ala Trp Pro Leu Met Gly Val Val Phe Glu Met  
 260 265 270  
 5 Asn Lys Gln Gly Gly Lys Ser Asp Ile Gly Phe Leu Ser Asn Phe Val  
 275 280 285  
 Asp Asn Asp Pro Glu Phe Gln Trp Ser Gly Pro Ile Lys Val Ser Glu  
 290 295 300  
 10 Ser Asp Met Ser Phe Ser Pro Lys Ile Gln Met Leu Leu Asp Glu Asp  
 305 310 315 320  
 Asn Asn Thr Ile Asn Gly Glu Ser Cys His Asn Phe Met Ile Thr Tyr  
 325 330 335  
 Ser Asp Tyr Asp Ser Glu Tyr Ser Asp Trp Asp Ile Arg Tyr Val Tyr  
 340 345 350  
 15 Pro Lys Lys Ser Phe Lys Tyr Glu Lys Gly Lys Thr Pro Thr Met Asp  
 355 360 365  
 Asp Leu Val Glu Ala Phe Leu Thr Ala Ser Tyr Gln Ser Glu Thr Asn  
 370 375 380  
 20 Ser Gly Leu Gly Tyr Asp Lys Asn Ala Asn His Tyr Leu Ile Thr Tyr  
 385 390 395 400  
 Ala Lys Lys Glu Glu Asn Gly Thr Asn Thr Leu Lys Tyr Arg Trp Ala  
 405 410 415  
 Asn Tyr Asp Lys Ile His Asn Lys Asp Leu Trp Ser Asp Thr Phe Thr  
 420 425 430  
 25 Tyr Thr Ser Ser Ala Asn Ala Leu Tyr Thr Pro Gln Val Asp Ile Asn  
 435 440 445  
 Pro Thr Lys Gly Leu Val Cys Trp Ser Trp Val Glu Tyr Leu Pro Gly  
 450 455 460  
 30 Lys Arg Ile Val Trp Ser Asp Thr Gln Trp Thr His Ala Asn Gly Val  
 465 470 475 480  
 Glu Asp Ile Val Met Gln Glu Gly Ser Met Lys Leu Tyr Pro Asn Pro  
 485 490 495  
 Ala Gln Glu Tyr Ala Val Ile Ser Leu Pro Thr Ala Ala Asn Cys Lys  
 500 505 510  
 35 Ala Val Val Tyr Asp Met Gln Gly Arg Val Val Ala Glu Ala Ser Phe  
 515 520 525  
 Ser Gly Asn Glu Tyr Arg Leu Asn Val Gln His Leu Ala Lys Gly Thr  
 530 535 540  
 40 Tyr Ile Leu Lys Val Val Ser Asp Thr Glu Arg Phe Val Glu Lys Leu  
 545 550 555 560  
 Ile Val Glu

- 45 (2) INFORMATION FOR SEQ ID NO:378  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 786 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 50 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 55 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 60 (B) LOCATION 1...786  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:378

65 Ile Val Tyr Leu Cys His Cys Met Asn His Arg Arg Ser Lys Thr Met  
 1 5 10 15  
 Leu Thr Ile Arg Asn Phe Leu Leu Phe Cys Cys Leu Ser Leu Ile Ala  
 20 25 30  
 Phe Ala Ala Asp Ala Gln Ser Ser Val Ser Ser Gly Arg Arg Leu Thr  
 35 40 45  
 70 Glu Tyr Val Asn Pro Phe Ile Gly Thr Ala Asn Tyr Gly Thr Thr Asn  
 50 55 60  
 Pro Gly Ala Val Leu Pro Asn Gly Leu Met Ser Val Thr Pro Phe Asn  
 65 70 75 80  
 75 Val Ser Gly Ser Thr Glu Asn Arg Phe Asp Lys Asp Ser Arg Trp Trp  
 85 90 95

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Ser Ala Pro Tyr Ser Ala Asp Asn Ser Tyr Cys Ile Gly Phe Ser His  
 100 105 110  
 Val Asn Leu Ser Gly Val Gly Cys Pro Glu Leu Ser Gly Ile Leu Leu  
 115 120 125  
 5 Met Ala Thr Ser Gly Thr Phe Asp Pro Asp Tyr Cys Tyr Gly Ser  
 130 135 140  
 Ser Leu Ser Arg Glu Tyr Ala Arg Pro Gly Glu Tyr Lys Ala Val Leu  
 145 150 155 160  
 10 Asp Lys Tyr Gly Ile Asp Ala Ala Val Thr Val Thr Glu Arg Thr Ala  
 165 170 175  
 Leu Thr Glu Phe Ala Phe Pro Glu Gly Glu Gly His Ile Leu Leu Asn  
 180 185 190  
 Leu Gly Gln Ala Leu Ser Asn Glu Ser Gly Ala Ser Val Arg Phe Leu  
 195 200 205  
 15 Asn Asp Ser Thr Val Val Gly Ser Arg Leu Met Gly Thr Phe Cys Tyr  
 210 215 220  
 Asn Pro Gln Ala Val Phe Arg Gln Tyr Phe Val Leu Gln Val Ser Arg  
 225 230 235 240  
 20 Arg Pro Ile Ser Ala Gly Tyr Trp Lys Lys Gln Pro Pro Met Thr Val  
 245 250 255  
 Glu Ala Gln Trp Asp Ser Thr Ala Gly Lys Tyr Lys Gln Tyr Asp Gly  
 260 265 270  
 Tyr Lys Arg Glu Met Ser Gly Asp Asp Ile Gly Val Arg Phe Ser Phe  
 275 280 285  
 25 Asn Cys Asp Gln Gly Glu Lys Ile Tyr Val Arg Ser Ala Val Ser Phe  
 290 295 300  
 Val Ser Glu Ala Asn Ala Leu Tyr Asn Leu Glu Ala Glu Gln Glu Glu  
 305 310 315 320  
 30 Val Phe Lys Ser Val Gly Gly Asn Pro Ala Lys Ala Phe Ser Ala Ile  
 325 330 335  
 Arg Ser Arg Ala Ile Glu Arg Trp Glu Glu Ala Leu Gly Thr Val Glu  
 340 345 350  
 Val Glu Gly Gly Thr Pro Asp Glu Lys Thr Ile Phe Tyr Thr Ala Leu  
 355 360 365  
 35 Tyr His Leu Leu Ile His Pro Asn Ile Leu Gln Asp Ala Asn Gly Glu  
 370 375 380  
 Tyr Pro Met Met Gly Ser Gly Lys Thr Gly Asn Thr Ala His Asp Arg  
 385 390 395 400  
 40 Tyr Thr Val Phe Ser Leu Trp Asp Thr Tyr Arg Asn Val His Pro Leu  
 405 410 415  
 Leu Cys Leu Leu Tyr Pro Glu Lys Gln Leu Asp Met Val Arg Thr Leu  
 420 425 430  
 Ile Asp Met Tyr Arg Glu Ser Gly Trp Leu Pro Arg Trp Glu Leu Tyr  
 435 440 445  
 45 Gly Gln Glu Thr Leu Thr Met Glu Gly Asp Pro Ser Leu Ile Val Ile  
 450 455 460  
 Asn Asp Thr Trp Gln Arg Gly Leu Arg Ala Phe Asp Thr Ala Thr Ala  
 465 470 475 480  
 Tyr Glu Ala Met Lys Lys Asn Ala Ser Ser Ala Gly Ala Thr His Pro  
 485 490 495  
 50 Ile Arg Pro Asp Asn Asp Asp Tyr Leu Thr Leu Gly Phe Val Pro Leu  
 500 505 510  
 Arg Glu Gln Tyr Asp Asn Ser Val Ser His Ala Leu Glu Tyr Tyr Leu  
 515 520 525  
 55 Ala Asp Trp Asn Leu Ser Arg Phe Ala His Ala Leu Gly His Lys Glu  
 530 535 540  
 Asp Ala Ala Leu Phe Gly Lys Arg Ser Leu Gly Tyr Arg His Tyr Tyr  
 545 550 555 560  
 60 Asn Lys Glu Tyr Gly Met Leu Cys Pro Leu Leu Pro Asp Gly Ser Phe  
 565 570 575  
 Leu Thr Pro Phe Asp Pro Lys Gln Gly Glu Asn Phe Glu Pro Asn Pro  
 580 585 590  
 Gly Phe His Glu Gly Ser Ala Tyr Asn Tyr Ala Phe Phe Val Pro His  
 595 600 605  
 65 Asp Ile Gln Gly Leu Ala Arg Leu Met Gly Gly Ala Lys Val Phe Ser  
 610 615 620  
 Glu Arg Leu Gln Lys Val Phe Asp Glu Gly Tyr Tyr Asp Pro Thr Asn  
 625 630 635 640  
 Glu Pro Asp Ile Ala Tyr Pro Tyr Leu Phe Ser Tyr Phe Pro Lys Glu  
 645 650 655  
 70 Ala Trp Arg Thr Gln Lys Leu Thr Arg Glu Leu Ile Asp Lys His Phe  
 660 665 670  
 Cys Asn Ala Pro Asn Gly Leu Pro Gly Asn Asp Asp Ala Gly Thr Met  
 675 680 685  
 75 Ser Ala Trp Leu Val Tyr Ser Met Leu Gly Phe Tyr Pro Asp Cys Pro

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690 695 700  
 Gly Ser Pro Thr Tyr Thr Leu Thr Ser Pro Val Phe Pro Arg Val Arg  
 705 710 715 720  
 5 Ile Arg Leu Asn Pro Gln Tyr Tyr Pro Gln Gly Glu Leu Ile Ile Thr  
 725 730 735  
 Thr Asn Thr Glu Asn Gln Pro Thr Asp Ser Ile Tyr Ile His Thr Val  
 740 745 750  
 Ser Leu Gly Asn Lys Thr Leu Pro His Gly Thr Arg His Ile Ser His  
 755 760 765  
 10 Ala Asp Leu Val Arg Cys Gly His Leu Arg Tyr Glu Leu Ser Asn Arg  
 770 775 780  
 Pro Arg  
 785  
 15 (2) INFORMATION FOR SEQ ID NO:379  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 814 amino acids  
 (B) TYPE: amino acid  
 20 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 25 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 30 (B) LOCATION 1...814  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:379  
 35 Pro Arg Phe His Pro Gly Gly Thr His Ala Gln Leu Cys Arg Asn Gly  
 1 5 10 15  
 Arg Arg Asn Gln Lys Ser Asn Gln Ser Ser Cys Phe Gly Gly Gly Thr  
 20 25 30  
 40 Ala Pro Arg Phe Phe Ile Met Cys Lys Ile Arg Phe Ser Leu Leu Gln  
 35 40 45  
 Ala Leu Val Val Cys Leu Leu Phe Thr Ser Phe Ser Leu Gln Ala Gln  
 50 55 60  
 Glu Glu Gly Ile Trp Asn Thr Leu Leu Ala Ile His Lys Thr Glu Lys  
 65 70 75 80  
 45 Ala Val Glu Thr Pro Lys Lys Val Phe Ala Val Ala Asn Gly Val Leu  
 85 90 95  
 Tyr Ser Val Gly Lys Glu Ala Pro His Glu Ala Lys Ile Phe Asp Arg  
 100 105 110  
 50 Ile Ser Gly Leu Ser Asp Thr Ser Val Ser Ser Ile Ala Tyr Ser Glu  
 115 120 125  
 Gln Leu Lys Ser Leu Val Ile Tyr Tyr Ala Ser Gly Asn Ile Asp Ile  
 130 135 140  
 Leu Asp Glu Ala Gly Arg Val Thr Asn Val Pro Ala Leu Lys Asp Asn  
 145 150 155 160  
 55 Ile Asp Leu Ile Asp Lys Thr Leu Asn Arg Leu Leu Ile Val Gly Asn  
 165 170 175  
 Arg Ala Tyr Leu Ala Gly Gly Phe Gly Leu Ser Val Leu Asp Val Ala  
 180 185 190  
 Glu Ala Arg Ile Pro Ala Thr Tyr Ala Lys Gly Thr Lys Val Thr Asp  
 195 200 205  
 60 Val Ala Lys Leu Asp Asn Asp Arg Leu Leu Met Leu Lys Glu Gly Gln  
 210 215 220  
 Leu Phe Ile Gly Lys Glu Thr Asp Asn Leu Gln Asp Pro Ala Ala Trp  
 225 230 235 240  
 65 Thr Ala Leu Ser Leu Asn Leu Pro Met Gly Ser Val Thr Gly Leu Gly  
 245 250 255  
 Ile Val Gly Glu Asp Ile Cys Phe Leu Leu Ala Asp Gly Arg Val Tyr  
 260 265 270  
 Val Ala Ala Asn Gln Ser Phe Glu Pro Glu Leu Leu Leu Ser Ser Ser  
 275 280 285  
 70 Ala Asp Ser Arg Leu Tyr Val Thr Asp Arg Gly Leu Phe Ile Cys Ala  
 290 295 300  
 Glu Asn Arg Ile Tyr Phe Ile Glu Lys Gly Arg Lys Thr Thr Gln Phe  
 305 310 315 320  
 75 Pro Ile Ala Asp Val Leu Gly Val Gly Ala Met Asn Glu Ser Asn Thr

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325 330 335  
 Ala Tyr Ile Ala Leu Gly Glu Glu Gly Leu Ala Ser Leu Leu Leu Ala  
 340 345 350  
 Glu Gly Ser Thr Ala Glu Ala Met Pro Val Ala Phe Asp Gly Pro Gly  
 355 360 365  
 5 Asp Asn Asp Phe Tyr Glu Met Arg Phe Ser His Gly Arg Leu Tyr Ala  
 370 375 380  
 Ala Ser Gly Leu Trp Gly Thr Asn Leu Met Gly His Ala Gly Met Val  
 385 390 395 400  
 10 Lys Leu Tyr Asp Gly Asn Arg Trp Thr Asn Phe Asp Lys Lys Thr Val  
 405 410 415  
 Gln Glu Gln Leu Gly Gly Gly Phe Ser Phe Asn Asp Ala Ile Asp Ile  
 420 425 430  
 15 Ala Val Ser Asn Gly Asp Pro Asp His Phe Phe Val Gly Thr Trp Gly  
 435 440 445  
 Asn Gly Leu Phe Glu Phe Lys Asp Gly Lys Ala Ile Ala Arg Tyr Ser  
 450 455 460  
 Gly Asn Glu Thr Ala Ile Ala Glu Cys Asn Pro Gly Asp Ala Arg Val  
 465 470 475 480  
 20 Lys Ala Ile Ala Phe Asp Asn Lys Gly Asn Leu Trp Gly Thr Leu Gly  
 485 490 495  
 Ala Val Gly Lys Asn Ile Phe Met Tyr Asp Pro Gln Ser Ser Thr Trp  
 500 505 510  
 25 His Ser Phe Ser Tyr Pro Asp Val Ala Asn Leu Ala Ser Phe Gly Asn  
 515 520 525  
 Met Ile Ile Leu Pro Asn Gly Asp Lys Trp Val Asn Ile Leu His Arg  
 530 535 540  
 Ser Gly Gly Ser Thr Arg Lys Gly Val Leu Ile Phe Asn Asp Arg Gly  
 545 550 555 560  
 30 Thr Pro Glu Thr Thr Ser Asp Asp Ser His Leu Tyr Val Glu Gln Phe  
 565 570 575  
 Val Asn Arg Leu Gly Ala Ala Ile Gly His Lys Thr Ile Tyr Ala Met  
 580 585 590  
 Ala Val Asp His Asn Gly Ser Val Trp Met Gly Ser Asp Ile Gly Ile  
 595 600 605  
 35 Phe Gly Val Tyr Asn Ala Ala Gly Val Leu Ser Ser Thr Ser Thr Pro  
 610 615 620  
 Ile Ala Val Arg Pro Val Gly Gly Glu Glu Pro Asn Leu Tyr Tyr Val  
 625 630 635 640  
 40 Leu Asp Lys Val Thr Val Thr Asp Ile Val Val Asp Lys Leu Asn His  
 645 650 655  
 Lys Trp Val Ala Thr Gln Gly Thr Gly Leu Tyr Leu Leu Ser Glu Asp  
 660 665 670  
 45 Cys Ser Lys Ile Leu Ala Gln Phe Thr Val Glu Asn Ser Pro Leu Leu  
 675 680 685  
 Ser Asn Asn Ile Leu Ser Leu Ala Leu Asn Asp Asp Asn Gly Leu Leu  
 690 695 700  
 Tyr Ile Gly Thr Ala Asp Gly Leu Met Thr Phe Gln Thr Gly Thr Gly  
 705 710 715 720  
 50 Ser Gly Ser Ala Ser Glu Leu Asp Gly Val Tyr Val Tyr Pro Asn Pro  
 725 730 735  
 Leu Arg Pro Glu Tyr Pro Asp Gly Val Thr Ile Ala Gly Leu Gln Ala  
 740 745 750  
 55 Gly Cys Ser Val Lys Ile Thr Asp Thr Thr Gly Arg Leu Leu Tyr Gln  
 755 760 765  
 Thr Glu Ser Val Thr Thr Glu Val Lys Trp Asn Ala Arg Gly Ala Asp  
 770 775 780  
 Gly Asn Arg Val Ala Ser Gly Val Tyr Ala Val Ala Val Tyr Asp Pro  
 785 790 795 800  
 60 Val Ser Lys Lys Ser Lys Leu Ile Arg Phe Ala Val Ile Arg  
 805 810

(2) INFORMATION FOR SEQ ID NO:380

- 65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1162 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 70 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 75 (A) ORGANISM: Porphyromonas gingivalis

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## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1162

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:380

	Ala	Ile	Ser	Gln	Met	Lys	Arg	Ile	Leu	Pro	Ile	Val	Ala	Phe	Leu	Ser	
	1				5				10					15			
10	Leu	Phe	Leu	Ala	Leu	Ala	Leu	Pro	Ala	Lys	Ala	Gln	Arg	Ala	Met	Gly	
				20				25						30			
	Lys	Thr	Ala	Asp	Arg	Ser	Leu	Met	Ala	Ser	Gly	His	Trp	Val	Lys	Ile	
				35				40						45			
15	Arg	Val	Asp	Ala	Ser	Gly	Val	Tyr	Arg	Leu	Thr	Asp	Glu	Gln	Leu	Arg	
				50				55						60			
	Ala	Asn	Gly	Phe	Ser	Asp	Pro	Ser	Lys	Val	Gly	Val	Phe	Gly	Tyr	Gly	
				65				70						75			
	Gly	Gly	Val	Leu	Pro	Glu	Asp	Leu	Ser	Arg	Ile	Thr	Thr	Asp	Asp	Leu	
						85					90			95			
20	Pro	Pro	Val	Pro	Val	Leu	Arg	Gln	Gly	Asn	Ala	Leu	Tyr	Phe	Tyr	Ala	
						100					105			110			
	Val	Gly	Pro	Val	Thr	Trp	Phe	Tyr	Asn	Pro	Ala	Lys	Thr	Thr	Met	Glu	
						115								125			
25	His	Thr	Val	Asn	Thr	Tyr	Ser	Thr	His	Gly	Tyr	Tyr	Phe	Leu	Ser	Asp	
						135								140			
	Ala	Ala	Gly	Ala	Pro	Leu	Gln	Met	Ser	Gln	Tyr	Thr	Gly	Gly	Gly	Ala	
						145								155			
	Ser	Ala	Glu	Ala	Leu	Ile	Asp	Tyr	Tyr	Asp	Glu	Leu	Met	Leu	His	Glu	
						165								175			
30	Gln	Glu	Leu	Tyr	Ser	Pro	Lys	Glu	Ser	Gly	Arg	Asp	Leu	Tyr	Gly	Glu	
						180								190			
	Ser	Phe	Ser	Ala	Val	Asn	Thr	Arg	Thr	Val	Lys	Phe	Pro	Leu	Arg	Gly	
						195								205			
	Asn	Thr	Arg	Ser	Ser	Gly	Glu	Leu	Gly	Thr	Val	Phe	Ser	Tyr	Ile	Ala	
						210								220			
35	Lys	Ala	Arg	Ser	Ala	Gly	Gly	Gly	Arg	Glu	Met	Ser	Leu	Ser	Ala	Asn	
						225								235			
	Gly	Ile	Leu	Ile	Phe	Ser	Asp	Pro	Phe	Ser	Met	Thr	Ser	Asn	Glu	Val	
						245								255			
40	Ser	Asn	Ser	Tyr	Leu	Ala	Gly	Lys	Lys	Arg	Arg	Leu	Tyr	His	Ser	Thr	
						260								270			
	Pro	Met	Asn	Ser	Leu	Val	Asn	Glu	Leu	Arg	Leu	Asp	Ala	Asn	Tyr	Ser	
						275								285			
45	Met	Thr	Gly	Asp	Ala	Val	Asn	Leu	Asp	Phe	Ile	Glu	Val	Ala	Thr	Gln	
						290								300			
	Asn	Asp	Leu	Arg	Tyr	Asp	Gly	Ala	Pro	Met	His	Ile	Arg	Arg	Phe	Ser	
						305								315			
	Asn	Leu	Pro	Val	Leu	Gly	Gly	Glu	Ser	Cys	Arg	Phe	Val	Ile	Ser	Glu	
						325								335			
50	Val	Pro	Glu	Ser	Leu	Val	Val	Leu	Gln	Ala	Asn	Ser	Ser	Leu	Thr	Ala	
						340								350			
	Ser	Leu	Val	Pro	Val	Lys	Thr	Val	Gly	Asp	Lys	Thr	Ile	Glu	Phe	Val	
						355								365			
55	Ala	Pro	Pro	Lys	Gly	Gln	Asp	Arg	Arg	Thr	Ile	Asn	Thr	Phe	Tyr	Ala	
						370								380			
	Val	Asp	Leu	Ser	Gln	Ala	Ser	Ala	Pro	Glu	Ile	Leu	Gly	Ala	Val	Pro	
						385								395			
	Asn	Gln	Asn	Leu	His	Gly	Glu	Glu	Ile	Pro	Asp	Leu	Ile	Ile	Val	Ser	
						405								415			
60	Thr	Gln	Ala	Leu	Leu	Leu	Glu	Ala	Asp	Arg	Leu	Ala	Thr	Tyr	Arg	Arg	
						420								430			
	Glu	Lys	Asn	Gly	Leu	Lys	Val	Leu	Val	Val	Leu	Gln	Glu	Gln	Val	Phe	
						435								445			
	Asn	Glu	Phe	Ser	Gly	Gly	Thr	Pro	Asp	Ala	Thr	Ala	Tyr	Arg	Leu	Phe	
						450								460			
65	Ala	Lys	Met	Phe	Tyr	Asp	Arg	Trp	Lys	Ala	Asn	Ala	Pro	Val	Gly	Glu	
						465								475			
	Thr	Phe	Pro	Met	Gln	Met	Leu	Leu	Phe	Gly	Asp	Gly	Ala	His	Asp	Asn	
						485								495			
70	Arg	Lys	Val	Ser	Val	Ala	Trp	Gln	Lys	Pro	Tyr	Leu	Gln	Gln	Thr	Glu	
						500								510			
	Phe	Leu	Leu	Thr	Phe	Gln	Ala	Val	Asn	Ser	Thr	Asn	Val	Asn	Ser	Tyr	
						515								525			
75	Val	Thr	Asp	Asp	Tyr	Phe	Gly	Leu	Leu	Asp	Asp	Gln	Pro	Ala	Ser	Val	
						530								540			



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	Asn	Ile	Gly	Trp	Arg	Asn	Tyr	Asn	Met	Ala	Val	Gly	Arg	Phe	Pro	Val
	545					550					555					560
	Arg	Thr	Pro	Ala	Glu	Ala	Arg	Ile	Ala	Val	Asp	Lys	Thr	Ile	Arg	Tyr
					565					570						575
5	Glu	Glu	Asp	Arg	Glu	Ser	Gly	Ala	Trp	Arg	Ile	Arg	Ala	Cys	Phe	Ala
				580					585					590		
	Ala	Asp	Asn	Gly	Asp	Lys	His	Ala	Thr	Glu	Thr	Ser	Arg	Leu	Ile	Asp
		595						600					605			
10	Thr	Val	Lys	Arg	Tyr	Ala	Pro	Ala	Ile	Met	Pro	Val	Arg	Ala	Phe	Gln
		610						615					620			
	Asp	Val	Tyr	Pro	His	Val	Ile	Glu	Asn	Gly	Leu	His	Ser	Ile	Pro	Gly
		625				630					635					640
	Ala	Lys	Lys	Lys	Met	Leu	Glu	Thr	Leu	Gln	Ser	Gly	Ile	Ile	Leu	Leu
				645						650						655
15	Asn	Tyr	Ala	Gly	His	Gly	Gly	Pro	Ala	Gly	Trp	Ser	Asp	Glu	His	Leu
				660					665					670		
	Leu	Thr	Leu	Asn	Asp	Ile	His	Lys	Phe	Asn	Tyr	Lys	His	Met	Pro	Ile
				675					680				685			
20	Trp	Ile	Thr	Ala	Thr	Cys	Asp	Phe	Ala	Asn	Tyr	Asp	Ser	Gln	Thr	Thr
		690					695						700			
	Ser	Ala	Gly	Glu	Glu	Val	Phe	Leu	His	Glu	Lys	Ser	Gly	Thr	Pro	Ile
		705				710					715					720
	Met	Phe	Ser	Thr	Thr	Arg	Val	Val	Tyr	Asn	Thr	Gln	Asn	Glu	Lys	Ile
				725							730					735
25	Asn	Gly	Phe	Met	Leu	Arg	Arg	Met	Phe	Glu	Lys	Ala	Lys	Asp	Gly	Arg
				740					745					750		
	Tyr	Arg	Thr	Met	Gly	Glu	Ile	Ile	Arg	Ser	Ala	Lys	Gln	Gly	Met	Leu
				755					760					765		
30	Ser	Thr	Val	Phe	Pro	Asp	Ser	Ile	Asn	Gln	Leu	Ser	Phe	Phe	Leu	Met
				770			775						780			
	Gly	Asp	Pro	Ser	Val	Arg	Met	Asn	Leu	Pro	Thr	His	Lys	Val	Gln	Leu
						790					795					800
	Thr	Ala	Ile	Asn	Gly	Gln	Asp	Pro	Glu	Gly	Gln	Tyr	Gly	Thr	Ile	Met
				805					810							815
35	Leu	Lys	Ser	Leu	Glu	Arg	Val	Ala	Leu	Lys	Gly	Lys	Val	Thr	Asp	Glu
				820					825					830		
	Lys	Gly	Thr	Phe	Asp	Glu	Thr	Phe	Ser	Gly	Lys	Val	Phe	Leu	Thr	Val
				835				840					845			
40	Phe	Asp	Gly	Arg	Lys	Lys	Met	Thr	Ala	Leu	Glu	Glu	Glu	Gly	Asn	Asp
		850					855						860			
	Leu	Ser	Leu	Val	Tyr	Tyr	Asp	Tyr	Pro	Asn	Val	Met	Tyr	Ala	Gly	Ile
						870					875					880
	Ala	Glu	Val	Lys	Asp	Gly	Leu	Phe	Glu	Thr	Ser	Phe	Ile	Val	Pro	Lys
				885						890						895
45	Asp	Val	Asn	Tyr	Ser	Glu	His	Glu	Gly	Arg	Ile	Asn	Leu	Tyr	Ala	Tyr
				900					905					910		
	Asn	Glu	Ser	Thr	Lys	Ala	Glu	Ala	Met	Gly	Val	Asp	Phe	Ser	Ile	Arg
				915					920					925		
50	Val	Gln	Pro	Gly	Ile	Pro	Asp	Glu	Val	Thr	Glu	Asp	Asn	Thr	Pro	Pro
				930									940			
	Glu	Ile	Ile	Ser	Cys	Phe	Leu	Asn	Asp	Ser	Thr	Phe	Arg	Ser	Gly	Asp
				945						950			955			960
	Glu	Val	Asn	Pro	Thr	Pro	Leu	Phe	Met	Ala	Glu	Val	Phe	Asp	Leu	Asn
					965					970						975
55	Gly	Ile	Asn	Ile	Thr	Gly	Ser	Gly	Val	Gly	His	Asp	Ile	Thr	Leu	Cys
				980						985						990
	Ile	Asp	Gly	Arg	Ala	Asp	Leu	Thr	Tyr	Asn	Leu	Asn	Ala	Tyr	Phe	Thr
				995					1000					1005		
60	Ser	Ser	Ala	Thr	Asp	Ala	Gly	Val	Gly	Thr	Ile	Leu	Phe	Met	Ile	Pro
				1010					1015							1020
	Ala	Leu	Ala	Glu	Gly	Asp	His	Thr	Ala	Arg	Leu	Thr	Val	Trp	Asp	Ile
						1030					1035					1040
	Phe	Asn	Asn	Ala	Val	His	His	Asp	Phe	Ser	Phe	Arg	Val	Val	Asp	Gly
				1045						1050						1055
65	Ile	Ala	Pro	Asp	Val	Ala	Asp	Val	Ile	Leu	Phe	Pro	Asn	Pro	Val	Arg
				1060						1065						1070
	Glu	Ser	Ala	Thr	Phe	Arg	Ile	Phe	His	Asn	Arg	Pro	Gly	Ser	Asp	Leu
				1075					1080					1085		
70	Asn	Val	Ala	Val	Glu	Ile	Tyr	Asp	Phe	Thr	Gly	Arg	Leu	Val	Asn	Ser
								1095						1100		
	Leu	Pro	Val	Lys	Thr	Tyr	Ser	Ser	Ser	Tyr	Gly	Glu	Pro	Ile	Glu	Ile
						1110						1115				1120
	Lys	Trp	Asp	Leu	Thr	Ser	Lys	Tyr	Gly	Val	Lys	Ile	Gly	Asn	Gly	Phe
						1125					1130					1135
75	Tyr	Leu	Tyr	Arg	Cys	Val	Val	Asn	Ser	Pro	Gly	Gly	Gln	Thr	Ala	Ser

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Met Ala Lys Lys Met Ile Val Val Gly Gln  
 1140 1145 1150  
 1155 1160

5 (2) INFORMATION FOR SEQ ID NO:381

(1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 973 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

10 (11) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

15 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (E) LOCATION 1...973

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:381

25 Phe Tyr Thr Gly Ile Asp Leu His Ile Glu Ser Gln Met Lys Lys Leu  
 1 5 10 15  
 Phe Pro Leu Leu Leu Ile Leu Ser Ile Leu Val Gly Cys Gly Lys  
 20 25 30  
 Lys Glu Lys His Ser Val Thr Glu Ile Ala Arg Glu Lys Lys Arg Ile  
 30 35 40 45  
 Thr Ala Leu Leu Tyr Glu Lys Glu Leu Pro Thr Asp Ser Val Lys Gln  
 50 55 60  
 Leu Tyr Glu Asn Ser Val Gln Asn Lys Asn Leu Val Gly Gln Met Leu  
 65 70 75 80  
 35 Phe Ala Ile Glu Val Gly Lys Arg Met Arg Asn Met Ser Gln Tyr Thr  
 85 90 95  
 Asp Ala Met Leu Tyr His Gln Lys Gly Leu Asn Ala Ala Leu Asn Leu  
 100 105 110  
 Arg Asp Thr Ile Val Ala Ala Gln Ala Trp Asn His Leu Gly Thr Asp  
 115 120 125  
 40 Ser Arg Arg Ile Gly Ala Leu Ala Glu Ala Ser Asp Tyr His Tyr Lys  
 130 135 140  
 Ala Leu Ser Leu Ile Glu Ser Phe Ser Gly Asn Gln Asn Arg Pro Ala  
 145 150 155 160  
 45 Ile Lys Ala Arg Ser Ala Ala Leu Asn Gly Ile Gly Asn Ile Asn Leu  
 165 170 175  
 Glu Leu Gly Tyr His Asp Glu Ala Glu Lys Asn Phe Leu Lys Ala Leu  
 180 185 190  
 Gln Gly Glu Lys Glu Leu Asp Ser Pro Leu Gly Gln Ala Ile Asn Tyr  
 195 200 205  
 50 Ala Asn Leu Gly Arg Ile Tyr Arg Gln Arg Lys Glu Tyr Asp Lys Ala  
 210 215 220  
 Arg Thr Tyr Phe Leu Leu Ser Leu Glu Gln Asn Asn Met Ala Glu Asn  
 225 230 235 240  
 55 Leu Met Gly Ile Gly Leu Cys Ser Ile Asn Leu Gly Glu Val Asp Glu  
 245 250 255  
 Glu Lys Gly Asp Tyr Gln Lys Ala Leu Gln Glu Tyr Ala Thr Ala Tyr  
 260 265 270  
 Lys Leu Met Glu Gln Leu Ser Asp Arg Trp His Trp Leu Asn Ser Cys  
 275 280 285  
 Ile Pro Met Ala Arg Ile Asn Leu Lys Gln Gly Asn Glu Arg Leu Tyr  
 290 295 300  
 Gln His Phe Ile Ser Leu Ala Glu Gly Thr Ala Lys Glu Ile Asn Ser  
 305 310 315 320  
 65 Thr Ser His Leu Ile Glu Ile Tyr Asn Leu Gln Tyr Glu Asn Leu Glu  
 325 330 335  
 Arg Lys Lys Glu Tyr Lys Gln Ala Leu Glu Ala Phe Cys Leu Ser Lys  
 340 345 350  
 Thr Leu Ser Asp Ser Met Ser Ile Ala His Lys Val Ser Ser Ile Gln  
 355 360 365  
 70 Glu Thr Arg Phe Asn Tyr Glu Arg Asn Lys Ser Gln Lys Glu Leu Glu  
 370 375 380  
 Glu Ile Gln Gln Val Ser Lys Ala Lys Gln Glu Lys Ser Lys Phe Ile  
 385 390 395 400  
 75 Leu Leu Ser Thr Leu Phe Ala Leu Phe Ile Ser Ile Leu Leu Ile Ser

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405 410 415  
 Val Leu Thr Tyr Ala Tyr Arg Gln Gly Lys Lys His Asn Lys Leu Ile  
 420 425 430  
 5 Lys Glu Thr Asp Lys Leu Arg Ser Gly Phe Phe Thr Gly Ile Thr His  
 435 440 445  
 Glu Phe Arg Thr Pro Ile Thr Val Ile Gln Gly Leu Asn Glu Lys Met  
 450 455 460  
 Ser Ser Ser Pro Asp Leu Gln Ala Ser Asp Arg Thr Glu Leu His Lys  
 465 470 475 480  
 10 Ile Ile Asp Arg Gln Ser Ser His Met Leu Asn Leu Val Asn Gln Leu  
 485 490 495  
 Leu Asp Ile Cys Lys Ile Arg Ser Gly Val Ser Thr Pro Glu Trp Arg  
 500 505 510  
 15 Asn Gly Asp Ile Val Ser Phe Val Gln Ile Leu Ile Asp Ser Phe Ala  
 515 520 525  
 Pro Tyr Ala Gln Ala Gln Asp Ile Thr Leu Glu Leu Gln Pro Glu Ser  
 530 535 540  
 Lys Pro Ile Val Val Asp Phe Val Pro Ser Tyr Leu Gln Lys Ile Ile  
 545 550 555 560  
 20 Ser Asn Leu Leu Ser Asn Ala Ile Lys Tyr Ser Leu Ala Gly Gly Arg  
 565 570 575  
 Val Val Ile Ser Leu Ala Lys Thr Lys Asn Glu Lys Asn Leu Ile Ile  
 580 585 590  
 25 Arg Val Ala Asp Asn Gly Ile Gly Ile Asp Lys Thr Asp Gln Ala His  
 595 600 605  
 Ile Phe Asp Ile Phe Tyr Arg Gly Gln Ser Ala Thr Glu Lys His Gly  
 610 615 620  
 Ser Gly Val Gly Leu Ser Phe Thr Asn Ile Leu Val Glu Asn Leu Arg  
 625 630 635 640  
 30 Gly Thr Ile Lys Val Glu Ser Gln Pro Gly Lys Gly Ser Ala Phe Thr  
 645 650 655  
 Ile Ser Ile Pro Thr Gln Asn Gln Ser Ser Ser Ala Glu Ile Leu Pro  
 660 665 670  
 35 Trp Leu Pro Ser Ser Asp Asp Ile Val Met Pro Val His Ile Ala Pro  
 675 680 685  
 Asp Asp Ser Pro Thr Ser Pro Met Val Ala Ala Leu Asn His Arg Phe  
 690 695 700  
 Glu Asp Glu Arg Pro Thr Ile Leu Leu Val Glu Asp Asn Lys Asp Ile  
 705 710 715 720  
 40 Asn Leu Leu Val Lys Leu Leu Leu Cys Asp Arg Tyr Asn Val Leu Ser  
 725 730 735  
 Ala Ala Asn Gly Lys Glu Gly Ile Ala Leu Ala Thr Glu His Ile Pro  
 740 745 750  
 45 Asp Ile Ile Ile Thr Asp Ile Met Met Pro Ile Met Asp Gly Ile Glu  
 755 760 765  
 Met Thr Ile Arg Met Lys Gln Ser Pro Leu Leu Cys His Ile Pro Ile  
 770 775 780  
 Val Ala Leu Thr Ala Lys Ser Thr Glu Gln Asp Arg Leu Glu Gly Ile  
 785 790 795 800  
 50 Lys Ser Gly Val Val Ser Tyr Leu Cys Lys Pro Phe Ser Pro Glu Glu  
 805 810 815  
 Leu Leu Met Arg Ile Glu Gln Leu Leu Lys Asp Arg Glu Leu Leu Lys  
 820 825 830  
 55 Lys Phe Tyr Met Gln Lys Leu Met Leu Asp Arg Lys Pro Glu Glu Glu  
 835 840 845  
 Pro Gln Pro Ile Asp Asp Ser Ser Met Gln Phe Leu Leu Ala Ala Lys  
 850 855 860  
 Asp Ala Val Ser Gly Gly Ile Lys Gln Asn Pro Asp Phe Ser Ala Gln  
 865 870 875 880  
 60 Asp Leu Ala Glu Lys Met Cys Met Ser Pro Ser Gln Leu Asn Arg Lys  
 885 890 895  
 Leu Thr Ser Val Val Gly Cys Ser Thr Ile Gly Tyr Ile Gln Gln Ile  
 900 905 910  
 65 Lys Ile Lys Leu Ala Cys Lys Leu Leu Ala Asp Glu Ser Lys Asn Ile  
 915 920 925  
 Ser Asp Ile Ser Ile Glu Ala Gly Phe Ser Asp Pro Ala Tyr Phe Ser  
 930 935 940  
 Arg Thr Phe Lys Arg Tyr Met Asn Cys Ser Pro Ser Gln Tyr Arg Gln  
 945 950 955 960  
 70 Lys Leu Leu Ala Met Pro Gly Ser Asp Lys Glu Thr Val  
 965 970

(2) INFORMATION FOR SEQ ID NO:382

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(1) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 563 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 10 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...563  
 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:382

20 His His Lys Thr Tyr Gln Thr Met Lys Lys Leu Leu Gln Ala Lys Ala  
 1 5 10 15  
 Leu Ile Leu Ala Leu Gly Leu Phe Gln Leu Pro Ala Ile Ala Gln Thr  
 20 25 30  
 Gln Met Gln Ala Asp Arg Thr Asn Gly Gln Phe Ala Thr Glu Glu Met  
 35 40 45  
 25 Gln Arg Ala Phe Gln Glu Thr Asn Pro Pro Ala Gly Pro Val Arg Ala  
 50 55 60  
 Ile Ala Glu Tyr Glu Arg Ser Ala Ala Val Leu Val Arg Tyr Pro Phe  
 65 70 75 80  
 Gly Ile Pro Met Glu Leu Ile Lys Glu Leu Ala Lys Asn Asp Lys Val  
 85 90 95  
 30 Ile Thr Ile Val Ala Ser Glu Ser Gln Lys Asn Thr Val Ile Thr Gln  
 100 105 110  
 Tyr Thr Gln Ser Gly Val Asn Leu Ser Asn Cys Asp Phe Ile Ile Ala  
 115 120 125  
 35 Lys Thr Asp Ser Tyr Trp Thr Arg Asp Tyr Thr Gly Trp Phe Ala Met  
 130 135 140  
 Tyr Asp Thr Asn Lys Val Gly Leu Val Asp Phe Ile Tyr Asn Arg Pro  
 145 150 155 160  
 Arg Pro Asn Asp Asp Glu Phe Pro Lys Tyr Glu Ala Gln Tyr Leu Gly  
 165 170 175  
 40 Ile Glu Met Phe Gly Met Lys Leu Lys Gln Thr Gly Gly Asn Tyr Met  
 180 185 190  
 Thr Asp Gly Tyr Gly Ser Ala Val Gln Ser His Ile Ala Tyr Thr Glu  
 195 200 205  
 45 Asn Ser Ser Leu Ser Gln Ala Gln Val Asn Gln Lys Met Lys Asp Tyr  
 210 215 220  
 Leu Gly Ile Thr His His Asp Val Val Gln Asp Pro Asn Gly Glu Tyr  
 225 230 235 240  
 Ile Asn His Val Asp Cys Trp Gly Lys Tyr Leu Ala Pro Asn Lys Ile  
 245 250 255  
 50 Leu Ile Arg Lys Val Pro Asp Asn His Pro Gln His Gln Ala Leu Glu  
 260 265 270  
 Asp Met Ala Ala Tyr Phe Ala Ala Gln Thr Cys Ala Trp Gly Thr Lys  
 275 280 285  
 55 Tyr Glu Val Tyr Arg Ala Leu Ala Thr Asn Glu Gln Pro Tyr Thr Asn  
 290 295 300  
 Ser Leu Ile Leu Asn Asn Arg Val Phe Val Pro Val Asn Gly Pro Ala  
 305 310 315 320  
 Ser Val Asp Asn Asp Ala Leu Asn Val Tyr Lys Thr Ala Met Pro Gly  
 325 330 335  
 60 Tyr Glu Ile Ile Gly Val Lys Gly Ala Ser Gly Thr Pro Trp Leu Gly  
 340 345 350  
 Thr Asp Ala Leu His Cys Arg Thr His Glu Val Ala Asp Lys Gly Tyr  
 355 360 365  
 65 Leu Tyr Ile Lys His Tyr Pro Ile Leu Gly Glu Gln Ala Gly Pro Asp  
 370 375 380  
 Tyr Lys Ile Glu Ala Asp Val Val Ser Cys Ala Asn Ala Thr Ile Ser  
 385 390 395 400  
 Pro Val Gln Cys Tyr Arg Ile Asn Gly Ser Gly Ser Phe Lys Ala  
 405 410 415  
 70 Ala Asp Met Thr Met Glu Ser Thr Gly His Tyr Thr Tyr Ser Phe Thr  
 420 425 430  
 Gly Leu Asn Lys Asn Asp Lys Val Glu Tyr Tyr Ile Ser Ala Ala Asp  
 435 440 445  
 75 Asn Ser Gly Arg Lys Glu Thr Tyr Pro Phe Ile Gly Glu Pro Asp Pro  
 450 455 460

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Phe Lys Phe Thr Cys Met Asn Glu Thr Asn Thr Cys Thr Val Thr Gly  
 465 470 475 480  
 Ala Ala Lys Ala Leu Arg Ala Trp Phe Asn Ala Gly Arg Ser Glu Leu  
 485 490 495  
 5 Ala Val Ser Val Ser Leu Asn Ile Ala Gly Thr Tyr Arg Ile Lys Leu  
 500 505 510  
 Tyr Asn Thr Ala Gly Glu Glu Val Ala Ala Met Thr Lys Glu Leu Val  
 515 520 525  
 10 Ala Gly Thr Ser Val Phe Ser Met Asp Val Tyr Ser Gln Ala Pro Gly  
 530 535 540  
 Thr Tyr Val Leu Val Val Glu Gly Asn Gly Ile Arg Glu Thr Met Lys  
 545 550 555 560  
 Ile Leu Lys

15 (2) INFORMATION FOR SEQ ID NO:383  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 437 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 20 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 25 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...437  
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:383  
 35 Thr Thr Asn Arg Lys Pro Asn Thr Asn Met Lys Leu Ser Ser Lys Lys  
 1 5 10 15  
 Ile Leu Ala Ile Ile Ala Leu Leu Thr Met Gly His Ala Val Gln Ala  
 20 25 30  
 40 Gln Phe Val Pro Ala Pro Thr Thr Gly Ile Arg Met Ser Val Thr Thr  
 35 40 45  
 Thr Lys Ala Val Gly Glu Lys Ile Glu Leu Leu Val His Ser Ile Glu  
 50 55  
 Lys Lys Gly Ile Trp Ile Asp Leu Asn Gly Asp Ala Thr Tyr Gln Gln  
 60 65 70 75 80  
 Gly Glu Glu Ile Thr Val Phe Asp Glu Ala Tyr His Glu Tyr Thr Ile  
 85 90 95  
 Gly Thr Gln Thr Leu Thr Ile Tyr Gly Asn Thr Thr Arg Leu Gly Cys  
 100 105 110  
 50 Arg Ser Thr Gly Ala Thr Ala Val Asp Val Thr Lys Asn Pro Asn Leu  
 115 120 125  
 Thr Tyr Leu Ala Cys Pro Lys Asn Asn Leu Lys Ser Leu Asp Leu Thr  
 130 135 140  
 Gln Asn Pro Lys Leu Leu Arg Val Trp Cys Asp Ser Asn Glu Ile Glu  
 145 150 155 160  
 55 Ser Leu Asp Leu Ser Gly Asn Pro Ala Leu Ile Ile Leu Gly Cys Asp  
 165 170 175  
 Arg Asn Lys Leu Thr Glu Leu Lys Thr Asp Asn Asn Pro Lys Leu Ala  
 180 185 190  
 60 Ser Leu Trp Cys Ser Asp Asn Asn Leu Thr Glu Leu Glu Ser Ala  
 195 200 205  
 Asn Pro Arg Leu Asn Asp Leu Trp Cys Phe Gly Asn Arg Ile Thr Lys  
 210 215 220  
 65 Leu Asp Leu Ser Ala Asn Pro Leu Leu Val Thr Leu Trp Cys Ser Asp  
 225 230 235 240  
 Asn Glu Leu Ser Thr Leu Asp Leu Ser Lys Asn Ser Asp Val Ala Tyr  
 245 250 255  
 Leu Trp Cys Ser Ser Asn Lys Leu Thr Ser Leu Asn Leu Ser Gly Val  
 260 265 270  
 70 Lys Gly Leu Ser Val Leu Val Cys His Ser Asn Gln Ile Ala Gly Glu  
 275 280 285  
 Glu Met Thr Lys Val Val Asn Ala Leu Pro Thr Leu Ser Pro Gly Ala  
 290 295 300  
 75 Gly Ala Gln Ser Lys Phe Val Val Val Asp Leu Lys Asp Thr Asp Glu  
 305 310 315 320

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Lys Asn Ile Cys Thr Val Lys Asp Val Glu Lys Ala Lys Ser Lys Asn  
 325 330 335  
 Trp Arg Val Phe Asp Phe Asn Gly Asp Ser Asp Asn Met Leu Pro Tyr  
 340 345 350  
 5 Glu Gly Ser Pro Thr Ser Asn Leu Ala Val Asp Ala Pro Thr Val Arg  
 355 360 365  
 Ile Tyr Pro Asn Pro Val Gly Arg Tyr Ala Leu Val Glu Ile Pro Glu  
 370 375 380  
 10 Ser Leu Leu Gly Gln Glu Ala Ala Leu Tyr Asp Met Asn Gly Val Lys  
 385 390 395 400  
 Val Tyr Ser Phe Ala Val Glu Ser Leu Arg Gln Asn Ile Asp Leu Thr  
 405 410 415  
 His Leu Pro Asp Gly Thr Tyr Phe Phe Arg Leu Asp Asn Tyr Thr Thr  
 420 425 430  
 15 Lys Leu Ile Lys Gln  
 435

(2) INFORMATION FOR SEQ ID NO:384

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 318 amino acids  
 (R) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 25 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...318  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:384

Asn His Leu Lys Thr Asn Ile Lys Met Arg Lys Thr Ile Ile Phe Cys  
 1 5 10 15  
 40 Leu Leu Leu Ala Leu Phe Gly Cys Ser Trp Ala Gln Glu Arg Val Asp  
 20 25 30  
 Glu Lys Val Phe Ser Ala Gly Thr Ser Ile Phe Arg Gly Ile Leu Glu  
 35 40 45  
 45 Lys Val Lys Ala Pro Leu Met Tyr Gly Asp Arg Glu Val Trp Gly Met  
 50 55 60  
 Ala Arg Ala Ser Glu Asp Phe Phe Phe Ile Leu Pro Val Thr Asp Asp  
 65 70 75 80  
 Leu Thr Pro Val Leu Phe Tyr Asn Arg Leu Thr Asn Glu Pro Cys Phe  
 85 90 95  
 50 Val Ser Asp Gln Gly Ile Thr Glu Tyr Phe Lys Phe Ala Gln Glu Gly  
 100 105 110  
 Asp Tyr Ile Glu Val Glu Gly Ser Ser Val Phe Met Ala Asn Leu Leu  
 115 120 125  
 55 Tyr Tyr Arg Phe Phe Pro Thr Arg Ile Thr Ser Tyr Asn Ala Pro Ile  
 130 135 140  
 Glu Gly Val Val Ser Lys Thr Gly Asn Pro Ala Phe Thr Ile Pro Met  
 145 150 155 160  
 Leu Pro Gly Val Ser Asp Cys Ile Glu Ile Ser Asn Asn Arg Lys Val  
 165 170 175  
 60 Phe Leu Thr Asn Gln Leu Gly Val Val Asn Ile Thr Asp Gly Met Glu  
 180 185 190  
 Pro Pro Ile Ile Ala Gly Val Ser Ala Ser Tyr Gly Ser Ser Val Arg  
 195 200 205  
 65 Val Tyr Gly His Val Ser Gln Arg Trp Asp Ile Ile Gly His Cys Tyr  
 210 215 220  
 Leu Asp Ile Tyr Pro Thr Asn Cys Tyr Pro Leu Ser Thr Lys Pro Val  
 225 230 235 240  
 Ala Gly Asp Asp Glu Val Phe Val Lys Gln Gly Arg Gln Ile Glu  
 245 250 255  
 70 Ile Asp Ser Asn Ser Pro Ile Val Gln Val Val Val Tyr Asp Leu Glu  
 260 265 270  
 Gly Lys Ser Val Phe Arg Lys Arg Met Thr Glu Asn Ala Tyr Thr Leu  
 275 280 285  
 75 Ser Phe Arg Ala Pro Met Leu Gly Phe Met Thr Ile Met Ile Glu Thr  
 290 295 300

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Gln Asn Ser Ile Ile Asn Lys Lys Leu Asn Val Thr Gln Leu  
305 310 315

5 (2) INFORMATION FOR SEQ ID NO:385

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 461 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

15 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

20 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385

25 Arg Arg Ala Val Lys Ile Arg Ser Pro Pro His Ile His Ser Leu Phe  
1 5 10 15  
Val Arg Lys Cys Leu Phe Ser Asp Phe Lys Tyr Leu Tyr Leu Ser Arg  
20 25 30  
Lys Ile Thr Gln Glu Arg Leu Gly Arg Leu Ser Ile Arg Leu Lys Ser  
35 40 45  
30 Tyr Asn Pro Ile Ile Ile Ile Glu Met Lys Lys Thr Thr Ile Ile Ser  
50 55 60  
Leu Ile Val Phe Gly Ala Phe Phe Ala Ala Val Gly Gln Thr Lys Asp  
65 70 75 80  
35 Asn Ser Ser Tyr Lys Pro Phe Ser Lys Glu Asp Ile Ala Gly Gly Val  
85 90 95  
Tyr Ser Leu Pro Thr Gln Asn Arg Ala Gln Lys Asp Asn Ala Glu Trp  
100 105 110  
Leu Leu Thr Ala Thr Val Ser Thr Asn Gln Ser Ala Asp Thr His Phe  
115 120 125  
40 Ile Phe Asp Glu Asn Asn Arg Tyr Ile Ala Arg Asp Ile Lys Ala Asn  
130 135 140  
Gly Val Arg Lys Ser Thr Asp Ser Ile Tyr Tyr Asp Ala Asn Gly Arg  
145 150 155 160  
45 Ile Ser His Val Asp Leu Tyr Ile Ser Phe Ser Gly Gly Glu Pro Ala  
165 170 175  
Leu Asp Thr Arg Phe Lys Tyr Thr Tyr Asp Asp Glu Gly Lys Met Thr  
180 185 190  
Val Arg Glu Val Phe Met Leu Val Met Asp Pro Asn Thr Pro Ile Ser  
195 200 205  
50 Arg Leu Glu Tyr His Tyr Asp Ala Gln Gly Arg Leu Thr His Trp Ile  
210 215 220  
Ser Phe Ala Phe Gly Ala Glu Ser Gln Lys Asn Thr Tyr His Tyr Asn  
225 230 235 240  
55 Glu Lys Gly Leu Leu Val Ser Glu Val Leu Ser Asn Ala Met Gly Thr  
245 250 255  
Thr Tyr Ser Asp Thr Gly Lys Thr Glu Tyr Ser Tyr Asp Asp Ala Asp  
260 265 270  
Asn Met Val Lys Ala Glu Tyr Phe Val Val Gln Gln Gly Lys Ala Trp  
275 280 285  
60 Gln Val Leu Lys Arg Glu Glu Tyr Thr Tyr Glu Asp Asn Ile Cys Ile  
290 295 300  
Gln Tyr Leu Ala Ile Asn Gly Thr Asp Thr Lys Val Tyr Lys Arg Asp  
305 310 315 320  
65 Ile Glu Ser Asp Lys Ser Ile Ser Ala Asn Val Ile Asp Ile Pro Ser  
325 330 335  
Met Pro Glu Gln Thr Trp Pro Asn Met Tyr Gly Phe Asn Ala Lys Arg  
340 345 350  
Leu Lys Glu Thr Tyr Ser Ser Tyr Glu Gly Asp Val Ala Thr Pro Ile  
355 360 365  
70 Phe Asp Tyr Ile Tyr Thr Tyr Lys Ala Leu Thr Ser Met Ala Thr Pro  
370 375 380  
Ser Thr Glu Ala Gln Val Ala Val Tyr Leu Asn Pro Ser Thr Asp Arg  
385 390 395 400  
75 Leu Val Ile Leu Ala Asn Gly Ile Thr His Leu Ser Met Tyr Asp Leu  
405 410 415

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Gln Gly Lys Leu Ile Arg Asp Cys Ala Leu Ser Gly Asp Lys Val Glu  
 420 425 430  
 Met Gly Val Gly Ser Leu Thr Lys Gly Thr Tyr Leu Leu Lys Val Asn  
 435 440 445  
 5 Thr Asp Gln Gly Ala Phe Val Arg Lys Val Val Ile Arg  
 450 455 460

(2) INFORMATION FOR SEQ ID NO:386

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 451 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES
- 20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...451
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:386

Met Ala Lys Val Ile Lys Thr Lys Lys Gly Leu Ala Leu Asn Leu Lys  
 1 5 10 15  
 30 Gly Lys Pro Leu Pro Glu Met Leu Ala Glu Pro Ala Gln Ser Pro Thr  
 20 25 30  
 Tyr Ala Val Val Pro Asp Asp Phe Glu Gly Val Ile Pro Lys Val Thr  
 35 40 45  
 Ala Arg Pro Gly Asp Lys Val Arg Ala Gly Ser Ala Leu Met His His  
 50 55 60  
 Lys Ala Tyr Pro Glu Met Lys Phe Thr Ser Pro Val Ser Gly Glu Val  
 65 70 75 80  
 Ile Ala Val Asn Arg Gly Ala Lys Arg Lys Val Leu Ser Ile Glu Val  
 85 90 95  
 40 Lys Pro Asp Gly Leu Asn Glu Tyr Glu Ser Phe Pro Val Gly Asp Pro  
 100 105 110  
 Ser Ala Leu Ser Ala Glu Gln Ile Lys Glu Leu Leu Ser Ser Gly  
 115 120 125  
 45 Met Trp Gly Phe Ile Lys Gln Arg Pro Tyr Asp Ile Val Ala Thr Pro  
 130 135 140  
 Asp Ile Ala Pro Arg Asp Ile Tyr Ile Thr Ala Asn Phe Thr Ala Pro  
 145 150 155 160  
 Leu Ala Pro Asp Phe Asp Phe Ile Val Arg Gly Glu Glu Arg Ala Leu  
 165 170 175  
 50 Gln Thr Ala Ile Asp Ala Leu Ala Lys Leu Thr Thr Gly Lys Val Tyr  
 180 185 190  
 Val Gly Leu Lys Pro Gly Ser Ser Leu Gly Leu His Asn Ala Glu Ile  
 195 200 205  
 55 Val Glu Val His Gly Pro His Pro Ala Gly Asn Val Gly Val Leu Ile  
 210 215 220  
 Asn His Thr Lys Pro Ile Asn Arg Gly Glu Thr Val Trp Thr Leu Lys  
 225 230 235 240  
 Ala Thr Asp Leu Ile Val Ile Gly Arg Phe Leu Leu Thr Gly Lys Ala  
 245 250 255  
 60 Asp Phe Thr Arg Met Ile Ala Met Thr Gly Ser Asp Ala Ala Ala His  
 260 265 270  
 Gly Tyr Val Arg Ile Met Pro Gly Cys Asn Val Phe Ala Ser Phe Pro  
 275 280 285  
 65 Gly Arg Leu Thr Ile Lys Glu Ser His Glu Arg Val Ile Asp Gly Asn  
 290 295 300  
 Val Leu Thr Gly Lys Lys Leu Cys Glu Lys Glu Pro Phe Leu Ser Ala  
 305 310 315 320  
 Arg Cys Asp Gln Ile Thr Val Ile Pro Glu Gly Asp Asp Val Asp Glu  
 325 330 335  
 70 Leu Phe Gly Trp Ala Ala Pro Arg Leu Asp Gln Tyr Ser Met Ser Arg  
 340 345 350  
 Ala Tyr Phe Ser Trp Leu Gln Gly Lys Asn Lys Glu Tyr Val Leu Asp  
 355 360 365  
 75 Ala Arg Ile Lys Gly Gly Glu Arg Ala Met Ile Met Ser Asn Glu Tyr  
 370 375 380

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Asp Arg Val Phe Pro Met Asp Ile Tyr Pro Glu Tyr Leu Leu Lys Ala  
 305 390 395 400  
 Ile Ile Ala Phe Asp Ile Asp Lys Met Glu Asp Leu Gly Ile Tyr Glu  
 405 410 415  
 5 Val Ala Pro Glu Asp Phe Ala Thr Cys Glu Phe Val Asp Thr Ser Lys  
 420 425 430  
 Ile Glu Leu Gln Arg Ile Val Arg Glu Gly Leu Asp Met Leu Tyr Lys  
 435 440 445  
 10 Glu Met Asn  
 450

## (2) INFORMATION FOR SEQ ID NO:387

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 195 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 20 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- 25 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...195
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:387

Met Asp Lys Val Ser Tyr Ala Leu Gly Leu Ser Ile Gly Asn Asn Phe  
 1 5 10 15  
 35 Lys Ser Ser Gly Ile Asp Ser Val Val Met Asp Asp Phe Met Gln Gly  
 20 25 30  
 Leu Ser Asp Val Leu Glu Glu Lys Ala Pro Gln Leu Ser Tyr Asp Glu  
 35 40 45  
 Ala Lys Arg Glu Ile Glu Ala Tyr Phe Met Asp Leu Gln Gln Lys Ala  
 50 55 60  
 40 Val Lys Leu Asn Lys Glu Ala Gly Glu Glu Phe Leu Lys Ile Asn Ala  
 65 70 75 80  
 His Lys Glu Gly Val Thr Thr Leu Pro Ser Gly Leu Gln Tyr Glu Val  
 85 90 95  
 45 Ile Lys Met Gly Glu Gly Pro Lys Pro Thr Leu Ser Asp Thr Val Thr  
 100 105 110  
 Cys His Tyr His Gly Thr Leu Ile Asn Gly Ile Val Phe Asp Ser Ser  
 115 120 125  
 Met Asp Arg Gly Glu Pro Ala Ser Phe Pro Leu Arg Gly Val Ile Ala  
 130 135 140  
 50 Gly Trp Thr Glu Ile Leu Gln Leu Met Pro Val Gly Ser Lys Trp Lys  
 145 150 155 160  
 Val Thr Ile Pro Ser Asp Leu Ala Tyr Gly Asp Arg Gly Ala Gly Glu  
 165 170 175  
 55 His Ile Lys Pro Gly Ser Thr Leu Ile Phe Ile Ile Glu Leu Leu Ser  
 180 185 190  
 Ile Asn Lys  
 195

## (2) INFORMATION FOR SEQ ID NO:388

- 60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 273 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 65 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 70 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...273
- 75

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      115      120      125
Thr Ala Phe Glu Tyr Val Gly Gly Thr Ile Gly Asn Gly Val Leu Leu
130      135      140
Met His Arg His Asp Ala Asp Ile Asn Asn Thr Glu Cys Val Tyr Lys
5 145      150      155      160
Lys Asp Phe Pro Asn Asn Arg Leu Met Gly Val Ala Ile Ala Ser Asn
      165      170      175
Tyr Arg Ala Pro Ser Pro Tyr Gly Leu Gly Gly Asp Pro Phe Ala Leu
      180      185      190
10 Ala Val Ala Val Ser Gly Ser Gly Ser Asp His Ser Phe Leu Asp Tyr
      195      200      205
Ile Phe Ser Leu Asp Gly Gly Val His Phe Glu Gln Lys Arg Ile Tyr
      210      215      220
Thr Arg Pro Gln Lys Leu Thr Ile Asn Arg Val Asp Leu Ser Leu Gly
15 225      230      235      240
Ser Thr Ser Pro Ser Leu Gly Phe Asn Thr Trp Pro Leu Met Gly Val
      245      250      255
Val Phe Glu Met Asn Lys Asn Leu Asp Gly Phe Asp Ile Gly Phe Ile
      260      265      270
20 Ser Asn Phe Val Asp Tyr Asp Pro Arg Tyr Ala Trp Ser Glu Pro Ile
      275      280      285
Ile Ile Glu Glu Asp Cys Gly Trp Thr Asp Phe Asn Pro Leu Gly Ala
      290      295      300
Leu Ser Ile Glu Ile Gln Met Met Leu Asp Asp Asn Ser Asp Asn Thr
25 305      310      315      320
Val Gly Gly Glu Arg Ser His Asn Phe Leu Ile Thr Tyr Pro Gly His
      325      330      335
Tyr Val Tyr Pro Lys Gln Ser Phe Asn Tyr Ser Pro Gly His Thr Pro
      340      345      350
30 Thr Lys Lys Asp Leu Val Phe Lys His Cys Ile Gly Ile Pro Ala Leu
      355      360      365
Ala Tyr Asp Lys Glu Gly Asp Arg Tyr Leu Thr Thr Phe Gln Asp His
      370      375      380
Asn Leu Met Arg Tyr Arg Trp Ile Lys Tyr Asp Asp Ile Asn Ser Phe
35 385      390      395      400
Tyr Gly Trp Ser Trp Pro Tyr Val Tyr Ala Lys Glu Ala Lys Asp Lys
      405      410      415
Lys Arg Arg Arg Pro Gln Val Ala Leu Asn Pro Thr Asn Gly Lys Ala
      420      425      430
40 Cys Trp Val Trp His Thr Arg Lys Ser Pro Tyr Asp Glu Thr Lys Pro
      435      440      445
His Pro Thr Pro Val Ile Ile Lys His Phe Leu Trp Ser Asp Thr Glu
      450      455      460
45 Trp Val His Ala Leu Asp Val Gly Asp Val Leu Gln Lys Glu Gly Ser
      465      470      475      480
Met Lys Leu Tyr Pro Asn Pro Ala Lys Glu Tyr Val Leu Ile Asn Leu
      485      490      495
Pro Lys Glu Gly Gly His Glu Ala Val Val Tyr Asp Met Gln Gly Arg
      500      505      510
50 Ile Val Glu Lys Val Ser Phe Ser Gly Lys Glu Tyr Lys Leu Asn Val
      515      520      525
Gln Tyr Leu Ser Lys Gly Thr Tyr Met Leu Lys Val Val Ala Asp Thr
      530      535      540
Glu Tyr Phe Val Glu Lys Ile Ile Val Glu
55 545      550

```

## (2) INFORMATION FOR SEQ ID NO:390

- 60 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 550 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 65 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- 70 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...550
- 75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:390

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Met Lys Leu Lys Ile Ala Leu Arg Leu Leu Leu Ala Thr Phe Ala Ile  
 1 5 10 15  
 Val Leu Phe Ser Pro Leu Ala Lys Ala Gln Met Asp Ile Gly Gly Asp  
 20 25 30  
 Asp Val Leu Ile Glu Thr Met Ser Thr Leu Ser Gly Tyr Ser Glu Asp  
 35 40 45  
 Phe Tyr Tyr Lys Met Ala Val Ala Asp Asn Gly Trp Ile Tyr Val Met  
 50 55 60  
 Leu Asp Phe Ser Arg Ile Tyr Phe Asp Asp Val Arg Leu Tyr Arg Ser  
 65 70 75 80  
 Lys Asp Gly Gly Ala Thr Tyr Gln Lys Leu Gly Ser Leu Gly Ser Leu  
 85 90 95  
 Val Pro Tyr Asp Phe Asp Val Ser His Cys Asp Phe Ile Val Thr Gly  
 100 105 110  
 Lys Asp Glu Asp Asp Ile Asn Val Trp Thr Val Met Thr Ala Phe Glu  
 115 120 125  
 Tyr Val Gly Gly Thr Ile Gly Asn Gly Val Leu Leu Met His Arg His  
 130 135 140  
 Asp Ala Asp Ile Asn Asn Thr Glu Cys Val Tyr Lys Lys Asp Phe Pro  
 145 150 155 160  
 Asn Asn Arg Leu Met Gly Val Ala Ile Ala Ser Asn Tyr Arg Ala Pro  
 165 170 175  
 Ser Pro Tyr Gly Leu Gly Gly Asp Pro Phe Ala Leu Ala Val Ala Val  
 180 185 190  
 Ser Gly Ser Gly Ser Asp His Ser Phe Leu Asp Tyr Ile Phe Ser Leu  
 195 200 205  
 Asp Gly Gly Val His Phe Glu Gln Lys Arg Ile Tyr Thr Arg Pro Gln  
 210 215 220  
 Lys Leu Thr Ile Asn Arg Val Asp Leu Ser Leu Gly Ser Thr Ser Pro  
 225 230 235 240  
 Ser Leu Gly Phe Asn Thr Trp Pro Leu Met Gly Val Val Phe Glu Met  
 245 250 255  
 Asn Lys Asn Leu Asp Gly Phe Asp Ile Gly Phe Ile Ser Asn Phe Val  
 260 265 270  
 Asp Tyr Asp Pro Arg Tyr Ala Trp Ser Glu Pro Ile Ile Glu Glu  
 275 280 285  
 Asp Cys Gly Trp Thr Asp Phe Asn Pro Leu Gly Ala Leu Ser Ile Glu  
 290 295 300  
 Ile Gln Met Met Leu Asp Asn Ser Asp Asn Thr Val Gly Gly Glu  
 305 310 315 320  
 Arg Ser His Asn Phe Leu Ile Thr Tyr Pro Gly His Tyr Val Tyr Pro  
 325 330 335  
 Lys Gln Ser Phe Asn Tyr Ser Pro Gly His Thr Pro Thr Lys Lys Asp  
 340 345 350  
 Leu Val Phe Lys His Cys Ile Gly Ile Pro Ala Leu Ala Tyr Asp Lys  
 355 360 365  
 Glu Gly Asp Arg Tyr Leu Thr Thr Phe Gln Asp His Asn Leu Met Arg  
 370 375 380  
 Tyr Arg Trp Ile Lys Tyr Asp Asp Ile Asn Ser Phe Tyr Gly Trp Ser  
 385 390 395 400  
 Trp Pro Tyr Val Tyr Ala Lys Glu Ala Lys Asp Lys Lys Arg Arg Arg  
 405 410 415  
 Pro Gln Val Ala Leu Asn Pro Thr Asn Gly Lys Ala Cys Trp Val Trp  
 420 425 430  
 His Thr Arg Lys Ser Pro Tyr Asp Glu Thr Lys Pro His Pro Thr Pro  
 435 440 445  
 Val Ile Ile Lys His Phe Leu Trp Ser Asp Thr Glu Trp Val His Ala  
 450 455 460  
 Leu Asp Val Gly Asp Val Leu Gln Lys Glu Gly Ser Met Lys Leu Tyr  
 465 470 475 480  
 Pro Asn Pro Ala Lys Glu Tyr Val Leu Ile Asn Leu Pro Lys Glu Gly  
 485 490 495  
 Gly His Glu Ala Val Val Tyr Asp Met Gln Gly Arg Ile Val Glu Lys  
 500 505 510  
 Val Ser Phe Ser Gly Lys Glu Tyr Lys Leu Asn Val Gln Tyr Leu Ser  
 515 520 525  
 Lys Gly Thr Tyr Met Leu Lys Val Val Ala Asp Thr Glu Tyr Phe Val  
 530 535 540  
 Glu Lys Ile Ile Val Glu  
 545 550

75 (2) INFORMATION FOR SEQ ID NO:391

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 390 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...390
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:391
- |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Arg | Leu | Leu | Pro | Phe | Leu | Leu | Leu | Ala | Gly | Leu | Val | Ala | Val |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Gly | Asn | Val | Ser | Ala | Gln | Ser | Pro | Arg | Ile | Pro | Gln | Val | Asp | Val | His |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Thr | Arg | Ile | Ala | Arg | Asn | Ala | Arg | Tyr | Arg | Leu | Asp | Lys | Ile | Ser | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Pro | Asp | Ser | Arg | Gln | Ile | Phe | Asp | Tyr | Phe | Tyr | Lys | Glu | Glu | Thr | Ile |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Pro | Thr | Lys | Ile | Gln | Thr | Thr | Thr | Gly | Gly | Ala | Ile | Thr | Ser | Ile | Asp |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Leu | Phe | Tyr | Glu | Asp | Asp | Arg | Leu | Val | Gln | Val | Arg | Tyr | Phe | Asp |
|     |     | 85  |     |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Asn | Asn | Leu | Glu | Leu | Lys | Gln | Ala | Glu | Lys | Tyr | Val | Tyr | Asp | Gly | Ser |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Leu | Val | Leu | Arg | Glu | Ile | Arg | Lys | Ser | Pro | Thr | Asp | Glu | Thr | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Lys | Lys | Val | Ser | Tyr | His | Tyr | Leu | Cys | Gly | Ser | Asp | Met | Pro | Phe |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Glu | Ile | Thr | Thr | Glu | Met | Ser | Asp | Gly | Tyr | Phe | Glu | Ser | His | Thr | Leu |
|     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Asn | Tyr | Leu | Asn | Gly | Lys | Ile | Ala | Arg | Ile | Asp | Ile | Met | Thr | Gln | Gln |
|     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Asn | Pro | Ser | Ala | Glu | Leu | Ile | Glu | Thr | Gly | Arg | Met | Val | Tyr | Glu | Phe |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asp | Ala | Asn | Asn | Asp | Ala | Val | Leu | Leu | Arg | Asp | Ser | Val | Phe | Leu | Pro |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Gln | Asn | Lys | Trp | Val | Glu | Met | Phe | Thr | His | Arg | Tyr | Thr | Tyr | Asp |
|     | 210 |     |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |
| Asn | Lys | His | Asn | Cys | Ile | Arg | Trp | Glu | Gln | Asp | Glu | Phe | Gly | Thr | Leu |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Thr | Leu | Ala | Asn | Asn | Phe | Glu | Tyr | Asp | Thr | Thr | Ile | Pro | Leu | Ser | Ser |
|     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Val | Leu | Phe | Pro | Thr | His | Glu | Glu | Phe | Phe | Arg | Pro | Leu | Leu | Pro | Asn |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     | 270 |     |     |     |
| Phe | Met | Lys | His | Met | Arg | Thr | Lys | Gln | Thr | Tyr | Phe | Asn | Asn | Ser | Gly |
|     | 275 |     |     |     |     |     | 280 |     |     |     | 285 |     |     |     |     |
| Glu | Gly | Leu | Ser | Glu | Val | Cys | Asp | Tyr | Asn | Tyr | Phe | Tyr | Thr | Asp | Met |
|     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |
| Gln | Gly | Asn | Ala | Leu | Thr | Asp | Val | Ala | Val | Asn | Glu | Ser | Ile | Lys | Ile |
|     | 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Tyr | Pro | Arg | Pro | Ala | Thr | Asp | Phe | Leu | Arg | Ile | Glu | Gly | Ser | Gln | Leu |
|     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |     |
| Leu | Arg | Leu | Ser | Leu | Phe | Asp | Met | Asn | Gly | Lys | Leu | Ile | Arg | Ala | Thr |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |
| Glu | Leu | Thr | Gly | Asp | Leu | Ala | Ile | Ile | Gly | Val | Ala | Ser | Leu | Pro | Arg |
|     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |     |
| Gly | Thr | Tyr | Ile | Ala | Glu | Ile | Thr | Ala | Ala | Asn | Ser | Lys | Thr | Ile | Arg |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Ala | Lys | Val | Ser | Leu | Arg |     |     |     |     |     |     |     |     |     |     |
|     | 385 |     |     |     | 390 |     |     |     |     |     |     |     |     |     |     |
- (2) INFORMATION FOR SEQ ID NO:392
- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 411 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392

Met Arg Gln His Leu Ser Leu Phe Pro Phe Ile Leu Phe Leu Leu Leu  
1 5 10 15  
Ala Phe Ser Tyr Val Gly Cys Arg Thr Val Arg Gln Thr Pro Lys Gln  
20 25 30  
Ser Glu Arg Tyr Val Val Val Leu Ser Leu Asp Gly Phe Arg Pro Asp  
35 40 45  
Tyr Thr Asp Arg Ala Arg Thr Pro Ala Leu Asp Arg Met Ala Gln Glu  
50 55 60  
Gly Leu Ser Gly Ser Leu Gln Pro Cys Phe Pro Ser Leu Thr Phe Pro  
65 70 75 80  
Asn His Tyr Ser Met Ala Thr Gly Leu Tyr Pro Asp His His Gly Ile  
85 90 95  
Val Ala Asn Glu Phe Val Asp Ser Leu Leu Gly Ile Phe Arg Ile Ser  
100 105 110  
Asp Arg Lys Ala Val Glu Thr Pro Gly Phe Trp Gly Gly Glu Pro Val  
115 120 125  
Trp Asn Thr Ala Ala Arg Gln Gly Ile Arg Thr Gly Val Tyr Phe Trp  
130 135 140  
Val Gly Ser Glu Thr Ala Val Asn Gly Asn Arg Pro Trp Arg Trp Lys  
145 150 155 160  
Lys Phe Ser Ser Thr Val Pro Phe Arg Asp Arg Ala Asp Ser Val Ile  
165 170 175  
Ala Trp Leu Gly Leu Pro Glu Lys Glu Arg Pro Arg Leu Leu Met Trp  
180 185 190  
Tyr Ile Glu Glu Pro Asp Met Ile Gly His Ser Gln Thr Pro Glu Ser  
195 200 205  
Pro Leu Thr Leu Ala Met Val Glu Arg Leu Asp Ser Val Val Gly Tyr  
210 215 220  
Phe Arg Lys Arg Leu Asp Ser Leu Pro Ile Ala Ala Gln Thr Asp Phe  
225 230 235 240  
Ile Ile Val Ser Asp His Gly Met Ala Thr Tyr Glu Asn Glu Lys Cys  
245 250 255  
Val Asn Leu Ser His Tyr Leu Pro Ala Asp Ser Phe Leu Tyr Met Ala  
260 265 270  
Thr Gly Ala Phe Thr His Leu Tyr Pro Lys Pro Ser Tyr Thr Glu Arg  
275 280 285 290  
Ala Tyr Glu Ile Leu Arg Ala Ile Pro His Ile Ser Val Tyr Arg Lys  
295 300 305  
Gly Glu Val Pro Lys Arg Leu Arg Cys Gly Thr Asn Pro Arg Leu Gly  
310 315 320  
Glu Leu Val Val Ile Pro Asp Ile Gly Ser Thr Val Phe Phe Ala Ile  
325 330 335  
Asn Glu Asp Val Arg Pro Gly Ala Ala His Gly Tyr Asp Asn Gln Ala  
340 345 350  
Pro Glu Met Arg Ala Leu Leu Arg Ala Val Gly Pro Asp Phe Arg Pro  
355 360 365  
Gly Ser Arg Val Glu Asn Leu Pro Asn Ile Thr Ile Tyr Pro Leu Ile  
370 375 380  
Cys Arg Leu Leu Gly Ile Glu Pro Ala Pro Asn Asp Ala Asp Glu Thr  
385 390 395 400  
Leu Leu Asn Gly Leu Ile Arg Asp Lys Arg Pro  
405 410

(2) INFORMATION FOR SEQ ID NO:393

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 246 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

5 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...246

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393

Met Lys Val Gly Leu Phe Ile Pro Cys Tyr Val Asn Ala Val Tyr Pro  
 1 5 10 15  
 15 Glu Val Gly Ile Ala Thr Tyr Lys Leu Lys Ser Leu Asp Ile Asp  
 20 25 30  
 Val Asp Tyr Pro Met Asp Gln Thr Cys Cys Gly Gln Pro Met Ala Asn  
 35 40 45  
 20 Ala Gly Phe Glu Gln Lys Ala Gln Lys Leu Ala Leu Arg Phe Glu Glu  
 50 55 60  
 Leu Phe Glu Ser Tyr Asp Val Val Val Gly Pro Ser Ala Ser Cys Val  
 65 70 75 80  
 Ala Phe Val Lys Glu Asn Tyr Asp His Ile Leu Arg Pro Thr Gly His  
 85 90 95  
 25 Val Cys Lys Ser Ala Ala Lys Val Arg Asp Ile Cys Glu Phe Leu His  
 100 105 110  
 Asp Asp Leu Lys Ile Thr Ser Leu Pro Ser Arg Phe Ala His Lys Val  
 115 120 125  
 30 Ser Leu His Asn Ser Cys His Gly Val Arg Glu Leu His Leu Ser Thr  
 130 135 140  
 Pro Ser Glu Val His Arg Pro Tyr His Asn Lys Val Arg Arg Leu Leu  
 145 150 155 160  
 Glu Met Val Gln Gly Ile Glu Val Phe Glu Pro Lys Arg Ile Asp Glu  
 165 170 175  
 35 Cys Cys Gly Phe Gly Gly Met Tyr Ser Val Glu Glu Pro Glu Val Ser  
 180 185 190  
 Thr Cys Met Gly His Asp Lys Val Leu Asp His Ile Ser Thr Gly Ala  
 195 200 205  
 40 Glu Tyr Ile Thr Gly Pro Asp Ser Ser Cys Leu Met His Met Gln Gly  
 210 215 220  
 Val Ile Asp Arg Glu Lys Leu Pro Ile Lys Thr Ile His Ala Val Glu  
 225 230 235 240  
 Ile Leu Ala Ala Asn Leu  
 245

45

(2) INFORMATION FOR SEQ ID NO:394

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids

50

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

55

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

60

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...246

65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394

Met Asp Ile Val Ser Met Ala Asp Lys Ala Leu Val Val Glu Met Arg  
 1 5 10 15  
 Asp Val Thr Leu Cys Gln Glu Glu Asn Val Ile Phe Gln Asn Leu Asn  
 20 25 30  
 70 Leu Thr Leu Ser Ala Gly Asp Phe Val Tyr Leu Ile Gly Ser Val Gly  
 35 40 45  
 Ser Gly Lys Ser Thr Leu Leu Lys Ala Leu Tyr Ala Glu Val Pro Ile  
 50 55 60  
 75 Ser Ala Gly Tyr Ala Arg Val Ile Asp Tyr Asp Leu Ala Lys Leu Lys  
 65 70 75 80

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Arg Lys Gln Leu Pro Tyr Leu Arg Arg Asn Leu Gly Ile Val Phe Gln  
 85 90 95  
 Asp Phe Gln Leu Leu Asn Gly Arg Thr Val Ala Glu Asn Leu Asp Phe  
 100 105 110  
 5 Val Leu Arg Ala Thr Asp Trp Lys Asn Arg Ala Asp Arg Glu Gln Arg  
 115 120 125  
 Ile Glu Glu Val Leu Thr Arg Val Gly Met Ser Arg Lys Ala Tyr Lys  
 130 135 140  
 10 Arg Pro His Glu Leu Ser Gly Gly Glu Gln Gln Arg Val Gly Ile Ala  
 145 150 155 160  
 Arg Ala Leu Leu Ala Lys Pro Ala Leu Ile Leu Ala Asp Glu Pro Thr  
 165 170 175  
 Gly Asn Leu Asp Ser Val Thr Gly Leu Gln Ile Ala Ser Leu Leu Tyr  
 180 185 190  
 15 Glu Ile Ser Lys Gln Gly Thr Ala Val Leu Met Ser Thr His Asn Ser  
 195 200 205  
 Ser Leu Leu Ser His Leu Pro Ala Arg Thr Leu Ala Val Arg Lys Asn  
 210 215 220  
 20 Gly Asp Ala Ser Ser Leu Val Glu Leu Ser Ala Asp Ala Val Ser Arg  
 225 230 235 240  
 Lys Asn Thr Glu Ile Asp

25 (2) INFORMATION FOR SEQ ID NO:395

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 241 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...241

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:395

45 Met Ala Asp Lys Ala Leu Val Val Glu Met Arg Asp Val Thr Leu Cys  
 1 5 10 15  
 Gln Glu Glu Asn Val Ile Phe Gln Asn Leu Asn Leu Thr Leu Ser Ala  
 20 25 30  
 Gly Asp Phe Val Tyr Leu Ile Gly Ser Val Gly Ser Gly Lys Ser Thr  
 35 40 45  
 50 Leu Leu Lys Ala Leu Tyr Ala Glu Val Pro Ile Ser Ala Gly Tyr Ala  
 50 55 60  
 Arg Val Ile Asp Tyr Asp Leu Ala Lys Leu Lys Arg Lys Gln Leu Pro  
 65 70 75 80  
 Tyr Leu Arg Arg Asn Leu Gly Ile Val Phe Gln Asp Phe Gln Leu Leu  
 85 90 95  
 55 Asn Gly Arg Thr Val Ala Glu Asn Leu Asp Phe Val Leu Arg Ala Thr  
 100 105 110  
 Asp Trp Lys Asn Arg Ala Asp Arg Glu Gln Arg Ile Glu Glu Val Leu  
 115 120 125  
 60 Thr Arg Val Gly Met Ser Arg Lys Ala Tyr Lys Arg Pro His Glu Leu  
 130 135 140  
 Ser Gly Gly Glu Gln Gln Arg Val Gly Ile Ala Arg Ala Leu Leu Ala  
 145 150 155 160  
 Lys Pro Ala Leu Ile Leu Ala Asp Glu Pro Thr Gly Asn Leu Asp Ser  
 165 170 175  
 65 Val Thr Gly Leu Gln Ile Ala Ser Leu Leu Tyr Glu Ile Ser Lys Gln  
 180 185 190  
 Gly Thr Ala Val Leu Met Ser Thr His Asn Ser Ser Leu Leu Ser His  
 195 200 205  
 70 Leu Pro Ala Arg Thr Leu Ala Val Arg Lys Asn Gly Asp Ala Ser Ser  
 210 215 220  
 Leu Val Glu Leu Ser Ala Asp Ala Val Ser Arg Lys Asn Thr Glu Ile  
 225 230 235  
 75 Asp



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## (2) INFORMATION FOR SEQ ID NO:396

5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 232 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

15 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...232

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:396

Met	Arg	Asp	Val	Thr	Leu	Cys	Gln	Glu	Glu	Asn	Val	Ile	Phe	Gln	Asn
1				5					10					15	
Leu	Asn	Leu	Thr	Leu	Ser	Ala	Gly	Asp	Phe	Val	Tyr	Leu	Ile	Gly	Ser
25				20				25					30		
Val	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Leu	Lys	Ala	Leu	Tyr	Ala	Glu	Val
	35						40					45			
Pro	Ile	Ser	Ala	Gly	Tyr	Ala	Arg	Val	Ile	Asp	Tyr	Asp	Leu	Ala	Lys
	50				55					60					
Leu	Lys	Arg	Lys	Gln	Leu	Pro	Tyr	Leu	Arg	Arg	Asn	Leu	Gly	Ile	Val
65					70				75				80		
Phe	Gln	Asp	Phe	Gln	Leu	Leu	Asn	Gly	Arg	Thr	Val	Ala	Glu	Asn	Leu
			85						90				95		
Asp	Phe	Val	Leu	Arg	Ala	Thr	Asp	Trp	Lys	Asn	Arg	Ala	Asp	Arg	Glu
			100						105				110		
Gln	Arg	Ile	Glu	Glu	Val	Leu	Thr	Arg	Val	Gly	Met	Ser	Arg	Lys	Ala
			115						120				125		
Tyr	Lys	Arg	Pro	His	Glu	Leu	Ser	Gly	Gly	Glu	Gln	Gln	Arg	Val	Gly
	130						135					140			
Ile	Ala	Arg	Ala	Leu	Leu	Ala	Lys	Pro	Ala	Leu	Ile	Leu	Ala	Asp	Glu
145					150					155				160	
Pro	Thr	Gly	Asn	Leu	Asp	Ser	Val	Thr	Gly	Leu	Gln	Ile	Ala	Ser	Leu
			165						170					175	
Leu	Tyr	Glu	Ile	Ser	Lys	Gln	Gly	Thr	Ala	Val	Leu	Met	Ser	Thr	His
			180					185					190		
Asn	Ser	Ser	Leu	Leu	Ser	His	Leu	Pro	Ala	Arg	Thr	Leu	Ala	Val	Arg
			195				200					205			
Lys	Asn	Gly	Asp	Ala	Ser	Ser	Leu	Val	Glu	Leu	Ser	Ala	Asp	Ala	Val
	210						215					220			
Ser	Arg	Lys	Asn	Thr	Glu	Ile	Asp								
225					230										

## (2) INFORMATION FOR SEQ ID NO:397

55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 219 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

65 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...219

70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:397

Met	Ile	Glu	Ile	Ser	Asn	Leu	Thr	Lys	Val	Phe	Arg	Thr	Glu	Glu	Ile
1				5					10				15		
Glu	Thr	Val	Ala	Leu	Asp	Gly	Val	Ser	Leu	Lys	Val	Asp	Lys	Gly	Glu

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      20      25      30
Phe Ile Ala Ile Met Gly Pro Ser Gly Cys Gly Lys Ser Thr Leu Leu
      35      40      45
5  Asn Ile Leu Gly Leu Leu Asp Asn Pro Thr Ser Gly Ile Tyr Lys Leu
      50      55      60
    Asp Gly Ala Glu Val Gly Asn Leu Arg Glu Lys Asp Arg Thr Ala Val
    65      70      75      80
    Arg Lys Gly Asn Ile Gly Phe Val Phe Gln Ser Phe Asn Leu Ile Glu
      85      90      95
10  Glu Met Thr Val Ser Glu Asn Val Glu Leu Pro Leu Val Tyr Leu Gly
      100      105      110
    Val Lys Ala Ser Glu Arg Lys Glu Arg Val Glu Glu Ala Leu Arg Lys
      115      120      125
15  Met Ser Ile Ser His Arg Ala Gly His Phe Pro Asn Gln Leu Ser Gly
      130      135      140
    Gly Gln Gln Gln Arg Val Ala Ile Ala Arg Ala Val Val Ala Asn Pro
    145      150      155      160
    Lys Leu Ile Leu Ala Asp Glu Pro Thr Gly Asn Leu Asp Ser Lys Asn
      165      170      175
20  Gly Ala Asp Val Met Glu Leu Leu Arg Gly Leu Asn Arg Glu Gly Ala
      180      185      190
    Thr Ile Val Met Val Thr His Ser Glu His Asp Ala Arg Ser Ala Gly
      195      200      205
25  Arg Ile Ile Asn Leu Phe Asp Gly Lys Ile Arg
      210      215

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(2) INFORMATION FOR SEQ ID NO:398

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30  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 595 amino acids
      (B) TYPE: amino acid
      (D) TOPOLOGY: linear

35  (ii) MOLECULE TYPE: protein

      (iii) HYPOTHETICAL: YES

      (vi) ORIGINAL SOURCE:
40  (A) ORGANISM: Porphyromonas gingivalis

      (ix) FEATURE:
      (A) NAME/KEY: misc_feature
      (B) LOCATION 1...595

45  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:398

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```

Met Lys Glu Phe Phe Lys Met Phe Phe Ala Ser Ile Leu Gly Val Ile
1  5 10 15
Thr Ala Gly Ile Ile Leu Phe Cys Ile Phe Leu Phe Ile Phe Phe Gly
20 25 30
50  Ile Val Ala Gly Ile Ala Ser Lys Ala Thr Gly Gly Thr Ile Pro Lys
      35      40      45
    Ile Glu Ala Asn Ser Ile Leu His Ile Unk Asn Ser Ser Phe Pro Glu
    50      55      60
55  Ile Val Ser Ala Asn Pro Trp Ser Met Leu Thr Gly Lys Asp Glu Ser
    65      70      75      80
    Val Ser Leu Ser Gln Ala Val Glu Ala Ile Gly Gln Ala Lys Asn Asn
      85      90      95
60  Pro Asn Ile Thr Gly Ile Phe Leu Asp Leu Asp Asn Leu Ser Val Gly
      100      105      110
    Met Ala Ser Ala Glu Glu Leu Arg Arg Ala Leu Gln Asp Phe Lys Met
    115      120      125
    Ser Gly Lys Phe Val Val Ser Tyr Ala Asp Arg Tyr Thr Gln Lys Gly
      130      135      140
65  Tyr Tyr Leu Ser Ser Ile Ala Asp Lys Leu Tyr Leu Asn Pro Lys Gly
      145      150      155      160
    Met Leu Gly Leu Ile Gly Ile Ala Thr Gln Thr Met Phe Tyr Lys Asp
      165      170      175
70  Ala Leu Asp Lys Phe Gly Val Lys Met Glu Ile Phe Lys Val Gly Thr
      180      185      190
    Tyr Lys Ala Ala Val Glu Pro Phe Met Leu Asn Arg Met Ser Asp Ala
      195      200      205
    Asn Arg Glu Gln Ile Thr Thr Tyr Ile Asn Gly Leu Trp Asp Lys Ile
      210      215      220
75  Thr Ser Asp Ile Ala Glu Ser Arg Lys Thr Ala Met Asp Ser Val Lys

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225 230 235 240  
 Met Phe Ala Asp Lys Gly Glu Met Phe Gly Leu Ala Glu Lys Ala Val  
 245 250 255  
 5 Glu Met Lys Leu Val Asp Glu Leu Ala Tyr Arg Thr Asp Val Glu Lys  
 260 265 270  
 Glu Leu Lys Lys Met Ser Gln Arg Gly Glu Lys Asp Glu Leu Arg Phe  
 275 280 285  
 Val Ser Leu Ser Gln Val Leu Ala Asn Gly Pro Met Asn Lys Thr Lys  
 290 295 300  
 10 Gly Ser Arg Ile Ala Val Leu Phe Ala Glu Gly Glu Ile Thr Glu Glu  
 305 310 315 320  
 Ile Ile Lys Lys Pro Phe Asp Thr Asp Gly Ser Ser Ile Thr Gln Glu  
 325 330 335  
 15 Leu Ala Lys Glu Ile Lys Ala Ala Ala Asp Asp Asp Ile Lys Ala  
 340 345 350  
 Val Val Leu Arg Val Asn Ser Pro Gly Gly Ser Ala Phe Thr Ser Glu  
 355 360 365  
 Gln Ile Trp Lys Gln Val Ala Asp Leu Lys Ala Lys Lys Pro Ile Val  
 370 375 380  
 20 Val Ser Met Gly Asp Val Ala Ala Ser Gly Gly Tyr Tyr Ile Ala Cys  
 385 390 395 400  
 Ala Ala Asn Ser Ile Val Ala Glu His Thr Thr Leu Thr Gly Ser Ile  
 405 410 415  
 25 Gly Ile Phe Gly Met Phe Pro Asn Phe Ala Gly Val Ala Lys Lys Ile  
 420 425 430  
 Gly Val Asn Met Asp Val Val Gln Thr Ser Lys Tyr Ala Asp Leu Gly  
 435 440 445  
 Asn Thr Phe Ala Pro Met Thr Val Glu Asp Arg Ala Leu Ile Gln Arg  
 450 455 460  
 30 Tyr Ile Glu Gln Gly Tyr Asp Leu Phe Leu Thr Arg Val Ser Glu Gly  
 465 470 475 480  
 Arg Asn Arg Thr Lys Ala Gln Ile Asp Ser Ile Ala Gln Gly Arg Val  
 485 490 495  
 35 Trp Leu Gly Asp Lys Ala Leu Ala Leu Gly Leu Val Asp Glu Leu Gly  
 500 505 510  
 Gly Leu Asp Thr Ala Ile Lys Arg Ala Ala Lys Leu Ala Gln Leu Gly  
 515 520 525  
 Gly Asn Tyr Ser Ile Glu Tyr Gly Lys Thr Lys Arg Asn Phe Phe Glu  
 530 535 540  
 40 Glu Leu Leu Ser Ser Ser Ala Ala Asp Met Lys Ser Ala Ile Leu Ser  
 545 550 555 560  
 Thr Ile Leu Ser Asp Pro Glu Ile Glu Val Leu Arg Glu Leu Arg Ser  
 565 570 575  
 45 Met Pro Pro Arg Pro Ser Gly Ile Gln Ala Arg Leu Pro Tyr Tyr Phe  
 580 585 590  
 Met Pro Tyr  
 595  
 (2) INFORMATION FOR SEQ ID NO:399  
 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 589 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 55 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 60 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 65 (B) LOCATION 1...589  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:399  
 70 Met Phe Phe Ala Ser Ile Leu Gly Val Ile Thr Ala Gly Ile Ile Leu  
 1 5 10 15  
 Phe Cys Ile Phe Leu Phe Ile Phe Phe Gly Ile Val Ala Gly Ile Ala  
 20 25 30  
 Ser Lys Ala Thr Gly Gly Thr Ile Pro Lys Ile Glu Ala Asn Ser Ile  
 35 40 45  
 75 Leu His Ile Unk Asn Ser Ser Phe Pro Glu Ile Val Ser Ala Asn Pro

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50 55 60  
 Trp Ser Met Leu Thr Gly Lys Asp Glu Ser Val Ser Leu Ser Gln Ala  
 65 70 75 80  
 Val Glu Ala Ile Gly Gln Ala Lys Asn Asn Pro Asn Ile Thr Gly Ile  
 85 90 95  
 Phe Leu Asp Leu Asp Asn Leu Ser Val Gly Met Ala Ser Ala Glu Glu  
 100 105 110  
 Leu Arg Arg Ala Leu Gln Asp Phe Lys Met Ser Gly Lys Phe Val Val  
 115 120 125  
 Ser Tyr Ala Asp Arg Tyr Thr Gln Lys Gly Tyr Tyr Leu Ser Ser Ile  
 130 135 140  
 Ala Asp Lys Leu Tyr Leu Asn Pro Lys Gly Met Leu Gly Leu Ile Gly  
 145 150 155 160  
 Ile Ala Thr Gln Thr Met Phe Tyr Lys Asp Ala Leu Asp Lys Phe Gly  
 165 170 175  
 Val Lys Met Glu Ile Phe Lys Val Gly Thr Tyr Lys Ala Ala Val Glu  
 180 185 190  
 Pro Phe Met Leu Asn Arg Met Ser Asp Ala Asn Arg Glu Gln Ile Thr  
 195 200 205  
 Thr Tyr Ile Asn Gly Leu Trp Asp Lys Ile Thr Ser Asp Ile Ala Glu  
 210 215 220  
 Ser Arg Lys Thr Ala Met Asp Ser Val Lys Met Phe Ala Asp Lys Gly  
 225 230 235 240  
 Glu Met Phe Gly Leu Ala Glu Lys Ala Val Glu Met Lys Leu Val Asp  
 245 250 255  
 Glu Leu Ala Tyr Arg Thr Asp Val Glu Lys Glu Leu Lys Lys Met Ser  
 260 265 270  
 Gln Arg Gly Glu Lys Asp Glu Leu Arg Phe Val Ser Leu Ser Gln Val  
 275 280 285  
 Leu Ala Asn Gly Pro Met Asn Lys Thr Lys Gly Ser Arg Ile Ala Val  
 290 295 300  
 Leu Phe Ala Glu Gly Glu Ile Thr Glu Glu Ile Ile Lys Lys Pro Phe  
 305 310 315 320  
 Asp Thr Asp Gly Ser Ser Ile Thr Gln Glu Leu Ala Lys Glu Ile Lys  
 325 330 335  
 Ala Ala Ala Asp Asp Asp Ile Lys Ala Val Val Leu Arg Val Asn  
 340 345 350  
 Ser Pro Gly Gly Ser Ala Phe Thr Ser Glu Gln Ile Trp Lys Gln Val  
 355 360 365  
 Ala Asp Leu Lys Ala Lys Lys Pro Ile Val Val Ser Met Gly Asp Val  
 370 375 380  
 Ala Ala Ser Gly Gly Tyr Tyr Ile Ala Cys Ala Ala Asn Ser Ile Val  
 385 390 395 400  
 Ala Glu His Thr Thr Leu Thr Gly Ser Ile Gly Ile Phe Gly Met Phe  
 405 410 415  
 Pro Asn Phe Ala Gly Val Ala Lys Lys Ile Gly Val Asn Met Asp Val  
 420 425 430  
 Val Gln Thr Ser Lys Tyr Ala Asp Leu Gly Asn Thr Phe Ala Pro Met  
 435 440 445  
 Thr Val Glu Asp Arg Ala Leu Ile Gln Arg Tyr Ile Glu Gln Gly Tyr  
 450 455 460  
 Asp Leu Phe Leu Thr Arg Val Ser Glu Gly Arg Asn Arg Thr Lys Ala  
 465 470 475 480  
 Gln Ile Asp Ser Ile Ala Gln Gly Arg Val Trp Leu Gly Asp Lys Ala  
 485 490 495  
 Leu Ala Leu Gly Leu Val Asp Glu Leu Gly Gly Leu Asp Thr Ala Ile  
 500 505 510  
 Lys Arg Ala Ala Lys Leu Ala Gln Leu Gly Gly Asn Tyr Ser Ile Glu  
 515 520 525  
 Tyr Gly Lys Thr Lys Arg Asn Phe Phe Glu Glu Leu Leu Ser Ser Ser  
 530 535 540  
 Ala Ala Asp Met Lys Ser Ala Ile Leu Ser Thr Ile Leu Ser Asp Pro  
 545 550 555 560  
 Glu Ile Glu Val Leu Arg Glu Leu Arg Ser Met Pro Pro Arg Pro Ser  
 565 570 575  
 Gly Ile Gln Ala Arg Leu Pro Tyr Tyr Phe Met Pro Tyr  
 580 585

(2) INFORMATION FOR SEQ ID NO:400

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 313 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

5 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
10 (A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400

15 Met Arg Ala Asn Ile Trp Gln Ile Leu Ser Val Ser Val Leu Phe Phe  
1 5 10 15  
Phe Gly Thr Ala Ile Gly Gln Ala Gln Ser Arg Asn Arg Thr Tyr Glu  
20 20 25 30  
Ala Tyr Val Lys Gln Tyr Ala Asp Glu Ala Ile Arg Gln Met Ser Arg  
35 40 45  
20 Tyr Asn Ile Pro Ala Ser Ile Thr Ile Ala Gln Ala Leu Val Glu Thr  
50 55 60  
Gly Ala Gly Ala Ser Thr Leu Ala Ser Val His Asn Asn His Phe Gly  
65 70 75  
Ile Lys Cys His Lys Ser Trp Thr Gly Lys Arg Thr Tyr Arg Thr Asp  
25 85 90 95  
Asp Ala Pro Asn Glu Cys Phe Arg Ser Tyr Ser Ala Ala Arg Glu Ser  
100 105 110  
Tyr Glu Asp His Ser Arg Phe Leu Leu Gln Pro Arg Tyr Arg Pro Leu  
115 120 125  
30 Phe Lys Leu Asp Arg Glu Asp Tyr Arg Gly Trp Ala Thr Gly Leu Gln  
130 135 140  
Arg Cys Gly Tyr Ala Thr Asn Arg Gly Tyr Ala Asn Leu Leu Ile Lys  
145 150 155 160  
Met Val Glu Leu Tyr Glu Leu Tyr Ala Leu Asp Arg Glu Lys Tyr Pro  
35 165 170 175  
Ser Trp Phe His Lys Ser Tyr Pro Gly Ser Asn Lys Lys Ser His Gln  
180 185 190  
Thr Thr Lys Gln Lys Gln Ser Gly Leu Lys His Glu Ala Tyr Phe Ser  
195 200 205  
40 Tyr Gly Leu Leu Tyr Ile Ile Ala Lys Gln Gly Asp Thr Phe Asp Ser  
210 215 220  
Leu Ala Glu Glu Phe Asp Met Arg Ala Ser Lys Leu Ala Lys Tyr Asn  
225 230 235 240  
Asp Ala Pro Val Asp Phe Pro Ile Glu Lys Gly Asp Val Ile Tyr Leu  
45 245 250 255  
Glu Lys Lys His Ala Cys Ser Ile Ser Lys His Thr Gln His Val Val  
260 265 270  
Arg Val Gly Asp Ser Met His Ser Ile Ser Gln Arg Tyr Gly Ile Arg  
275 280 285  
50 Met Lys Asn Leu Tyr Lys Leu Asn Asp Lys Asp Gly Glu Tyr Ile Pro  
290 295 300  
Gln Glu Gly Asp Ile Leu Arg Leu Arg  
305 310

55 (2) INFORMATION FOR SEQ ID NO:401

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 523 amino acids  
60 (B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

65 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
70 (A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401

75 Met Asp Gly Arg Arg Tyr Ser Asp Gly Leu His Gln Ala Ile Glu Ala

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1 Lys Glu His Val Lys Val Glu Ala Ala Thr Gln Thr Phe Ala Thr Ile  
 20 25 30  
 5 Thr Leu Gln Asn Tyr Phe Arg Met Tyr His Lys Leu Ala Gly Met Thr  
 35 40 45  
 Gly Thr Ala Glu Thr Glu Ala Gly Glu Leu Trp Asp Ile Tyr Lys Leu  
 50 55 60  
 Asp Val Val Val Ile Pro Thr Asn Lys Pro Ile Ala Arg Lys Asp Met  
 65 70 75 80  
 10 Asn Asp Arg Ile Tyr Lys Thr Ala Arg Glu Lys Tyr Ala Ala Val Ile  
 85 90 95  
 Glu Glu Ile Val Arg Leu Val Glu Glu Gly Arg Pro Val Leu Val Gly  
 100 105 110  
 15 Thr Thr Ser Val Glu Ile Ser Glu Leu Leu Ser Arg Met Leu Arg Leu  
 115 120 125  
 Arg Gly Ile Gln His Asn Val Leu Asn Ala Lys Leu His Gln Lys Glu  
 130 135 140  
 Ala Glu Ile Val Ala Gln Ala Gly Gln Lys Gly Thr Val Thr Ile Ala  
 145 150 155 160  
 20 Thr Asn Met Ala Gly Arg Gly Thr Asp Ile Lys Leu Ser Ala Glu Val  
 165 170 175  
 Lys Lys Ala Gly Gly Leu Ala Ile Ile Gly Thr Glu Arg His Glu Ser  
 180 185 190  
 25 Arg Arg Val Asp Arg Gln Leu Arg Gly Arg Ser Gly Arg Gln Gly Asp  
 195 200 205  
 Pro Gly Ser Ser Ile Phe Tyr Val Ser Leu Glu Asp His Leu Met Arg  
 210 215 220  
 Leu Phe Ala Thr Glu Lys Ile Ala Ser Leu Met Asp Arg Leu Gly Phe  
 225 230 235 240  
 30 Lys Glu Gly Glu Val Leu Glu Asn Asn Met Leu Ser Lys Ser Val Glu  
 245 250 255  
 Arg Ala Gln Lys Lys Val Glu Glu Asn Asn Phe Gly Ile Arg Lys His  
 260 265 270  
 35 Leu Leu Glu Tyr Asp Asp Val Met Asn Ser Gln Arg Glu Val Ile Tyr  
 275 280 285  
 Thr Arg Arg Arg His Ala Leu Met Gly Glu Arg Ile Gly Met Asp Val  
 290 295 300  
 Leu Asn Thr Ile Tyr Asp Val Cys Lys Ala Leu Ile Asp Asn Tyr Ala  
 305 310 315 320  
 40 Glu Ala Asn Asp Phe Glu Gly Phe Lys Glu Asp Leu Met Arg Ala Leu  
 325 330 335  
 Ala Ile Glu Ser Pro Ile Thr Gln Glu Ile Phe Arg Gly Lys Lys Ala  
 340 345 350  
 45 Glu Glu Leu Thr Asp Met Leu Phe Asp Glu Ala Tyr Lys Ser Phe Gln  
 355 360 365  
 Arg Lys Met Asp Leu Ile Ala Glu Val Ala His Pro Val Val His Gln  
 370 375 380  
 Val Phe Glu Thr Gln Ala Ala Val Tyr Glu Arg Ile Leu Ile Pro Ile  
 385 390 395 400  
 50 Thr Asp Gly Lys Arg Val Tyr Asn Ile Gly Cys Asn Leu Arg Glu Ala  
 405 410 415  
 Asp Glu Thr Gln Gly Lys Ser Ile Ile Lys Glu Phe Glu Lys Ala Ile  
 420 425 430  
 55 Val Leu His Thr Ile Asp Glu Ser Trp Lys Glu His Leu Arg Glu Met  
 435 440 445  
 Asp Glu Leu Arg Asn Ser Val Gln Asn Ala Ser Tyr Glu Asn Lys Asp  
 450 455 460  
 Pro Leu Leu Ile Tyr Lys Leu Glu Ser Tyr Glu Leu Phe Arg Lys Met  
 465 470 475 480  
 60 Val Glu Ala Met Asn Arg Lys Thr Val Ala Ile Leu Met Arg Ala Arg  
 485 490 495  
 Ile Pro Val Pro Glu Ala Pro Ser Gln Glu Glu Leu Glu His Arg Arg  
 500 505 510  
 65 Gln Ile Glu Ile Arg His Ala Thr Gln Gln Arg  
 515 520

(2) INFORMATION FOR SEQ ID NO:402

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 375 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

5

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...375

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402

```

Met Asn Phe Leu Lys Lys Glu Pro Phe Lys Ile Phe Ser Met Ile Tyr
1      5      10      15
Leu Leu Leu Asp Thr Ile Thr Asn Arg Ala Gly Thr Glu Arg Ala Val
15     20     25     30
Ile Asn Leu Ala Asn Asn Leu His Ala Asn Gly His Arg Val Ser Leu
35     40     45
Val Ser Val Cys Thr Lys Glu Gly Glu Pro Ser Phe Gln Val Glu Lys
50     55     60
Gly Ile Glu Val His His Leu Gly Ile Arg Leu Tyr Gly Asn Ala Leu
65     70     75     80
Ala Arg Lys Thr Val Tyr Phe Lys Ala Tyr Arg Arg Ile Lys Ala Leu
85     90     95
Tyr Lys Lys Arg Glu Pro Val Leu Leu Ile Gly Thr Asn Ile Phe Ile
100    105    110
Asn Thr Ile Leu Ser Gln Ile Ser Asn Arg Gly Arg Ile Phe Thr Ile
115    120    125
Gly Cys Glu His Ile Ser Tyr Asp Ile Ala Arg Pro Ile Thr Lys Arg
130    135    140
Ile Arg Gly Phe Leu Tyr Ser Gly Leu Asp Ala Val Val Ala Leu Thr
145    150    155    160
Lys Arg Asp Gln Gln Ser Phe Glu Ala Ile Leu Arg Gly Arg Ser Lys
165    170    175
Ala Tyr Val Ile Pro Asn Gln Val Ser Phe Thr Thr Val Gln Arg Asp
180    185    190
Ala Thr Thr His Lys Gln Met Leu Ala Ile Gly Arg Leu Thr Tyr Gln
195    200    205
Lys Gly Phe Glu Phe Met Ile Glu Asp Ala Ser Arg Val Leu Arg Glu
210    215    220
Arg Pro Asp Trp Lys Leu Ile Ile Val Gly Asp Gly Glu Asn Glu Ser
225    230    235    240
Met Leu Arg Lys Glu Ile Ala Ser Arg Asn Met Glu Ser Gln Ile Glu
245    250    255
Ile His Pro Ser Thr Pro Glu Ile Arg Lys Tyr Tyr Glu Ser Ser Ala
260    265    270
Ile Tyr Leu Met Thr Ser Arg Phe Glu Gly Leu Pro Met Val Leu Leu
275    280    285
Glu Ala Glu Ala Tyr Ala Leu Pro Ile Ile Ser Tyr Asp Cys Pro Thr
290    295    300
Gly Pro Arg Glu Leu Ile Glu Asn Gly Arg Asn Gly Phe Leu Val Pro
305    310    315    320
Met Glu Ala His Glu Asp Phe Ala Asp Lys Leu Arg Leu Leu Met Asp
325    330    335
Asp Glu Thr Leu Arg Lys Lys Met Gly Gln Glu Ser Glu Leu Met Val
340    345    350
Lys Ser Tyr Ser Pro Ala Asn Ile Tyr Glu Cys Trp Lys Lys Leu Phe
355    360    365
Val Glu Ile Gly Tyr Met Asn
370    375

```

60

(2) INFORMATION FOR SEQ ID NO:403

(1) SEQUENCE CHARACTERISTICS:

65

(A) LENGTH: 362 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

70

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

75

(ix) FEATURE:

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(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403

5 Met Ile Tyr Leu Leu Asp Thr Ile Thr Asn Arg Ala Gly Thr Glu  
1 5 10 15  
Arg Ala Val Ile Asn Leu Ala Asn Asn Leu His Ala Asn Gly His Arg  
20 25 30  
10 Val Ser Leu Val Ser Val Cys Thr Lys Glu Gly Glu Pro Ser Phe Gln  
35 40 45  
Val Glu Lys Gly Ile Glu Val His His Leu Gly Ile Arg Leu Tyr Gly  
50 55 60  
15 Asn Ala Leu Ala Arg Lys Thr Val Tyr Phe Lys Ala Tyr Arg Arg Ile  
65 70 75 80  
Lys Ala Leu Tyr Lys Lys Arg Glu Pro Val Leu Leu Ile Gly Thr Asn  
85 90 95  
Ile Phe Ile Asn Thr Ile Leu Ser Gln Ile Ser Asn Arg Gly Arg Ile  
100 105 110  
20 Phe Thr Ile Gly Cys Glu His Ile Ser Tyr Asp Ile Ala Arg Pro Ile  
115 120 125  
Thr Lys Arg Ile Arg Gly Phe Leu Tyr Ser Gly Leu Asp Ala Val Val  
130 135 140  
25 Ala Leu Thr Lys Arg Asp Gln Gln Ser Phe Glu Ala Ile Leu Arg Gly  
145 150 155 160  
Arg Ser Lys Ala Tyr Val Ile Pro Asn Gln Val Ser Phe Thr Thr Val  
165 170 175  
Gln Arg Asp Ala Thr Thr His Lys Gln Met Leu Ala Ile Gly Arg Leu  
180 185 190  
30 Thr Tyr Gln Lys Gly Phe Glu Phe Met Ile Glu Asp Ala Ser Arg Val  
195 200 205  
Leu Arg Glu Arg Pro Asp Trp Lys Leu Ile Ile Val Gly Asp Gly Glu  
210 215 220  
35 Asn Glu Ser Met Leu Arg Lys Glu Ile Ala Ser Arg Asn Met Glu Ser  
225 230 235 240  
Gln Ile Glu Ile His Pro Ser Thr Pro Glu Ile Arg Lys Tyr Tyr Glu  
245 250 255  
Ser Ser Ala Ile Tyr Leu Met Thr Ser Arg Phe Glu Gly Leu Pro Met  
260 265 270  
40 Val Leu Leu Glu Ala Glu Ala Tyr Ala Leu Pro Ile Ile Ser Tyr Asp  
275 280 285  
Cys Pro Thr Gly Pro Arg Glu Leu Ile Glu Asn Gly Arg Asn Gly Phe  
290 295 300  
45 Leu Val Pro Met Glu Ala His Glu Asp Phe Ala Asp Lys Leu Arg Leu  
305 310 315 320  
Leu Met Asp Asp Glu Thr Leu Arg Lys Lys Met Gly Gln Glu Ser Glu  
325 330 335  
Leu Met Val Lys Ser Tyr Ser Pro Ala Asn Ile Tyr Glu Cys Trp Lys  
340 345 350  
50 Lys Leu Phe Val Glu Ile Gly Tyr Met Asn  
355 360

(2) INFORMATION FOR SEQ ID NO:404

55 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 640 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

65 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404

75 Met Gly Lys Ile Ile Gly Ile Asp Leu Gly Thr Thr Asn Ser Cys Val  
1 5 10 15  
Ser Val Leu Glu Gly Asn Glu Pro Ile Val Ile Thr Asn Ser Glu Gly



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20 25 30  
 Lys Arg Thr Thr Pro Ser Val Val Ala Phe Val Asp Gly Gly Glu Arg  
 35 40 45  
 5 Lys Val Gly Asp Pro Ala Lys Arg Gln Ala Ile Thr Asn Pro Thr Lys  
 50 55 60  
 Thr Ile Tyr Ser Ile Lys Arg Phe Met Gly Glu Thr Tyr Asp Gln Val  
 65 70 75 80  
 Ser Arg Glu Val Glu Arg Val Pro Phe Lys Val Val Arg Gly Asp Asn  
 85 90 95  
 10 Asn Thr Pro Arg Val Asp Ile Asp Gly Arg Leu Tyr Thr Pro Gln Glu  
 100 105 110  
 Ile Ser Ala Met Ile Leu Gln Lys Met Lys Lys Thr Ala Glu Asp Tyr  
 115 120 125  
 15 Leu Gly Gln Glu Val Thr Glu Ala Val Ile Thr Val Pro Ala Tyr Phe  
 130 135 140  
 Asn Asp Ala Gln Arg Gln Ala Thr Lys Glu Ala Gly Glu Ile Ala Gly  
 145 150 155 160  
 Leu Lys Val Arg Arg Ile Val Asn Glu Pro Thr Ala Ala Ser Leu Ala  
 165 170 175  
 20 Tyr Gly Leu Asp Lys Ser Asn Lys Asp Met Lys Ile Ala Val Phe Asp  
 180 185 190  
 Leu Gly Gly Thr Phe Asp Ile Ser Ile Leu Glu Leu Gly Asp Gly  
 195 200 205  
 25 Val Phe Glu Val Lys Ser Thr Asn Gly Asp Thr His Leu Gly Gly Asp  
 210 215 220  
 Asp Phe Asp His Val Ile Ile Asp Trp Leu Ala Glu Glu Phe Lys Ser  
 225 230 235 240  
 Gln Glu Gly Val Asp Leu Arg Gln Asp Pro Met Ala Met Gln Arg Leu  
 245 250 255  
 30 Lys Glu Ala Ala Glu Lys Ala Lys Ile Glu Leu Ser Ser Thr Ser Ser  
 260 265 270  
 Thr Glu Ile Asn Leu Pro Tyr Ile Met Pro Val Asn Gly Ile Pro Lys  
 275 280 285  
 35 His Leu Val Met Thr Leu Thr Arg Ala Lys Phe Glu Gln Leu Ala Asp  
 290 295 300  
 Arg Leu Ile Gln Ala Cys Val Ala Pro Cys Glu Thr Ala Leu Lys Asp  
 305 310 315 320  
 Ala Gly Met Ser Arg Gly Asp Ile Asp Glu Val Ile Leu Val Gly Gly  
 325 330 335  
 40 Ser Thr Arg Ile Pro Ala Ile Gln Glu Ile Val Glu Lys Ile Phe Gly  
 340 345 350  
 Lys Ala Pro Ser Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly  
 355 360 365  
 45 Ala Ala Ile Gln Gly Gly Val Leu Thr Gly Glu Val Lys Asp Val Leu  
 370 375 380  
 Leu Leu Asp Val Thr Pro Leu Ser Leu Gly Ile Glu Thr Met Gly Gly  
 385 390 395 400  
 Val Met Thr Arg Leu Ile Asp Ala Asn Thr Thr Ile Pro Thr Lys Lys  
 405 410 415  
 50 Ser Glu Ile Phe Thr Thr Ala Val Asp Asn Gln Pro Ser Val Glu Ile  
 420 425 430  
 His Val Leu Gln Gly Glu Arg Ser Leu Ala Lys Asp Asn Lys Ser Ile  
 435 440 445  
 55 Gly Arg Phe Asn Leu Asp Gly Ile Ala Pro Ala Pro Arg Gln Thr Pro  
 450 455 460  
 Gln Ile Glu Val Thr Phe Asp Ile Asp Ala Asn Gly Ile Leu Asn Val  
 465 470 475 480  
 Thr Ala His Asp Lys Ala Thr Gly Lys Lys Gln Asn Ile Arg Ile Glu  
 485 490 495  
 60 Ala Ser Ser Gly Leu Ser Asp Asp Glu Ile Lys Arg Met Lys Glu Glu  
 500 505 510  
 Ala Gln Ala Asn Ala Glu Ala Asp Lys Lys Glu Lys Glu Arg Ile Asp  
 515 520 525  
 65 Lys Ile Asn Gln Ala Asp Ser Met Ile Phe Gln Thr Glu Lys Gln Leu  
 530 535 540  
 Lys Glu Leu Gly Asp Lys Phe Pro Ala Asp Lys Lys Ala Pro Ile Asp  
 545 550 555 560  
 Thr Ala Leu Asp Lys Leu Lys Glu Ala His Lys Ala Gln Asp Val Ala  
 565 570 575  
 70 Ala Ile Asp Thr Ala Met Ala Glu Leu Gln Thr Ala Leu Ser Ala Ala  
 580 585 590  
 Gly Glu Glu Leu Tyr Lys Asn Ala Gly Ala Ala Gln Gly Gly Ala Gln  
 595 600 605  
 75 Pro Gly Pro Asp Phe Gly Gly Ala Gln Gly Pro Ser Ala Gly Asp Gln  
 610 615 620

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Pro Ser Asp Asp Lys Asn Val Thr Asp Val Asp Phe Glu Glu Val Lys  
 625 630 635 640

(2) INFORMATION FOR SEQ ID NO:405

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 449 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405

Met Arg Tyr Asp Leu Ala Ile Ile Gly Gly Gly Pro Ala Gly Tyr Thr  
 1 8 10 15  
 Ala Ala Glu Arg Ala Ala Lys Gly Gly Leu Lys Thr Leu Leu Ile Glu  
 20 25 30  
 Lys Asn Ala Leu Gly Gly Val Cys Leu Asn Glu Gly Cys Ile Pro Thr  
 35 40 45  
 Lys Thr Leu Leu Tyr Ser Ala Lys Val Leu His Gln Ile Ala Thr Ala  
 50 55 60  
 Ser Lys Tyr Ala Val Ser Gly Thr Ala Asp Gly Leu Asp Leu Gly Lys  
 65 70 75 80  
 Val Ile Ala Arg Lys Gly Lys Ile Ile Arg Lys Leu Thr Ala Gly Ile  
 85 90 95  
 Arg Ser Arg Leu Thr Glu Ala Gly Val Glu Met Val Thr Ala Glu Ala  
 100 105 110  
 Thr Val Thr Gly Cys Asp Ala Asp Gly Ile Ile Gly Ile Thr Ala Gly  
 115 120 125  
 Glu Ala Gln Tyr Lys Ala Ala Asn Leu Leu Leu Cys Thr Gly Ser Glu  
 130 135 140  
 Thr Phe Ile Pro Pro Ile Pro Gly Val Glu Gln Thr Glu Tyr Trp Thr  
 145 150 155 160  
 Asn Arg Glu Ala Leu Gln Asn Lys Glu Ile Pro Thr Ser Leu Val Ile  
 165 170 175  
 Ile Gly Gly Gly Val Ile Gly Met Glu Phe Ala Ser Phe Phe Asn Gly  
 180 185 190  
 Ile Gly Thr Gln Val His Val Val Glu Met Leu Pro Glu Ile Leu Asn  
 195 200 205  
 Gly Ile Asp Pro Glu His Ala Ala Met Leu Arg Ala His Tyr Glu Lys  
 210 215 220  
 Glu Gly Ile Lys Phe Tyr Leu Gly His Lys Val Thr Ser Val Arg Asn  
 225 230 235 240  
 Gly Ala Val Thr Val Glu Tyr Glu Gly Glu Ser Lys Glu Ile Glu Gly  
 245 250 255  
 Glu Arg Ile Leu Met Ser Val Gly Arg Arg Pro Val Leu Gln Gly Phe  
 260 265 270  
 Glu Ser Leu Gly Leu Val Leu Ala Gly Lys Gly Val Lys Thr Asn Glu  
 275 280 285  
 Arg Met Gln Thr Ser Leu Pro Asn Val Tyr Ala Ala Gly Asp Ile Thr  
 290 295 300  
 Gly Phe Ser Leu Leu Ala His Thr Ala Val Arg Glu Ala Glu Val Ala  
 305 310 315 320  
 Val Asp Gln Ile Leu Gly Lys Thr Asp Glu Thr Met Ser Tyr Arg Ala  
 325 330 335  
 Val Pro Gly Val Val Tyr Thr Asn Pro Glu Val Ala Gly Val Gly Glu  
 340 345 350  
 Thr Glu Glu Ser Leu Arg Lys Ala Gly Arg Ala Tyr Thr Val Arg Arg  
 355 360 365  
 Leu Pro Met Ala Phe Ser Gly Arg Phe Val Ala Glu Asn Glu Gln Gly  
 370 375 380  
 Asn Gly Glu Cys Lys Leu Leu Leu Asp Glu Glu Asn Arg Leu Ile Gly  
 385 390 395 400  
 Ala His Leu Ile Gly Asn Pro Ala Gly Glu Leu Ile Val Thr Ala Ala  
 405 410 415



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Lys Gly Glu Tyr Asp Arg Ala Arg Thr Asn Val Leu Lys Arg Tyr Glu  
 385 390 395 400  
 Asn Gln Tyr Asn Glu Arg Asp Lys Arg Lys Asn Asn Ala Tyr Ala Asn  
 405 410 415  
 5 Glu Tyr Ser Thr Tyr Phe Thr Asp Gly Gly Tyr Ile Pro Gly Ile Glu  
 420 425 430  
 Val Glu Tyr Gln Thr Val Asn Ala Phe Ala Pro Gln Val Pro Leu Glu  
 435 440 445  
 10 Ala Phe Asn Gln Ala Ile Ala Gln Met Ile Asp Pro Val Lys Asn Ala  
 450 455 460  
 Val Val Thr Leu Thr Gly Pro Ser Lys Ala Glu Ala Lys Ile Pro Ser  
 465 470 475 480  
 Glu Ala Asp Phe Leu Ala Ala Phe Lys Ala Ala Arg Gln Gln Lys Val  
 485 490 495  
 15 Glu Ala Lys Lys Asp Glu Val Ser Asp Gln Lys Leu Met Glu Lys Ala  
 500 505 510  
 Pro Lys Ala Gly Lys Ile Val Ser Glu Lys Lys Asp Gln Lys Phe Gly  
 515 520 525  
 20 Thr Thr Glu Leu Thr Leu Ser Asn Gly Ile Lys Val Tyr Leu Lys Lys  
 530 535 540  
 Thr Asp Phe Lys Ser Asn Glu Ile Leu Met Ser Ala Leu Ser Pro Gly  
 545 550 555 560  
 Gly Ile Leu Ser Gly Lys His Ala Pro Asn Gln Ser Val Met Asn Ser  
 565 570 575  
 25 Phe Met Asn Val Gly Gly Leu Gly Asn Phe Asp Ala Ile Gln Leu Asp  
 580 585 590  
 Lys Val Leu Thr Gly Arg Ser Ala Ser Val Ser Pro Ser Leu Ser Leu  
 595 600 605  
 30 Leu Ser Glu Gly Leu Ser Gly Lys Thr Thr Val Glu Asp Met Glu Thr  
 610 615 620  
 Phe Phe Gln Leu Ile Tyr Leu Gln Met Thr Ala Asn Arg Lys Asp Pro  
 625 630 635 640  
 Glu Ala Phe Lys Ala Thr Gln Glu Lys Leu Tyr Asn Asn Leu Lys Asn  
 645 650 655  
 35 Gln Glu Ala Asn Pro Met Ala Ala Leu Met Asp Ser Ile Arg His Thr  
 660 665 670  
 Met Tyr Gly Asp Asn Pro Met Met Lys Pro Met Lys Ala Ala Asp Val  
 675 680 685  
 40 Glu Lys Val Asn Tyr Asp Gln Val Met Ala Phe Tyr Asn Glu Arg Phe  
 690 695 700  
 Ala Asp Ala Gly Asp Phe Met Phe Phe Phe Ile Gly Asn Leu Asp Glu  
 705 710 715 720  
 Ala Lys Met Lys Pro Leu Ile Glu Thr Tyr Leu Ala Ser Leu Pro Asn  
 725 730 735  
 45 Leu Lys Arg Gly Asp Lys Met Asn Lys Ala Gln Val Pro Ala Ala Arg  
 740 745 750  
 Ser Gly Lys Ile Asp Cys Lys Phe Glu Lys Glu Met Asp Thr Pro Ser  
 755 760 765  
 50 Thr Thr Ile Phe Asp Val Val Ser Gly Asn Val Glu Tyr Thr Leu Lys  
 770 775 780  
 Asn Ser Leu Leu Leu Glu Val Phe Ser Ala Val Met Asp Gln Val Tyr  
 785 790 795 800  
 Thr Ala Thr Val Arg Glu Lys Glu Gly Gly Ala Tyr Ser Val Ala Ala  
 805 810 815  
 55 Phe Gly Gly Leu Glu Gln Tyr Pro Gln Pro Lys Ala Leu Met Gln Ile  
 820 825 830  
 Tyr Phe Pro Thr Asp Pro Ala Arg Ala Glu Glu Met Asn Ala Ile Val  
 835 840 845  
 60 Phe Ala Glu Leu Glu Lys Leu Ala Lys Glu Gly Pro Asn Val Glu Tyr  
 850 855 860  
 Phe Lys Lys Thr Ile Glu Asn Leu Asn Lys Gln His Lys Glu Ser Leu  
 865 870 875 880  
 Arg Glu Asn Arg Phe Trp Leu Glu Ala Met Lys Ala Ser Phe Phe Glu  
 885 890 895  
 65 Gly Asn Asp Phe Ile Thr Asp Tyr Glu Ser Val Leu Asn Gly Leu Thr  
 900 905 910  
 Pro Ala Glu Leu Gln Lys Phe Ala Ala Asp Leu Leu Lys Gln Gln Asn  
 915 920 925  
 70 Arg Val Val Val Met Met Ala Pro Val Ala Lys Ala Gln  
 930 935 940

(2) INFORMATION FOR SEQ ID NO:407

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 684 amino acids

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(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
(A) NAME/KEY: misc feature  
(B) LOCATION 1...684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407

```

Met Ser Lys Lys Gly Thr Ile Gly Val Thr Ser Asp Asn Ile Phe Pro
1      5      10      15
Val Ile Lys Lys Phe Leu Tyr Ser Asp His Glu Ile Phe Leu Arg Glu
20     20     25     30
Ile Val Ser Asn Ala Val Asp Ala Thr Gln Lys Leu Lys Thr Leu Thr
35     40     45
Ser Val Gly Glu Phe Lys Gly Glu Thr Gly Asp Leu Arg Val Thr Val
50     55     60
Ser Val Asp Glu Val Ala Arg Thr Ile Thr Val Ser Asp Arg Gly Val
25     65     70     75     80
Gly Met Thr Glu Glu Val Glu Lys Tyr Ile Asn Gln Ile Ala Phe
85     90     95
Ser Ser Ala Glu Glu Phe Leu Glu Lys Tyr Lys Asp Asp Lys Ala Ala
100    105    110
30   Ile Ile Gly His Phe Gly Leu Gly Phe Tyr Ser Ala Phe Met Val Ser
115    120    125
Glu Arg Val Asp Val Ile Thr Arg Ser Phe Arg Glu Asp Ala Thr Ala
130    135    140
35   Val Lys Trp Ser Cys Asp Gly Ser Pro Glu Tyr Thr Leu Glu Pro Ala
145    150    155    160
Asp Lys Ala Asp Arg Gly Thr Asp Ile Val Met His Ile Asp Glu Glu
165    170    175
40   Asn Ser Glu Phe Leu Lys Lys Glu Lys Ile Glu Gly Leu Leu Gly Lys
180    185    190
Tyr Cys Lys Phe Leu Thr Val Pro Ile Ile Phe Gly Lys Lys Gln Glu
195    200    205
Trp Lys Asp Gly Lys Met Gln Asp Thr Asp Glu Asp Asn Gln Ile Asn
210    215    220
45   Asp Thr His Pro Ala Trp Thr Lys Lys Pro Ala Asp Leu Lys Asp Glu
225    230    235    240
Asp Tyr Lys Glu Phe Tyr Arg Ser Leu Tyr Pro Met Ser Glu Glu Pro
245    250    255
50   Leu Phe Trp Ile His Leu Asn Val Asp Tyr Pro Phe Asn Leu Thr Gly
260    265    270
Ile Leu Tyr Phe Pro Lys Ile Lys Asn Asn Leu Asp Leu Gln Arg Asn
275    280    285
Lys Ile Gln Leu Tyr Cys Asn Gln Val Tyr Val Thr Asp Glu Val Gln
290    295    300
55   Gly Ile Val Pro Asp Phe Leu Thr Leu Leu His Gly Val Ile Asp Ser
305    310    315    320
Pro Asp Ile Pro Leu Asn Val Ser Arg Ser Tyr Leu Gln Ser Asp Ala
325    330    335
60   Asn Val Lys Lys Ile Ser Ser His Ile Thr Lys Lys Val Ala Asp Arg
340    345    350
Leu Glu Glu Ile Phe Lys Asn Asp Arg Pro Thr Phe Glu Glu Lys Trp
355    360    365
Asp Ser Leu Lys Leu Phe Val Glu Tyr Gly Met Leu Thr Asp Glu Lys
370    375    380
65   Phe Tyr Glu Arg Ala Ala Lys Phe Phe Leu Phe Thr Asp Met Asp Gly
385    390    395    400
His Lys Tyr Thr Phe Asp Glu Tyr Arg Thr Leu Val Glu Gly Val Gln
405    410    415
Thr Asp Lys Asp Gly Gln Val Val Tyr Leu Tyr Ala Thr Asp Lys His
420    425    430
70   Gly Gln Tyr Ser His Val Lys Arg Ala Ser Asp Lys Gly Tyr Ser Val
435    440    445
Met Leu Leu Asp Gly Gln Leu Asp Pro His Ile Val Ser Leu Leu Glu
450    455    460
75   Gln Lys Leu Glu Lys Thr His Phe Val Arg Val Asp Ser Asp Thr Ile

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210 215 220  
 Glu Ser Leu Phe Glu Ser Glu Leu Phe Gly His Lys Lys Gly Ala Phe  
 225 230 235 240  
 Thr Asn Ala Phe Ser Asp Arg Lys Gly Arg Phe Glu Leu Ala Asp Gly  
 245 250 255  
 5 Gly Thr Ile Phe Leu Asp Glu Ile Gly Glu Leu Pro Val Gly Asn Gln  
 260 265 270  
 Val Lys Leu Leu Arg Val Leu Gln Glu Gln Thr Phe Glu Pro Leu Gly  
 275 280 285  
 10 Glu Ser Val Ser His Arg Val Asp Ile Arg Val Val Ser Ala Thr Asn  
 290 295 300  
 Ala Ser Leu Glu Arg Met Val Ala Glu Gly Arg Phe Arg Glu Asp Leu  
 305 310 315 320  
 Tyr Tyr Arg Ile Asn Leu Ile His Leu His Leu Pro Pro Leu Arg Glu  
 325 330 335  
 15 Arg Gln Glu Asp Ile Gln Leu Leu Val Glu Ala Phe Ser Glu Ala Phe  
 340 345 350  
 Ala Gln Ser Asn Gly Leu Pro His Ala Val Trp Ser Ala Glu Ala Met  
 355 360 365  
 20 Arg Arg Ile Cys Ala Met Pro Leu Pro Gly Asn Val Arg Glu Leu Lys  
 370 375 380  
 Asn Val Val Glu Arg Thr Leu Leu Ser Gly Ser Arg Glu Ile Ser  
 385 390 395 400  
 25 Ala Arg Asp Val Ala Asp Phe Gly Ser Gln Val Thr Ala Ala Asp His  
 405 410 415  
 Ser Asp Glu Arg Ala Leu Thr Asp Met Glu Glu Ala Ala Ile Arg Glu  
 420 425 430  
 Thr Leu Thr Lys Tyr Asn Gly Asn Val Ser Arg Ala Ala Arg Ala Leu  
 435 440 445  
 30 Gly Leu Ser Arg Ala Ala Leu Tyr Arg Arg Met Glu Lys Tyr Gly Leu  
 450 455 460

(2) INFORMATION FOR SEQ ID NO:409

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 250 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 40 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 45 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...250  
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:409

Met Leu Lys Ile Lys Asn Leu His Ala Thr Val Gln Gly Lys Glu Ile  
 1 5 10 15  
 55 Leu Lys Gly Ile Asn Leu Glu Ile Asn Ala Gly Glu Ile His Ala Ile  
 20 25 30  
 Met Gly Pro Asn Gly Ser Gly Lys Ser Thr Leu Ser Ser Val Leu Val  
 35 40 45  
 60 Gly His Pro Ser Phe Glu Val Thr Glu Gly Glu Val Thr Phe Asn Gly  
 50 55 60  
 Ile Asp Leu Leu Glu Leu Glu Pro Glu Glu Arg Ala His Leu Gly Leu  
 65 70 75 80  
 Phe Leu Ser Phe Gln Tyr Pro Val Glu Ile Pro Gly Val Ser Met Val  
 85 90 95  
 65 Asn Phe Met Arg Ala Ala Val Asn Glu His Arg Lys Ala Ile Gly Ala  
 100 105 110  
 Glu Pro Val Ser Ala Ser Asp Phe Leu Lys Met Met Arg Glu Lys Arg  
 115 120 125  
 70 Ala Ile Val Glu Leu Asp Asn Lys Leu Ala Ser Arg Ser Val Asn Glu  
 130 135 140  
 Gly Phe Ser Gly Gly Glu Lys Lys Arg Asn Glu Ile Phe Gln Met Ala  
 145 150 155 160  
 Met Leu Glu Pro Lys Leu Ala Ile Leu Asp Glu Thr Asp Ser Gly Leu  
 165 170 175  
 75 Asp Ile Asp Ala Leu Arg Ile Val Ala Gly Gly Val Asn Arg Leu Arg

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180 185 190  
 Ser Pro Glu Asn Ala Ala Ile Val Ile Thr His Tyr Gln Arg Leu Leu  
 195 200 205  
 Glu Tyr Ile Lys Pro Asp Phe Val His Val Leu Tyr Lys Gly Arg Ile  
 210 215 220  
 Val Lys Ser Gly Gly Ala Glu Leu Ala Leu Thr Leu Glu Glu Lys Gly  
 225 230 235 240  
 Tyr Asp Trp Ile Lys Glu Glu Ile Gly Glu  
 245 250

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(2) INFORMATION FOR SEQ ID NO:410  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 461 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...461  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:410

Met Ala Lys Glu Lys Thr Ile Tyr Val Cys Arg Ser Cys Gly Thr Lys  
 1 5 10 15  
 Tyr Ala Lys Trp Gln Gly Asn Cys Asn Ala Cys Gly Glu Trp Asn Cys  
 20 25 30  
 Ile Asp Glu Glu Lys Val Pro Ala Pro Ala Ser Gly Lys His Ala Ala  
 35 40 45  
 Lys Ser Phe Met Pro Arg Glu Gln Asp Asn Arg Pro Arg Leu Leu Gln  
 50 55 60  
 Asp Val Glu Ser Gly Asp Glu Glu Arg Ile Arg Leu Gly Asp Glu Glu  
 65 70 75 80  
 Phe Asp Arg Val Leu Gly Gly Gly Ile Val Lys Gly Ala Phe Val Leu  
 85 90 95  
 Leu Gly Gly Glu Pro Gly Ile Gly Lys Ser Thr Leu Ile Leu Gln Thr  
 100 105 110  
 Val Leu Arg Leu Pro Gln Leu Arg Thr Leu Tyr Val Ser Gly Glu Glu  
 115 120 125  
 Ser Ala Arg Gln Leu Lys Met Arg Ala Glu Arg Leu Gly Gln Ala Met  
 130 135 140  
 Asn Gly Cys Tyr Val Tyr Cys Glu Thr Asn Ile Glu Arg Ile Leu Ser  
 145 150 155 160  
 Arg Ala Glu Glu Leu Thr Pro Asp Leu Leu Val Ile Asp Ser Ile Gln  
 165 170 175  
 Thr Val Tyr Thr Glu Glu Met Glu Ser Ser Ala Gly Ser Val Gly Gln  
 180 185 190  
 Ile Arg Glu Cys Ala Ala Leu Leu Leu Lys Tyr Cys Lys Thr Thr Gly  
 195 200 205  
 Ile Pro Val Ile Val Ile Gly His Ile Thr Lys Glu Gly Ser Ile Ala  
 210 215 220  
 Gly Pro Lys Val Leu Glu His Ile Val Asp Thr Val Leu Leu Phe Asp  
 225 230 235 240  
 Gly Asp Lys His His Leu Tyr Arg Ile Leu Arg Gly Gln Lys Asn Arg  
 245 250 255  
 Tyr Gly Ser Thr Ser Glu Leu Gly Ile Tyr Glu Met Arg Gln Asp Gly  
 260 265 270  
 Leu Arg Gly Val Glu Asn Pro Ser Glu His Leu Ile Thr Arg Asn Arg  
 275 280 285  
 Glu Asp Leu Ser Gly Ile Ala Ile Ala Val Ala Met Glu Gly Ile Arg  
 290 295 300  
 Pro Ile Leu Ile Glu Ala Gln Ala Leu Val Ser Ser Ala Ile Tyr Ala  
 305 310 315 320  
 Asn Pro Gln Arg Ser Ala Thr Gly Phe Asp Ile Arg Arg Met Asn Met  
 325 330 335  
 Leu Leu Ala Val Leu Glu Lys Arg Ala Gly Phe Lys Leu Ile Gln Lys  
 340 345 350  
 Asp Val Phe Leu Asn Ile Ala Gly Gly Ile Lys Ile Ala Asp Pro Ala

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355 360 365  
 Thr Asp Leu Ala Val Ile Ser Ala Val Leu Ala Ser Ser Leu Asp Ile  
 370 375 380  
 Val Ile Pro Pro Ala Val Cys Met Thr Gly Glu Val Gly Leu Ser Gly  
 385 390 395 400  
 Glu Ile Arg Pro Val Ser Arg Ile Glu Gln Arg Ile Thr Glu Ala Arg  
 405 410 415  
 Arg Ile Gly Phe Lys Glu Ile Leu Val Pro Ala Asp Asn Phe Arg Gln  
 420 425 430  
 10 Glu Asp Ala Gly Arg Phe Gly Ile Arg Leu Val Pro Val Arg Lys Val  
 435 440 445  
 Glu Glu Ala Phe Arg His Leu Phe Ser Lys Gly Arg Glu  
 450 455 460

## 15 (2) INFORMATION FOR SEQ ID NO:411

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 271 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES

25 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

30 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411

35 Met Asn Ser Arg His Leu Thr Ile Thr Ile Ala Gly Leu Ser Leu  
 1 5 10 15  
 Phe Val Leu Thr Leu Gly Gly Cys Ser Val Ala Gln Gln Asp Thr Gln  
 20 25 30  
 Trp Thr Leu Gly Gly Lys Leu Phe Thr Ser Ala Trp Ile Gln Arg Ser  
 35 40 45  
 40 Ala Glu Tyr Gln Ala Leu Cys Ile Gln Ala Tyr Asn Ile Ala Thr Glu  
 50 55 60  
 Arg Val Asp Ala Leu Pro Ala Glu Arg Lys Gln Gly Asp Arg Pro Tyr  
 65 70 75 80  
 45 Ala Ile Val Thr Asp Ile Arg Glu Thr Ile Leu Asp Asn Thr Pro Asn  
 85 90 95  
 Ser Val Tyr Gln Ala Leu Arg Gly Lys Asp Tyr Asp Glu Glu Thr Trp  
 100 105 110  
 50 Gly Lys Trp Cys Ala Gln Ala Asp Ala Asp Thr Leu Ala Gly Ala Leu  
 115 120 125  
 Ser Phe Phe Leu His Ala Ala Asn Lys Gly Ile Glu Val Phe Tyr Val  
 130 135 140  
 Thr Asn Arg Arg Asp Asn Leu Arg Glu Ala Thr Leu Gln Asn Leu Gln  
 145 150 155 160  
 55 Arg Tyr Gly Phe Pro Phe Ala Asp Glu Glu His Leu Leu Thr Thr His  
 165 170 175  
 Gly Pro Ser Asp Lys Glu Pro Arg Arg Leu Lys Ile Gln Glu Gln Tyr  
 180 185 190  
 60 Glu Ile Val Leu Leu Ile Gly Asp Asn Leu Gly Asp Phe His His Phe  
 195 200 205  
 Phe Asn Thr Lys Glu Glu Ser Gly Arg Lys Gln Ala Leu Gly Leu Thr  
 210 215 220  
 Ala Gly Glu Phe Gly Arg His Phe Ile Met Leu Pro Asn Pro Asn Tyr  
 225 230 235 240  
 65 Gly Ser Trp Glu Pro Ala Trp Tyr Gly Gly Lys Tyr Pro Pro Leu Pro  
 245 250 255  
 Glu Arg Asp Lys Ala Leu Lys Gln Leu His Ser Gln Asn Ser Arg  
 260 265 270

## 70 (2) INFORMATION FOR SEQ ID NO:412

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 417 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412

15	Met Ser Thr Asn Ile Asp Val Gln Gln Ile Lys Gln Arg Phe Gly Ile
	1 5 10 15
	Ile Gly Ser Ser Pro Leu Met Glu His Ala Ile Arg Val Ala Ala Gln
	20 25 30
20	Val Ala Pro Thr Asp Met Ser Val Leu Val Thr Gly Glu Ser Gly Ser
	35 40 45
	Gly Lys Glu Phe Phe Pro Gln Ile Ile His Tyr Tyr Ser Ala Arg Lys
	50 55 60
	His His Ser Tyr Ile Ala Val Asn Cys Gly Ala Ile Pro Glu Gly Thr
	65 70 75 80
25	Ile Asp Ser Glu Leu Phe Gly His Arg Lys Gly Ser Phe Thr Gly Ala
	85 90 95
	Val Ser Asp Arg Lys Gly Tyr Phe Glu Glu Ala Ser Gly Gly Thr Ile
	100 105 110
	Phe Leu Asp Glu Val Gly Glu Leu Pro Leu Pro Thr Gln Ala Arg Leu
	115 120 125
30	Leu Arg Val Leu Glu Thr Gly Glu Phe Ile Pro Val Gly Ala Ser Gln
	130 135 140
	Ser Gln Lys Thr Asp Val Arg Ile Val Ala Ala Thr Asn Val Asn Leu
	145 150 155 160
35	Lys Glu Ala Val Ala Asn Gly Lys Phe Arg Glu Asp Leu Phe Phe Arg
	165 170 175
	Leu Asn Thr Val Pro Ile Glu Val Pro Ala Leu Arg Met Arg Pro Asp
	180 185 190
	Asp Val Pro Leu Leu Phe Arg Arg Phe Ala Ala Asp Ser Ala Glu Lys
	195 200 205
40	Tyr Arg Met Pro Pro Leu Arg Leu Ser Asp Glu Ala Arg Thr Ile Leu
	210 215 220
	Met Arg Tyr Arg Trp Pro Gly Asn Val Arg Glu Leu Arg Asn Ile Thr
	225 230 235 240
45	Asp Arg Leu Ser Ile Leu Glu Glu Glu Arg Thr Val Ser Ala Glu Thr
	245 250 255
	Ile Thr Arg Tyr Leu Asp Ala Glu Gly Met Gln Asp Leu His Pro Val
	260 265 270
50	Val Ile Arg Arg Asn Glu Thr Thr Glu Ala Asp Lys Gln Ile Pro His
	275 280 285
	Tyr Glu Arg Glu Ile Ile Tyr Gln Val Leu Tyr Asp Met Lys Lys Glu
	290 295 300
	Ile Ala Asp Leu Lys Gly Met Met Asn Arg Leu Ala His His Glu Gln
	305 310 315 320
55	Pro Ser Trp Pro Val Gly Ser Asp Val Trp Gly Asn Asp Asp Lys Arg
	325 330 335
	Thr Ala Asp Pro Lys Trp Gly Val Ser Thr His Lys Ala Pro Ile Ala
	340 345 350
	Asn Ala Ala Glu Pro Val Glu Pro Ile Gln Glu Ala Ser Glu Tyr Thr
	355 360 365
60	Glu Asp Pro Val Ser Leu Glu Glu Val Gln Lys Lys Met Ile Ser Leu
	370 375 380
	Ala Leu Glu Arg His Gly Gly Arg Arg Lys Gln Thr Ala Glu Glu Leu
	385 390 395 400
65	Lys Ile Ser Glu Arg Thr Leu Tyr Arg Lys Ile Lys Glu Tyr Gly Leu
	405 410 415
	Glu

(2) INFORMATION FOR SEQ ID NO:413

(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 602 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413

Met Ile Leu Leu Phe Gly Gly Thr Thr Glu Gly Arg Ala Ala Ala Arg  
1 5 10 15  
Val Leu Asp Glu Ala Gly Ser Pro Phe Phe Tyr Ser Thr Lys Gly Asn  
20 25 30  
Leu Gln Glu Ile Gln Ser Ser His Gly His Arg Leu Thr Gly Ala Met  
35 40 45  
Thr Val Ala Asp Met Val Ser Phe Cys Arg Lys Glu Ile Arg Leu  
50 55 60  
Ile Val Asp Ala Ala His Pro Phe Ala Glu Glu Leu His Ala Ser Val  
65 70 75 80  
Ala Glu Ala Ser Glu Gln Thr Gly Ile Pro Val Val Arg Tyr Glu Arg  
85 90 95  
Gln Tyr Pro Pro Arg Glu Glu Gly Ile Val Trp Cys Ala Asn Tyr Asp  
100 105 110  
Thr Ala Ala Glu Arg Met Leu Gly Asp Gly Val Gln Arg Leu Leu Met  
115 120 125  
Leu Thr Gly Val Asn Thr Ile Pro Lys Leu Ala Ala Phe Trp Lys Glu  
130 135 140  
Arg Thr Thr Phe Cys Arg Ile Leu Lys Arg Asp Glu Ser Val Ala Leu  
145 150 155 160  
Ala Glu Lys Asn Gly Phe Pro Ala Glu Arg Ile Val Phe Phe Glu Pro  
165 170 175  
His Ala Asp Glu Glu Leu Met Gln Ala Val Arg Pro Asp Ala Ile Ile  
180 185 190  
Thr Lys Glu Ser Gly Glu Ser Gly Tyr Phe Arg Glu Lys Ile Glu Ala  
195 200 205  
Ala Arg Arg Met Gly Ile Arg Ile Tyr Ala Val Val Arg Pro Pro Leu  
210 215 220  
Pro Pro Ser Phe Ile Pro Val Gly Gly Pro Val Gly Leu Arg Arg Ala  
225 230 235 240  
Val Glu Arg Leu Val Pro Gly Phe Phe Ser Leu Arg Ser Gly Phe Thr  
245 250 255  
Thr Gly Thr Thr Ala Thr Ala Val Val Ala Ala Met Tyr Arg Leu  
260 265 270  
Met Gly Leu Gly Ser Leu Ala Glu Ala Pro Val Glu Leu Pro Ser Gly  
275 280 285  
Glu Ile Val Ser Leu Pro Ile Ala Glu Ile Arg Glu Glu Glu Asp Ala  
290 295 300  
Val Val Ser Ala Val Leu Lys Asp Ala Gly Asp Asp Pro Asp Val Thr  
305 310 315 320  
Asn Gly Met Ala Val Cys Ala Thr Ile Arg Leu Asn Pro Glu His Glu  
325 330 335  
Glu Val Arg Phe Leu Gln Gly Glu Gly Val Gly Val Val Thr Leu Pro  
340 345 350  
Gly Leu Gly Leu Glu Val Gly Gly Pro Ala Ile Asn Leu Val Pro Arg  
355 360 365  
Arg Met Met Thr Ala Glu Val Arg Arg Leu Tyr Ala Gln Gly Gly Val  
370 375 380  
Asp Ile Thr Ile Ser Val Pro Glu Gly Arg Glu Ala Ala Thr Gln Thr  
385 390 395 400  
Phe Asn Pro Arg Leu Gly Ile Arg Asp Gly Ile Ser Ile Ile Gly Thr  
405 410 415  
Ser Gly Val Val Lys Pro Phe Ser Ala Glu Ala Phe Val Gly Ala Ile  
420 425 430  
Arg Lys Gln Val Gly Ile Ala Thr Ala Leu Gly Ala Asn His Ile Val  
435 440 445  
Leu Asn Ser Gly Ala Lys Ser Glu Arg Tyr Val Lys Gly Ala Tyr Pro  
450 455 460  
Ala Leu Ile Pro Gln Ala Phe Val Gln Tyr Gly Asn Phe Val Gly Glu  
465 470 475 480  
Ser Leu Ser Cys Val Ala Ser Phe Pro Ser Val Arg Ser Val Thr Val



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290 295 300  
 Leu Glu Ile Ile Asn Ser Asp Lys Tyr Ala Asp Asp Asp Ala Arg Glu  
 305 310 315  
 Gln Ala Leu Lys Gln Leu Ser Ser Tyr Arg Tyr Ile Leu Asp Gln Ile  
 5 325 330 335  
 Tyr Pro Asn Leu Arg Arg Asn Thr Ile Thr Met Gly Tyr Ile Val Arg  
 340 345 350  
 Asp Tyr Thr Leu Glu Glu Ala Arg Glu Ile Ile Lys Thr Ala Pro Lys  
 355 360 365  
 10 Glu Leu Ser Glu Ala Glu Met Tyr Arg Val Ala Met Ser Tyr Pro Glu  
 370 375 380  
 Gly His Gln Glu Arg Leu Phe Ala Leu Asn Thr Thr Leu Lys Tyr Phe  
 385 390 395 400  
 15 Pro Glu Ser Val Thr Gly Arg Ile Asn Leu Ala Val Ala Phe Asn  
 405 410 415  
 Gly Gly Asp Val Gln Gln Ala Ile Ala Leu Leu Ser Pro Ile Gln Thr  
 420 425 430  
 Glu Lys Gly Val Ser Asn Ile Leu Gly Ala Ala Tyr Ala Arg Thr Gly  
 435 440 445  
 20 Asp Phe Ala Arg Ala Glu Thr Phe Phe Arg Lys Ala Val Ala Glu Gly  
 450 455 460  
 Asp Ala Asn Ala Gln Arg Asn Leu Asp Met Leu Leu Gly Lys Lys  
 465 470 475  
 25 (2) INFORMATION FOR SEQ ID NO:416  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 383 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 40 (B) LOCATION 1...383  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:416  
 45 Met Ala Glu Lys Arg Asp Tyr Tyr Glu Val Leu Gly Val Ser Lys Asn  
 1 5 10 15  
 Ala Thr Asp Asp Glu Leu Lys Lys Ala Tyr Arg Lys Lys Ala Ile Gln  
 20 25 30  
 50 Tyr His Pro Asp Lys Asn Pro Gly Asp Lys Glu Ala Glu Glu His Phe  
 35 40 45  
 Lys Glu Val Ala Glu Ala Tyr Asp Val Leu Ser Asp Pro Gln Lys Arg  
 50 55 60  
 Ser Gln Tyr Asp Gln Phe Gly His Ala Gly Leu Gly Gly Ala Ala Gly  
 65 70 75 80  
 55 Gly Gly Phe Ser Gly Gly Gly Met Ser Met Glu Asp Ile Phe Ser Arg  
 85 90 95  
 Phe Gly Asp Leu Phe Gly Gly Phe Gly Gly Phe Gly Gly Phe Ser Asp  
 100 105 110  
 60 Met Gly Gly Gly Ser Arg Arg Arg Val Arg Arg Gly Ser Asp Leu Arg  
 115 120 125  
 Val Arg Val Lys Leu Ser Leu Ala Asp Ile Ser Lys Gly Val Glu Lys  
 130 135 140  
 Lys Val Lys Val Lys Lys Gln Val Val Cys Ser Lys Cys Arg Gly Asp  
 145 150 155 160  
 65 Gly Thr Glu Glu Ala Asn Gly Lys Thr Thr Cys Gln Thr Cys His Gly  
 165 170 175  
 Thr Gly Val Val Thr Arg Val Ser Asn Thr Phe Leu Gly Ala Met Gln  
 180 185 190  
 70 Thr Gln Ser Thr Cys Pro Thr Cys His Gly Glu Gly Glu Ile Ile Thr  
 195 200 205  
 Lys Pro Cys Ser Lys Cys Lys Gly Glu Gly Val Glu Ile Gly Glu Glu  
 210 215 220  
 Val Ile Ser Phe His Ile Pro Ala Gly Val Ala Glu Gly Met Gln Met  
 225 230 235 240  
 75 Ser Val Asn Gly Lys Gly Asn Ala Ala Pro Arg Gly Gly Val Asn Gly

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245 250 255  
 Asp Leu Ile Val Val Ile Ala Glu Glu Pro Asp Pro Asn Leu Ile Arg  
 260 265 270  
 Asn Gly Asn Asp Leu Ile Tyr Asn Leu Leu Ile Ser Val Pro Leu Ala  
 275 280 285  
 5 Ile Lys Gly Gly Ser Val Glu Val Pro Thr Ile Asp Gly Arg Ala Lys  
 290 295 300  
 Ile Arg Ile Glu Ala Gly Thr Gln Pro Gly Lys Met Leu Arg Leu Arg  
 305 310 315 320  
 10 Asn Lys Gly Leu Pro Ser Val Asn Gly Tyr Gly Met Gly Asp Gln Leu  
 325 330 335  
 Val Asn Val Asn Val Tyr Ile Pro Glu Ser Ile Asp Ala Lys Asp Glu  
 340 345 350  
 15 Gln Ala Ile Ala Ala Met Glu Asn Ser Asp Ser Phe Lys Pro Thr Asp  
 355 360 365  
 Ala Ala Arg Lys Asp Ile Asp Lys Lys Tyr Arg Glu Met Leu Asp  
 370 375 380

(2) INFORMATION FOR SEQ ID NO:417

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 293 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417

40 Met Lys Lys Leu Ile Leu Ala Thr Leu Gly Leu Met Ala Ile Ala Met  
 1 5 10 15  
 Leu Ser Cys Ser Ser Asn Asn Lys Asp Leu Glu Asn Lys Gly Glu Ala  
 20 25 30  
 Thr Leu Leu Val Thr Phe Gly Ser Ser Tyr Lys Ala Pro Arg Glu Thr  
 35 40 45  
 45 Tyr Ala Lys Ile Glu Lys Thr Phe Ala Ala Tyr Pro Asp Gln Arg  
 50 55 60  
 Ile Ser Trp Thr Tyr Thr Ser Ser Ile Ile Arg Lys Lys Leu Ala Gln  
 65 70 75 80  
 50 Gln Gly Ile Tyr Ile Asp Ala Pro Asp Glu Ala Leu Glu Lys Leu Ala  
 85 90 95  
 Arg Leu Gly Tyr Lys Lys Ile Asn Val Gln Ser Leu His Val Ile Pro  
 100 105 110  
 Gly Arg Glu Tyr Asp Glu Met Ile Asp Phe Val Asn Lys Phe Lys Ala  
 115 120 125  
 55 Ala His Ser Asp Ile Thr Val Lys Val Gly Ala Pro Leu Phe Asp Thr  
 130 135 140  
 Asp Glu Asp Met Arg Glu Val Ala Glu Ile Leu His Lys Arg Phe Gln  
 145 150 155 160  
 60 Gln Thr Ile Glu Lys Gly Glu Ala Ile Val Phe Met Gly His Gly Thr  
 165 170 175  
 Glu His Ala Ala Asn Asp Arg Tyr Ala Arg Ile Asn Lys Ile Met Lys  
 180 185 190  
 Asn Tyr Ser Lys Phe Met Ile Val Gly Thr Val Glu Ser Asp Pro Ser  
 195 200 205  
 65 Ile Asn Asp Val Ile Ala Glu Leu Lys Glu Thr Gly Ala Thr Ala Val  
 210 215 220  
 Thr Met Met Pro Leu Met Ser Val Ala Gly Asp His Ala Thr Asn Asp  
 225 230 235 240  
 70 Met Ala Gly Asp Glu Asp Asp Ser Trp Lys Thr Leu Leu Thr Asn Ala  
 245 250 255  
 Gly Tyr Thr Val Ser Ile Asp Lys Leu Asp Asn Gly Asn Phe Ser Ala  
 260 265 270  
 Leu Gly Asp Ile Glu Glu Ile Arg Asn Ile Trp Leu Lys His Met Lys  
 275 280 285  
 75 Ala Thr Ser Ala Arg

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(2) INFORMATION FOR SEQ ID NO:418

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 356 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...356

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419

Met Thr Ser Val Ser His Leu Arg Thr Ile Ser Val Ala Gly Ile Leu  
 1 5 10 15  
 25 Ala Ala Leu Gly Gly Ala Val Leu Ile Leu Phe Gly Val Asn Leu Phe  
 20 25 30  
 Leu Gly Ser Val Ala Ile Pro Met Ser Glu Ile Phe Arg His Leu Phe  
 35 40 45  
 30 Ser Asp Arg Pro Glu Gly Gly Glu Ala Leu Val His Tyr Asn Ile Leu  
 50 55 60  
 Trp Lys Ser Arg Leu Pro Glu Ala Leu Thr Ala Ala Phe Ala Gly Ala  
 65 70 75 80  
 Gly Leu Ser Val Ser Gly Leu Gln Met Gln Thr Val Phe Arg Asn Pro  
 85 90 95  
 35 Leu Ala Gly Pro Ser Val Leu Gly Ile Ser Ser Gly Ala Ser Leu Gly  
 100 105 110  
 Val Ala Leu Val Val Leu Leu Ser Gly Ser Leu Gly Gly Val Ala Leu  
 115 120 125  
 40 Ser Ser Leu Gly Tyr Met Gly Glu Val Ala Met Asn Ile Ala Ala Ala  
 130 135 140  
 Val Gly Ser Leu Ala Val Met Gly Leu Ile Val Phe Val Ser Thr Lys  
 145 150 155 160  
 Val Arg Ser His Val Thr Leu Leu Ile Ile Gly Val Met Ile Gly Tyr  
 165 170 175  
 45 Val Ala Thr Ala Val Ile Gly Val Phe Lys Phe Phe Ser Ile Glu Glu  
 180 185 190  
 Asp Ile Arg Ala Tyr Val Ile Trp Gly Leu Gly Ser Phe Ser Arg Ala  
 195 200 205  
 50 Thr Asp Ser Gln Leu Ser Phe Phe Ala Ile Leu Met Leu Ile Phe Ile  
 210 215 220  
 Pro Ala Gly Met Leu Leu Val Lys Gln Leu Asn Leu Leu Leu Gly  
 225 230 235 240  
 Glu Ser Tyr Ala Arg Asn Leu Gly Leu Asn Thr Arg Arg Ala Arg Leu  
 245 250 255  
 55 Leu Val Ile Ser Ser Ala Gly Leu Leu Ile Ala Thr Val Thr Ala Tyr  
 260 265 270  
 Cys Gly Pro Ile Gly Phe Leu Gly Met Ala Val Pro His Leu Ala Arg  
 275 280 285  
 60 Val Ile Phe His Thr Ser Asp His Arg Ile Leu Met Pro Ala Thr Cys  
 290 295 300  
 Leu Ile Gly Ser Ala Leu Ala Leu Phe Cys Asn Ile Ile Ala Arg Met  
 305 310 315 320  
 Pro Gly Phe Glu Gly Ala Leu Pro Val Asn Ser Val Thr Ala Leu Val  
 325 330 335  
 65 Gly Ala Pro Ile Ile Val Thr Val Leu Phe Arg Arg Arg Arg Phe Lys  
 340 345 350  
 Glu Glu Thr Asp  
 355

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(2) INFORMATION FOR SEQ ID NO:419

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 757 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(iv) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419

15	Met Arg Thr Lys Thr Ile Phe Phe Ala Ile Ile Ser Phe Ile Ala Leu
	1 5 10 15
	Leu Ser Ser Ser Leu Ser Ala Gln Ser Lys Ala Val Leu Thr Gly Ser
	20 25 30
20	Val Ser Asp Ala Glu Thr Gly Glu Pro Leu Ala Gly Ala Arg Ile Glu
	35 40 45
	Val Lys His Thr Asn Ile Val Ala Gly Ala Asp Ala Gly Gly His Phe
	50 55 60
	Glu Ile Lys Asn Leu Pro Ala Gly Gln His Thr Ile Ile Cys Ser Leu
	65 70 75 80
25	Gly Gly Tyr Gly Gln Lys Glu Glu Val Val Ala Ile Glu Ala Gly Gln
	85 90 95
	Thr Lys Thr Ile Ser Phe Ala Leu Arg Leu Arg Thr Asn Asn Leu Glu
	100 105 110
30	Glu Val Val Val Thr Gly Thr Gly Thr Arg Tyr Arg Leu Val Asp Ala
	115 120 125
	Pro Val Ala Thr Glu Val Leu Thr Ala Lys Asp Ile Ala Ser Phe Ser
	130 135 140
	Ala Pro Thr Ser Glu Ala Leu Leu Gln Gly Leu Ser Pro Ser Phe Asp
	145 150 155 160
35	Phe Gly Pro Asn Leu Met Gly Ser Phe Met Gln Leu Asn Gly Leu Ser
	165 170 175
	Ser Lys Tyr Ile Leu Ile Leu Ile Asp Gly Lys Arg Val Tyr Gly Asp
	180 185 190
40	Val Gly Gly Gln Ala Asp Leu Ser Arg Ile Ser Pro Asp Gln Ile Glu
	195 200 205
	Arg Ile Glu Leu Val Lys Gly Ala Ser Ser Ser Leu Tyr Gly Ser Asp
	210 215 220
	Ala Ile Ala Gly Val Ile Asn Val Ile Thr Lys Lys Asn Thr Asn Arg
	225 230 235 240
45	Leu Ser Ala Tyr Thr Ser His Arg Ile Ser Lys Tyr Asn Asp Arg Gln
	245 250 255
	Thr Asn Thr Ser Leu Asp Ile Asn Ile Gly Lys Phe Ser Ser Asn Thr
	260 265 270
50	Asn Tyr Phe Phe Tyr His Thr Asp Gly Trp Gln Asn Ser Pro Phe Glu
	275 280 285
	Ile Lys Lys Lys Lys Gly Ser Gly Glu Pro Val Leu Glu Glu Thr Tyr
	290 295 300
	Lys Lys Thr Phe Arg Ala Gln Glu Asn Gln Gly Val Ser Gln Ser Leu
	305 310 315 320
55	Ser Tyr Tyr Ala Thr Asn Asn Leu Ser Phe Ser Gly Asn Val Gln Tyr
	325 330 335
	Asn Lys Arg Gln Ile Phe Thr Pro Thr Phe Ser Glu Lys Lys Ala Tyr
	340 345 350
60	Asp Met Asp Tyr Arg Ala Leu Thr Ala Ser Leu Gly Thr Asn Tyr Leu
	355 360 365
	Phe Pro Asn Gly Leu His Thr Leu Ser Phe Asp Ala Val Tyr Asp Arg
	370 375 380
	Phe Arg Phe Gly Tyr Leu Tyr His Asp Lys Asp Ser Ser Glu Ser Leu
	385 390 395 400
65	Ile Asn Asn Gln Gly Gln Thr Glu Gln Pro Thr Phe Phe Pro Gly Gln
	405 410 415
	Leu Arg Asn Lys Asn Asp Gln Ile Arg Tyr Thr Ala Glu Ala Arg Gly
	420 425 430
70	Val Phe Thr Leu Pro Tyr Ala Gln Lys Leu Thr Gly Gly Leu Glu Tyr
	435 440 445
	Phe Arg Glu Glu Leu Ile Ser Pro Tyr Asn Leu Ile Thr Asp Lys Ala
	450 455 460
	Asp Ala Ser Thr Leu Ser Ala Tyr Val Gln Asp Glu Trp Lys Pro Leu
	465 470 475 480
75	Asp Trp Phe Asn Met Thr Ala Gly Phe Arg Leu Val His His Gln Glu

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485 490 495  
 Phe Gly Thr Arg Met Thr Pro Lys Val Ser Ile Leu Ala Lys Tyr Gly  
 500 505 510  
 5 15 30 35 40 45 50 55 60 65 70 75  
 Pro Leu Asn Phe Arg Ala Thr Tyr Ala Asn Gly Tyr Lys Thr Pro Thr  
 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755  
 Leu Lys Glu Leu Phe Ala Arg Asn Glu Leu Thr Thr Met Gly Ser His  
 Asn Leu Tyr Leu Gly Asn Ala Asp Leu Lys Pro Gln Met Ser Asp Tyr  
 Tyr Ala Leu Gly Leu Glu Tyr Asn Gln Gly Pro Ile Ser Phe Ser Ala  
 Thr Val Tyr Asp Asn Glu Leu Arg Asn Leu Ile Ser Phe Met Asp Ile  
 Pro Thr Ser Pro Glu His Glu Ala Gln Gly Ile Lys Lys Thr Lys Gln  
 Tyr Ala Asn Ile Gly Lys Ala Arg Ser Arg Gly Leu Asp Val Leu Cys  
 Asp Ala Ser Ile Gly Trp Gly Ile Lys Leu Gly Ala Gly Tyr Ser Leu  
 Val Glu Ala Lys Asn Leu Gln Thr Asp Glu Trp Leu Glu Gly Ala Ala  
 Arg His Arg Ala Asn Val His Ala Asp Trp Val His Tyr Trp Gly Gln  
 Tyr Arg Leu Gly Val Ser Leu Phe Gly Arg Ile Gln Ser Glu Arg Tyr  
 Tyr Lys Asp Gly Asn Ala Pro Asp Tyr Thr Leu Trp Arg Leu Ala Thr  
 Ser His Arg Phe Ala His Phe Arg His Ile Ile Leu Asp Gly Thr Leu  
 Gly Ile Asp Asn Leu Phe Asp Tyr Val Asp Asp Arg Pro Met Gly Val  
 Asn Tyr Ala Thr Val Thr Pro Gly Arg Thr Phe Phe Ala Gln Ile Ala  
 Ile Arg Phe Asn Asn

(2) INFORMATION FOR SEQ ID NO:420

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 331 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...331  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:420

Met Thr Asp Asn Lys Gln Arg Asn Ile Val Phe Pro Ala Phe Leu Leu  
 1 5 10 15  
 Leu Leu Gly Val Ile Ala Val Val Thr Ile Val Gly Phe Phe Met Leu  
 20 25 30  
 Arg Pro Ala Glu Glu Ile Ile Gln Gly Gln Ile Glu Val Thr Glu Tyr  
 35 40 45  
 Arg Val Ser Ser Lys Val Pro Gly Arg Ile Lys Glu Leu Arg Val Ser  
 50 55 60  
 Glu Gly Gln Gln Val Gln Ala Gly Asp Thr Leu Ala Val Ile Glu Ala  
 65 70 75 80  
 Pro Asp Val Ala Ala Lys Met Glu Gln Ala Lys Ala Ala Glu Ala Ala  
 85 90 95  
 Ala Gln Ala Gln Asn Ala Lys Ala Leu Lys Gly Ala Arg Ser Glu Gln  
 100 105 110  
 Ile Gln Ala Ala Tyr Glu Met Trp Gln Lys Ala Gln Ala Gly Val Ala  
 115 120 125  
 Ile Ala Thr Lys Thr His Gln Arg Val Gln Asn Leu Tyr Asp Gln Gly  
 130 135 140  
 Val Val Pro Ala Gln Lys Leu Asp Glu Ala Thr Ala Gln Arg Asp Ala

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145 150 155 160  
 Ala Ile Ala Thr Gln Lys Ala Ala Glu Ala Gln Tyr Asn Met Ala Arg  
 165 170 175  
 Asn Gly Ala Glu Arg Glu Asp Lys Leu Ala Ala Ser Ala Leu Val Asp  
 180 185 190  
 Arg Ala Arg Gly Ala Val Ala Glu Val Glu Ser Tyr Ile Asn Glu Thr  
 195 200 205  
 Tyr Leu Ile Ala Pro Arg Ala Gly Glu Val Ser Glu Ile Phe Pro Lys  
 210 215 220  
 10 Ala Gly Glu Leu Val Gly Thr Gly Ala Pro Ile Met Asn Ile Ala Glu  
 225 230 235 240  
 Met Gly Asp Met Trp Ala Ser Phe Ala Val Arg Glu Asp Phe Leu Ser  
 245 250 255  
 15 Ser Met Thr Met Gly Ala Val Leu Glu Thr Val Val Pro Ala Leu Asn  
 260 265 270  
 Glu Glu Lys Val Arg Phe Lys Ile Thr Phe Ile Lys Asn Met Gly Thr  
 275 280 285  
 Tyr Ala Ala Trp Lys Ala Thr Lys Thr Thr Gly Gln Tyr Asp Leu Lys  
 290 295 300  
 20 Thr Phe Glu Val Lys Ala Thr Leu Ala Asp Lys Asp Lys Ala Gln Lys  
 305 310 315 320  
 Leu Arg Pro Gly Met Ser Val Ile Ile Arg Lys  
 325 330

25 (2) INFORMATION FOR SEQ ID NO:421

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 267 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

35 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

40 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421

45 Met Arg Ile Val Ser Asn Phe Leu Phe Val Ser Phe Ser Val Leu Leu  
 1 5 10 15  
 Phe Ala Ser Cys Arg Ser Gln Arg Glu Lys Val Val Tyr Leu Gln Asp  
 20 25 30  
 50 Ile Gln Thr Phe Asn Arg Glu Ile Ile Ala Lys Pro Tyr Asp Val Lys  
 35 40 45  
 Ile Glu Lys Asp Asp Val Leu Asn Ile Leu Val Ser Ser Arg Asp Pro  
 50 55 60  
 Glu Leu Ser Thr Pro Tyr Asn Gln Val Leu Thr Thr Arg Ala Leu Ala  
 65 70 75 80  
 55 Arg Asn Gly Tyr Gly Thr Asn Ser Asn Glu Gly Phe Leu Val Asp Ser  
 85 90 95  
 Lys Gly Tyr Ile Asn Tyr Pro Ile Leu Gly Gln Ile Tyr Val Glu Gly  
 100 105 110  
 60 Leu Thr Arg Thr Glu Leu Glu Lys Glu Ile Gln Lys Arg Ile Ile Ser  
 115 120 125  
 Ser Gly Phe Ile Lys Asp Pro Thr Val Thr Val Glu Leu Gln Asn Phe  
 130 135 140  
 Lys Val Ser Val Leu Gly Glu Val Asn His Pro Gly Ser Met Ser Val  
 145 150 155 160  
 65 Lys Gly Glu Arg Ile Thr Leu Leu Glu Ala Ile Gly Met Ala Gly Asp  
 165 170 175  
 Leu Thr Ile Tyr Gly Arg Arg Asp Arg Val Phe Val Ile Arg Glu Thr  
 180 185 190  
 70 Asp Gly His Arg Glu Val Phe Gln Thr Asp Leu Arg Lys Ala Asp Leu  
 195 200 205  
 Leu Ala Ser Pro Val Tyr Tyr Leu His Gln Asn Asp Val Ile Tyr Val  
 210 215 220  
 Glu Pro Asn Asp Lys Lys Thr Gln Met Ser Glu Ile Asn Gln Asn Asn  
 225 230 235 240  
 75 Asn Val Asn Val Trp Leu Ser Val Thr Ser Thr Leu Val Ser Ile Ser

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245 250 255  
 Thr Leu Thr Ile Thr Ile Ile Asp Lys Thr Lys  
 260 265

5 (2) INFORMATION FOR SEQ ID NO:422  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 569 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 10  
 (ii) MOLECULE TYPE: protein  
 15 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 20 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...569  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:422

25 Met Lys Lys Thr Asn Leu Phe Leu Ser Leu Leu Val Ile Phe Ile Thr  
 1 5 10 15  
 Gly Ser Phe Met Thr Ala Cys Ala Gln Lys Ser Lys Thr Asn Lys Leu  
 20 25 30  
 30 Thr Glu Glu Asp Arg Ser Arg Asn Glu Tyr Val Gln Ser Met Asp Val  
 35 40 45  
 Leu Ser Asn Ile Ile Gly Asn Val Arg Leu Tyr Phe Val Asp Thr Ile  
 50 55 60  
 Ser Ile Lys His Met Thr Arg Arg Gly Ile Asp Ala Met Leu Gly Gly  
 65 70 75 80  
 35 Leu Asp Pro Tyr Thr Glu Tyr Ile Pro Tyr Glu Glu Met Asp Glu Leu  
 85 90 95  
 Lys Leu Met Thr Thr Gly Glu Tyr Ala Gly Val Gly Ala Ile Ile Ser  
 100 105 110  
 40 Gln Arg Pro Asp Ser Ala Val Ile Ile Gln Arg Pro Met Glu Gly Met  
 115 120 125  
 Pro Ala Asp Glu Ala Gly Leu Ile Ala Gly Asp Arg Ile Leu Thr Ile  
 130 135 140  
 Asp Gly Lys Asp Phe Arg Lys Ser Thr Thr Pro Lys Val Ser Gln Ala  
 145 150 155 160  
 45 Leu Lys Gly Ile Ala Gly Thr Val Ala Lys Val Thr Val Met Arg Tyr  
 165 170 175  
 Gly Glu Thr Lys Pro Arg Thr Phe Ser Val Lys Arg Gln Lys Val Ile  
 180 185 190  
 50 Met Asn Ser Val Thr Tyr Ser Gly Met Leu Asp Gly Ser Ile Gly Tyr  
 195 200 205  
 Ile Arg Leu Asn Asn Phe Thr Asp Lys Ser Ala Glu Glu Val Arg Thr  
 210 215 220  
 Ala Leu Leu Asp Leu Arg Asp Lys Gln Gly Ala Lys Gly Leu Ile Leu  
 225 230 235 240  
 55 Asp Leu Arg Gly Asn Gly Gly Leu Met Gln Ala Ala Ile Glu Ile  
 245 250 255  
 Val Asn Leu Phe Val Pro Lys Gly Lys Glu Val Val Thr Thr Lys Gly  
 260 265 270  
 60 Arg Ile Ala Glu Ser Ala Ser Val Phe Arg Thr Leu Thr Glu Pro Ile  
 275 280 285  
 Asp Thr Lys Leu Pro Ile Val Val Leu Ile Asp Gly Gln Ser Ala Ser  
 290 295 300  
 Ser Ser Glu Ile Val Ala Gly Ala Leu Gln Asp Met Asp Arg Ala Val  
 305 310 315 320  
 65 Leu Met Gly Gln Lys Ser Tyr Gly Lys Gly Leu Val Gln Thr Thr Arg  
 325 330 335  
 Gln Leu Pro Tyr Asn Gly Val Ile Lys Leu Thr Thr Ala Lys Tyr Tyr  
 340 345 350  
 70 Ile Pro Ser Gly Arg Cys Ile Gln Arg Leu Asp Tyr Ser Arg Thr Asn  
 355 360 365  
 Arg Thr Gly Met Ala Thr Ala Ile Pro Asp Ser Leu His Lys Ile Phe  
 370 375 380  
 Tyr Thr Ala Ala Gly Arg Arg Val Glu Asp Ala Gly Gly Ile Leu Pro  
 385 390 395 400  
 75 Asp Ile Glu Val Lys Gln Asp Thr Ala Ala Thr Leu Leu Tyr Tyr Met

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405 410 415  
 Ala Ile Asn Asn Asp Val Phe Asp Phe Val Thr Gly Tyr Val Leu Lys  
 420 425 430  
 His Lys Thr Ile Ala Lys Pro Glu Asp Phe Ser Ile Thr Asn Glu Asp  
 435 440 445  
 Tyr Ala Ala Phe Cys Lys Met Met Glu Glu Lys Lys Phe Asp Tyr Asp  
 450 455 460  
 Arg Gln Ser Gly Lys Met Leu Asp Lys Leu Glu Glu Leu Ala Lys Ile  
 465 470 475 480  
 10 Glu Gly Tyr Leu Pro Glu Ala Asn Ser Glu Leu Lys Ala Leu Arg Glu  
 485 490 495  
 Lys Leu Lys Pro Asn Leu Ser Arg Asp Leu Leu Arg Phe Lys Lys Glu  
 500 505 510  
 15 Ile Thr Asn Tyr Leu Asn Asn Glu Ile Val Thr Arg Tyr Tyr Tyr Glu  
 515 520 525  
 Arg Gly Ser Ile Arg Gln Ser Leu Pro Glu Asp Lys Val Val Lys Glu  
 530 535 540  
 Ala Ile Lys Leu Leu Lys Asp His Pro Glu Gln Ile Arg Gln Ile Leu  
 545 550 555 560  
 20 Ala Ala Pro Lys Ala Glu Asn Lys Gly  
 565

## (2) INFORMATION FOR SEQ ID NO:423

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 981 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 35 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...981  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:423

Met Gln Asn Lys Gly Phe Val Ile Val Ile Thr Ser Ala Leu Ala Ile  
 1 5 10 15  
 45 Ile Cys Ala Phe Tyr Leu Ser Phe Ser Phe Val Thr Asn Arg Tyr Glu  
 20 25 30  
 Lys Lys Ala Lys Ala Met Gly Asp Val Ala Gly Met Ala Tyr Leu Asp  
 35 40 45  
 50 Ser Met Ser Asn Glu Lys Val Trp Phe Gly Tyr Thr Leu Lys Glu Ala  
 50 55 60  
 Gln Ala Gln Gln Ile Gly Leu Gly Leu Asp Leu Lys Gly Gly Met Asn  
 65 70 75 80  
 Val Ile Leu Lys Leu Asn Ala Ser Asp Leu Leu Arg Asn Leu Ser Asn  
 85 90 95  
 55 Lys Ser Leu Asp Pro Asn Phe Asn Lys Ala Leu Glu Asn Ala Ala Lys  
 100 105 110  
 Ser Thr Glu Gln Ser Asp Phe Ile Asp Ile Phe Val Lys Glu Tyr Arg  
 115 120 125  
 60 Lys Leu Asp Pro Asn Gly Arg Leu Ala Val Ile Phe Gly Ser Gly Asp  
 130 135 140  
 Leu Arg Asp Gln Ile Thr Ala Lys Ser Thr Asp Ala Asp Val Val Arg  
 145 150 155 160  
 Leu Leu Lys Glu Lys Tyr Asn Ser Ala Val Glu Ala Ser Phe Asn Val  
 165 170 175  
 65 Leu Arg Ala Arg Ile Asp Ala Phe Gly Val Val Ala Pro Asn Leu Gln  
 180 185 190  
 Arg Leu Glu Gly Gln Gly Arg Ile Leu Val Glu Leu Pro Gly Val Lys  
 195 200 205  
 70 Asp Pro Glu Arg Val Arg Thr Leu Leu Gln Arg Ser Ala Asn Leu Gln  
 210 215 220  
 Phe Trp Arg Thr Tyr Lys Phe Glu Glu Val Ser Gly Asp Leu Ile Ala  
 225 230 235 240  
 Ala Asn Asp Arg Leu Ser Glu Leu Ala Met Asn Asn Thr Asp Ala Thr  
 245 250 255  
 75 Pro Glu Thr Glu Pro Ala Thr Thr Asp Ser Val Ala Ala Thr Ala Asp

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		260		265		270
	Ser	Ala	Ala	Val	Gln	Ala
		275		280		285
5	Glu	Ala	Lys	Asp	Ala	Thr
		290		295		300
	Pro	Val	Asn	Arg	Gly	Ala
		305		310		315
	Met	Ala	Gln	Ile	Ser	Glu
		320		325		330
10	Thr	Arg	Glu	Asp	Val	Leu
		335		340		345
	Pro	Glu	Thr	Lys	Glu	Thr
		350		355		360
15	Thr	Asn	Arg	Thr	Gly	Asp
		365		370		375
	Ala	Lys	Ser	Asp	Ile	Gln
		380		385		390
	Ser	Met	Thr	Met	Asn	Glu
		395		400		405
20	Lys	Asp	Asn	Val	Gly	Arg
		410		415		420
	Tyr	Ser	Ala	Pro	Asn	Val
		425		430		435
25	Ile	Ser	Gly	His	Phe	Thr
		440		445		450
	Leu	Asn	Ser	Gly	Lys	Met
		455		460		465
	Val	Ile	Gly	Pro	Thr	Leu
		470		475		480
30	Ser	Phe	Leu	Leu	Ala	Leu
		485		490		495
	Tyr	Gly	Phe	Leu	Pro	Gly
		500		505		510
35	Ser	Phe	Thr	Leu	Gly	Val
		515		520		525
	Leu	Ser	Gly	Ile	Ala	Gly
		530		535		540
	Ala	Asn	Val	Leu	Ile	Phe
		545		550		555
40	Lys	Thr	Pro	Ile	Arg	Ala
		560		565		570
	Ala	Ile	Phe	Asp	Ser	Asn
		575		580		585
45	Phe	Leu	Tyr	Gly	Thr	Gly
		590		595		600
	Ile	Gly	Leu	Ile	Ala	Ser
		605		610		615
	Val	Phe	Glu	Lys	Leu	Ala
		620		625		630
50	Thr	Thr	Ser	Ile	Thr	Arg
		635		640		645
	Leu	Gly	Lys	Arg	Lys	Thr
		650		655		660
55	Leu	Gly	Leu	Ile	Ala	Ser
		665		670		675
	Phe	Ser	Gly	Gly	Arg	Asn
		680		685		690
	Ser	Glu	Ala	Val	Arg	Ser
		695		700		705
60	Leu	Val	Thr	Ser	Ile	Gly
		710		715		720
	Asn	Tyr	Lys	Ile	Gln	Glu
		725		730		735
65	Asp	Lys	Leu	Tyr	Gln	Ser
		740		745		750
	Ala	Asp	Gln	Phe	Leu	Asp
		755		760		765
	Ser	Met	Ser	Ser	Asp	Ile
		770		775		780
70	Ser	Met	Ile	Phe	Met	Ala
		785		790		795
	Ser	Phe	Ser	Ala	Gly	Val
		800		805		810
	Ile	Ile	Ala	Leu	Tyr	Ala
		815		820		825
75	Ile	Ile	Ala	Leu	Tyr	Ala
		830		835		840
		845		850		855

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Glu Ile Asp Gln Asn Phe Ile Ala Ala Ile Leu Ala Ile Ile Gly Tyr  
 865 870 875 880  
 Ser Leu Asn Asp Thr Val Val Val Phe Asp Arg Ile Arg Glu Thr Met  
 885 890 895  
 5 Lys Leu Tyr Pro Asn Arg Asp Arg Tyr Gln Val Ile Asn Asp Ala Leu  
 900 905 910  
 Asn Ser Thr Leu Gly Arg Thr Leu Asn Thr Ser Leu Thr Thr Phe Ile  
 915 920 925  
 10 Val Met Leu Val Ile Phe Ile Phe Gly Gly Ala Thr Met Arg Ser Phe  
 930 935 940  
 Thr Phe Ser Ile Leu Leu Gly Ile Val Ile Gly Thr Tyr Ser Thr Leu  
 945 950 955 960  
 Phe Val Ala Thr Pro Leu Ala Tyr Glu Ile Gln Lys Arg Lys Leu Asn  
 965 970 975  
 15 Lys Ala Ala Lys Lys  
 980

(2) INFORMATION FOR SEQ ID NO:424

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1017 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 25 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1017  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:424

Met Lys Arg Met Thr Leu Phe Phe Leu Cys Leu Leu Thr Ser Ile Gly  
 1 5 10 15  
 40 Trp Ala Met Ala Gln Asn Arg Thr Val Lys Gly Thr Val Ile Ser Ser  
 20 25 30  
 Glu Asp Asn Glu Pro Leu Ile Gly Ala Asn Val Val Val Val Gly Asn  
 35 40 45  
 45 Thr Thr Ile Gly Ala Ala Thr Asp Leu Asp Gly Asn Phe Thr Leu Ser  
 50 55 60  
 Val Pro Ala Asn Ala Lys Met Leu Arg Val Ser Tyr Ser Gly Met Thr  
 65 70 75 80  
 Thr Lys Glu Val Ala Ile Ala Asn Val Met Lys Ile Val Leu Asp Pro  
 85 90 95  
 50 Asp Ser Lys Val Leu Glu Gln Val Val Val Leu Gly Tyr Gly Thr Gly  
 100 105 110  
 Gln Lys Leu Ser Thr Val Ser Gly Ser Val Ala Lys Val Ser Ser Glu  
 115 120 125  
 55 Lys Leu Ala Glu Lys Pro Val Ala Asn Ile Met Asp Ala Leu Gln Gly  
 130 135 140  
 Gln Val Ala Gly Met Gln Val Met Thr Thr Ser Gly Asp Pro Thr Ala  
 145 150 155 160  
 Val Ala Ser Val Glu Ile His Gly Thr Gly Ser Leu Gly Ala Ser Ser  
 165 170 175  
 60 Ala Pro Leu Tyr Ile Val Asp Gly Met Gln Thr Ser Leu Asp Val Val  
 180 185 190  
 Ala Thr Met Asn Pro Asn Asp Phe Glu Ser Met Ser Val Leu Lys Asp  
 195 200 205  
 65 Ala Ser Ala Thr Ser Ile Tyr Gly Ala Arg Ala Ala Asn Gly Val Val  
 210 215 220  
 Phe Ile Gln Thr Lys Lys Gly Lys Met Ser Glu Arg Gly Arg Ile Thr  
 225 230 235 240  
 Phe Asn Ala Ser Tyr Gly Ile Ser Gln Ile Leu Asn Thr Lys Pro Leu  
 245 250 255  
 70 Asp Asn Met Met Thr Gly Asp Glu Leu Leu Asp Phe Gln Val Lys Ala  
 260 265 270  
 Gly Phe Trp Gly Asn Asn Gln Thr Val Gln Lys Val Lys Asp Met Ile  
 275 280 285  
 75 Leu Ala Gly Ala Glu Asp Leu Tyr Gly Asn Tyr Asp Ser Leu Lys Asp  
 290 295 300

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Glu Tyr Gly Lys Thr Leu Phe Pro Val Asp Phe Asn His Asp Ala Asp  
 305 310 315 320  
 Trp Leu Lys Ala Leu Phe Lys Thr Ala Pro Thr Ser Gln Gly Asp Ile  
 325 330 335  
 5 Ser Phe Ser Gly Gly Ser Gln Gly Thr Ser Tyr Tyr Ala Ser Ile Gly  
 340 345 350  
 Tyr Phe Asp Gln Glu Gly Met Ala Arg Glu Pro Ala Asn Phe Lys Arg  
 355 360 365  
 10 Tyr Ser Gly Arg Leu Asn Phe Glu Ser Arg Ile Asn Glu Trp Leu Lys  
 370 375 380  
 Val Gly Ala Asn Leu Ser Gly Ala Ile Ala Asn Arg Arg Ser Ala Asp  
 385 390 395 400  
 Tyr Phe Gly Lys Tyr Tyr Met Gly Ser Gly Thr Phe Gly Val Leu Thr  
 405 410 415  
 15 Met Pro Arg Tyr Tyr Asn Pro Phe Asp Val Asn Gly Asp Leu Ala Asp  
 420 425 430  
 Val Tyr Tyr Met Tyr Gly Ala Thr Arg Pro Ser Met Thr Glu Pro Tyr  
 435 440 445  
 20 Phe Ala Lys Met Arg Pro Phe Ser Ser Glu Ser His Gln Ala Asn Val  
 450 455 460  
 Asn Gly Phe Ala Gln Ile Thr Pro Ile Lys Gly Leu Thr Leu Lys Ala  
 465 470 475 480  
 Gln Ala Gly Val Asp Ile Thr Asn Thr Arg Thr Ser Ser Lys Arg Met  
 485 490 495  
 25 Pro Asn Asn Pro Tyr Asp Ser Thr Pro Leu Gly Glu Arg Arg Glu Arg  
 500 505 510  
 Ala Tyr Arg Asp Val Ser Lys Ser Phe Thr Asn Thr Ala Glu Tyr Lys  
 515 520 525  
 30 Phe Ser Ile Asp Glu Lys His Asp Leu Thr Ala Leu Met Gly His Glu  
 530 535 540  
 Tyr Ile Glu Tyr Glu Gly Asp Val Ile Gly Ala Ser Ser Lys Gly Phe  
 545 550 555 560  
 Glu Ser Asp Lys Leu Met Leu Leu Ser Gln Gly Lys Thr Gly Asn Ser  
 565 570 575  
 35 Leu Ser Leu Pro Glu His Arg Val Ala Glu Tyr Ala Tyr Leu Ser Phe  
 580 585 590  
 Phe Ser Arg Phe Asn Tyr Gly Phe Asp Lys Trp Met Tyr Ile Asp Phe  
 595 600 605  
 40 Ser Val Arg Asn Asp Gln Ser Ser Arg Phe Gly Ser Asn Asn Arg Ser  
 610 615 620  
 Ala Trp Phe Tyr Ser Val Gly Gly Met Phe Asp Ile Tyr Asn Lys Phe  
 625 630 635 640  
 Ile Gln Glu Ser Asn Trp Leu Ser Asp Leu Arg Leu Lys Met Ser Tyr  
 645 650 655  
 45 Gly Thr Thr Gly Asn Ser Glu Ile Gly Asn Tyr Asn His Gln Ala Leu  
 660 665 670  
 Val Thr Val Asn Asn Tyr Thr Glu Asp Ala Met Gly Leu Ser Ile Ser  
 675 680 685  
 50 Thr Ala Gly Asn Pro Asp Leu Ser Trp Glu Lys Gln Ser Gln Phe Asn  
 690 695 700  
 Phe Gly Leu Ala Ala Gly Ala Phe Asn Asn Arg Leu Ser Ala Glu Val  
 705 710 715 720  
 Asp Phe Tyr Val Arg Thr Thr Asn Asp Met Leu Ile Asp Val Pro Met  
 725 730 735  
 55 Pro Tyr Ile Ser Gly Phe Phe Ser Gln Tyr Gln Asn Val Gly Ser Met  
 740 745 750  
 Lys Asn Thr Gly Val Asp Leu Ser Leu Lys Gly Thr Ile Tyr Gln Asn  
 755 760 765  
 60 Lys Asp Trp Asn Val Tyr Ala Ser Ala Asn Phe Asn Tyr Asn Arg Gln  
 770 775 780  
 Glu Ile Thr Lys Leu Phe Phe Gly Leu Asn Lys Tyr Met Leu Pro Asn  
 785 790 795 800  
 Thr Gly Thr Ile Trp Glu Ile Gly Tyr Pro Asn Ser Phe Tyr Met Ala  
 805 810 815  
 65 Glu Tyr Ala Gly Ile Asp Lys Lys Thr Gly Lys Gln Leu Trp Tyr Val  
 820 825 830  
 Pro Gly Gln Val Asp Ala Asp Gly Asn Lys Val Thr Thr Ser Gln Tyr  
 835 840 845  
 70 Ser Ala Asp Leu Glu Thr Arg Ile Asp Lys Ser Val Thr Pro Pro Ile  
 850 855 860  
 Thr Gly Gly Phe Ser Leu Gly Ala Ser Trp Lys Gly Leu Ser Leu Asp  
 865 870 875 880  
 Ala Asp Phe Ala Tyr Ile Val Gly Lys Trp Met Ile Asn Asn Asp Arg  
 885 890 895  
 75 Tyr Phe Thr Glu Asn Ala Gly Gly Leu Met Gln Leu Asn Lys Asp Lys



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5 Met Leu 900 Asn Ala Trp Thr 905 Glu Asp Asn Lys Glu Thr 910 Asp Val Pro  
 915 920 925  
 Lys Leu Gly Gln Ser Pro Gln Phe Asp Thr His Leu Leu Glu Asn Ala  
 930 935 940  
 Ser Phe Leu Arg Leu Lys Asn Leu Lys Leu Thr Tyr Val Leu Pro Asn  
 945 950 955 960  
 Ser Leu Phe Ala Gly Gln Asn Val Ile Gly Gly Ala Arg Val Tyr Leu  
 965 970 975  
 10 Met Ala Arg Asn Leu Leu Thr Val Thr Lys Tyr Lys Gly Phe Asp Pro  
 980 985 990  
 Glu Ala Gly Gly Asn Val Gly Lys Asn Gln Tyr Pro Asn Ser Lys Gln  
 995 1000 1005  
 15 Tyr Val Ala Gly Ile Gln Leu Ser Phe  
 1010 1015  
 (2) INFORMATION FOR SEQ ID NO:425  
 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1014 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 25 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 30 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1014  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:425  
 Met Thr Leu Phe Phe Leu Cys Leu Leu Thr Ser Ile Gly Trp Ala Met  
 1 5 10 15  
 40 Ala Gln Asn Arg Thr Val Lys Gly Thr Val Ile Ser Ser Glu Asp Asn  
 20 25 30  
 Glu Pro Leu Ile Gly Ala Asn Val Val Val Val Gly Asn Thr Thr Ile  
 35 40 45  
 Gly Ala Ala Thr Asp Leu Asp Gly Asn Phe Thr Leu Ser Val Pro Ala  
 50 55 60  
 45 Asn Ala Lys Met Leu Arg Val Ser Tyr Ser Gly Met Thr Thr Lys Glu  
 65 70 75 80  
 Val Ala Ile Ala Asn Val Met Lys Ile Val Leu Asp Pro Asp Ser Lys  
 85 90 95  
 50 Val Leu Glu Gln Val Val Val Leu Gly Tyr Gly Thr Gly Gln Lys Leu  
 100 105 110  
 Ser Thr Val Ser Gly Ser Val Ala Lys Val Ser Ser Glu Lys Leu Ala  
 115 120 125  
 Glu Lys Pro Val Ala Asn Ile Met Asp Ala Leu Gln Gly Gln Val Ala  
 130 135 140  
 55 Gly Met Gln Val Met Thr Thr Ser Gly Asp Pro Thr Ala Val Ala Ser  
 145 150 155 160  
 Val Glu Ile His Gly Thr Gly Ser Leu Gly Ala Ser Ser Ala Pro Leu  
 165 170 175  
 60 Tyr Ile Val Asp Gly Met Gln Thr Ser Leu Asp Val Val Ala Thr Met  
 180 185 190  
 Asn Pro Asn Asp Phe Glu Ser Met Ser Val Leu Lys Asp Ala Ser Ala  
 195 200 205  
 Thr Ser Ile Tyr Gly Ala Arg Ala Ala Asn Gly Val Val Phe Ile Gln  
 210 215 220  
 65 Thr Lys Lys Gly Lys Met Ser Glu Arg Gly Arg Ile Thr Phe Asn Ala  
 225 230 235 240  
 Ser Tyr Gly Ile Ser Gln Ile Leu Asn Thr Lys Pro Leu Asp Asn Met  
 245 250 255  
 70 Met Thr Gly Asp Glu Leu Leu Asp Phe Gln Val Lys Ala Gly Phe Trp  
 260 265 270  
 Gly Asn Asn Gln Thr Val Gln Lys Val Lys Asp Met Ile Leu Ala Gly  
 275 280 285  
 Ala Glu Asp Leu Tyr Gly Asn Tyr Asp Ser Leu Lys Asp Glu Tyr Gly  
 290 295 300  
 75 Lys Thr Leu Phe Pro Val Asp Phe Asn His Asp Ala Asp Trp Leu Lys

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305  
 Ala Leu Phe Lys Thr 310  
 325  
 Gly Gly Ser Gln Gly Thr Ser Tyr Tyr 330  
 340  
 Gln Glu Gly Met Ala Arg Glu Pro Ala Asn Phe Lys Arg Tyr Ser Gly 350  
 355  
 Arg Leu Asn Phe Glu Ser Arg Ile Asn Glu Trp Leu Lys Val Gly Ala 360  
 370  
 375  
 10 Asn Leu Ser Gly Ala Ile Ala Asn Arg Arg Ser Ala Asp Tyr Phe Gly 380  
 385 390  
 Lys Tyr Tyr Met Gly Ser Gly Thr Phe Gly Val Leu Thr Met Pro Arg 400  
 405  
 15 Tyr Tyr Asn Pro Phe Asp Val Asn Gly Asp Leu Ala Asp Val Tyr Tyr 415  
 420  
 425  
 Met Tyr Gly Ala Thr Arg Pro Ser Met Thr Glu Pro Tyr Phe Ala Lys 430  
 435  
 440  
 Met Arg Pro Phe Ser Ser Glu Ser His Gln Ala Asn Val Asn Gly Phe 445  
 450  
 455  
 20 Ala Gln Ile Thr Pro Ile Lys Gly Leu Thr Leu Lys Ala Gln Ala Gly 460  
 465 470  
 Val Asp Ile Thr Asn Thr Arg Thr Ser Ser Lys Arg Met Pro Asn Asn 480  
 485  
 25 Pro Tyr Asp Ser Thr Pro Leu Gly Glu Arg Arg Glu Arg Ala Tyr Arg 490  
 500  
 505  
 Asp Val Ser Lys Ser Phe Thr Asn Thr Ala Glu Tyr Lys Phe Ser Ile 510  
 515  
 520  
 Asp Glu Lys His Asp Leu Thr Ala Leu Met Gly His Glu Tyr Ile Glu 525  
 530  
 535  
 30 Tyr Glu Gly Asp Val Ile Gly Ala Ser Ser Lys Gly Phe Glu Ser Asp 540  
 545 550  
 Lys Leu Met Leu Leu Ser Gln Gly Lys Thr Gly Asn Ser Leu Ser Leu 560  
 565  
 570  
 35 Pro Glu His Arg Val Ala Glu Tyr Ala Tyr Leu Ser Phe Phe Ser Arg 580  
 585  
 590  
 Phe Asn Tyr Gly Phe Asp Lys Trp Met Tyr Ile Asp Phe Ser Val Arg 600  
 595  
 600  
 Asn Asp Gln Ser Ser Arg Phe Gly Ser Asn Asn Arg Ser Ala Trp Phe 610  
 615  
 40 Tyr Ser Val Gly Gly Met Phe Asp Ile Tyr Asn Lys Phe Ile Gln Glu 620  
 625 630  
 Ser Asn Trp Leu Ser Asp Leu Arg Leu Lys Met Ser Tyr Gly Thr Thr 640  
 645  
 45 Gly Asn Ser Glu Ile Gly Asn Tyr Asn His Gln Ala Leu Val Thr Val 650  
 655  
 660  
 670  
 Asn Asn Tyr Thr Glu Asp Ala Met Gly Leu Ser Ile Ser Thr Ala Gly 680  
 675  
 685  
 Asn Pro Asp Leu Ser Trp Glu Lys Gln Ser Gln Phe Asn Phe Gly Leu 690  
 695  
 700  
 50 Ala Ala Gly Ala Phe Asn Asn Arg Leu Ser Ala Glu Val Asp Phe Tyr 710  
 715  
 720  
 Val Arg Thr Thr Asn Asp Met Leu Ile Asp Val Pro Met Pro Tyr Ile 730  
 725  
 735  
 55 Ser Gly Phe Phe Ser Gln Tyr Gln Asn Val Gly Ser Met Lys Asn Thr 740  
 745  
 750  
 Gly Val Asp Leu Ser Leu Lys Gly Thr Ile Tyr Gln Asn Lys Asp Trp 755  
 760  
 765  
 Asn Val Tyr Ala Ser Ala Asn Phe Asn Tyr Asn Arg Gln Glu Ile Thr 770  
 775  
 780  
 60 Lys Leu Phe Phe Gly Leu Asn Lys Tyr Met Leu Pro Asn Thr Gly Thr 785  
 790  
 795  
 Ile Trp Glu Ile Gly Tyr Pro Asn Ser Phe Tyr Met Ala Glu Tyr Ala 800  
 805  
 810  
 65 Gly Ile Asp Lys Lys Thr Gly Lys Gln Leu Trp Tyr Val Pro Gly Gln 820  
 825  
 830  
 Val Asp Ala Asp Gly Asn Lys Val Thr Thr Ser Gln Tyr Ser Ala Asp 835  
 840  
 845  
 Leu Glu Thr Arg Ile Asp Lys Ser Val Thr Pro Ile Thr Gly Gly 850  
 855  
 860  
 70 Phe Ser Leu Gly Ala Ser Trp Lys Gly Leu Ser Leu Asp Ala Asp Phe 865  
 870  
 875  
 Ala Tyr Ile Val Gly Lys Trp Met Ile Asn Asn Asp Arg Tyr Phe Thr 880  
 885  
 890  
 75 Glu Asn Ala Gly Gly Leu Met Gln Leu Asn Lys Asp Lys Met Leu Leu 900  
 905  
 910

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Asn Ala Trp Thr Glu Asp Asn Lys Glu Thr Asp Val Pro Lys Leu Gly  
 915 920 925  
 Gln Ser Pro Gln Phe Asp Thr His Leu Leu Glu Asn Ala Ser Phe Leu  
 930 935 940  
 5 Arg Leu Lys Asn Leu Lys Leu Thr Tyr Val Leu Pro Asn Ser Leu Phe  
 945 950 955 960  
 Ala Gly Gln Asn Val Ile Gly Gly Ala Arg Val Tyr Leu Met Ala Arg  
 965 970 975  
 10 Asn Leu Leu Thr Val Thr Lys Tyr Lys Gly Phe Asp Pro Glu Ala Gly  
 980 985 990  
 Gly Asn Val Gly Lys Asn Gln Tyr Pro Asn Ser Lys Gln Tyr Val Ala  
 995 1000 1005  
 Gly Ile Gln Leu Ser Phe  
 1010  
 15  
 (2) INFORMATION FOR SEQ ID NO:426  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 821 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 20  
 (ii) MOLECULE TYPE: protein  
 25 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 30 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...821  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:426  
 35 Met Lys Lys Lys Asn Phe Leu Leu Leu Gly Ile Phe Val Ala Leu Leu  
 1 5 10 15  
 Thr Phe Ile Gly Ser Met Gln Ala Gln Ala Lys Asp Tyr Phe Asn  
 20 25 30  
 40 Phe Asp Glu Arg Gly Glu Ala Tyr Phe Ser Phe Lys Val Pro Asp Arg  
 35 40 45  
 Ala Val Leu Gln Glu Leu Ala Leu Ile Met Ser Ile Asp Glu Phe Asp  
 50 55 60  
 Pro Val Thr Asn Glu Ala Ile Ala Tyr Ala Ser Glu Glu Glu Phe Glu  
 45 65 70 75 80  
 Ala Phe Leu Arg Tyr Gly Leu Lys Pro Thr Phe Leu Thr Pro Pro Ser  
 85 90 95  
 Met Gln Arg Ala Val Glu Met Phe Asp Tyr Arg Ser Gly Glu Lys Tyr  
 100 105 110  
 50 Glu Trp Asn Ala Tyr Pro Thr Tyr Glu Ala Tyr Ile Ser Met Met Glu  
 115 120 125  
 Glu Phe Gln Thr Lys Tyr Pro Ser Leu Cys Thr Thr Ser Val Ile Gly  
 130 135 140  
 Lys Ser Val Lys Asp Arg Lys Leu Met Ile Cys Lys Leu Thr Ser Ser  
 145 150 155 160  
 55 Ala Asn Thr Gly Lys Lys Pro Arg Val Leu Tyr Thr Ser Thr Met His  
 165 170 175  
 Gly Asp Glu Thr Thr Gly Tyr Val Val Leu Leu Arg Leu Ile Asp His  
 180 185 190  
 60 Leu Leu Ser Asn Tyr Glu Ser Asp Pro Arg Ile Lys Asn Ile Leu Asp  
 195 200 205  
 Lys Thr Gln Val Trp Ile Cys Pro Leu Thr Asn Pro Asp Gly Ala Tyr  
 210 215 220  
 65 Arg Ala Gly Asn His Thr Val Gln Gly Ala Thr Arg Tyr Asn Ala Asn  
 225 230 235 240  
 Asn Val Asp Leu Asn Arg Asn Phe Lys Asp Asp Val Ala Gly Asp His  
 245 250 255  
 Pro Asp Gly Lys Pro Trp Gln Pro Glu Ala Thr Ala Phe Met Asp Leu  
 260 265 270  
 70 Glu Gly Asn Thr Ser Phe Val Leu Gly Ala Asn Ile His Gly Gly Thr  
 275 280 285  
 Glu Val Val Asn Tyr Pro Trp Asp Asn Lys Lys Glu Arg His Ala Asp  
 290 295 300  
 75 Asp Glu Trp Tyr Lys Leu Ile Ser Arg Asn Tyr Ala Ala Ala Cys Gln  
 305 310 315 320

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Ser Ile Ser Ala Ser Tyr Met Thr Ser Glu Thr Asn Ser Gly Ile Ile  
 325 330 335  
 Asn Gly Ser Asp Trp Tyr Val Ile Arg Gly Ser Arg Gln Asp Asn Ala  
 340 345 350  
 5 Asn Tyr Phe His Arg Leu Arg Glu Ile Thr Leu Glu Ile Ser Asn Thr  
 355 360 365  
 Lys Leu Val Pro Ala Ser Gln Leu Pro Lys Tyr Trp Asn Leu Asn Lys  
 370 375 380  
 10 Glu Ser Leu Leu Ala Leu Ile Glu Glu Ser Leu Tyr Gly Ile His Gly  
 385 390 400  
 Thr Val Thr Ser Ala Ala Asn Gly Gln Pro Leu Lys Cys Gln Ile Leu  
 405 410 415  
 Ile Glu Asn His Asp Lys Arg Asn Ser Asp Val Tyr Ser Asp Ala Thr  
 420 425 430  
 15 Thr Gly Tyr Tyr Val Arg Pro Ile Lys Ala Gly Thr Tyr Thr Val Lys  
 435 440 445  
 Tyr Lys Ala Glu Gly Tyr Pro Glu Ala Thr Arg Thr Ile Thr Ile Lys  
 450 455 460  
 20 Asp Lys Glu Thr Val Ile Met Asp Ile Ala Leu Gly Asn Ser Val Pro  
 465 470 475  
 Leu Pro Val Pro Asp Phe Thr Ala Ser Pro Met Thr Ile Ser Val Gly  
 485 490 495  
 Glu Ser Val Gln Phe Gln Asp Gln Thr Thr Asn Asn Pro Thr Asn Trp  
 500 505 510  
 25 Glu Trp Thr Phe Glu Gly Gly Gln Pro Ala Met Ser Thr Glu Gln Asn  
 515 520 525  
 Pro Leu Val Ser Tyr Ser His Pro Gly Gln Tyr Asp Val Thr Leu Lys  
 530 535 540  
 30 Val Trp Asn Ala Ser Gly Ser Asn Thr Ile Thr Lys Glu Lys Phe Ile  
 545 550 555  
 Thr Val Asn Ala Val Met Pro Val Ala Glu Phe Val Gly Thr Pro Thr  
 565 570 575  
 Glu Ile Glu Glu Gly Gln Thr Val Ser Phe Gln Asn Gln Ser Thr Asn  
 580 585 590  
 35 Ala Thr Asn Tyr Val Trp Ile Phe Asp Gly Gly Thr Pro Ala Thr Ser  
 595 600 605  
 Glu Asp Glu Asn Pro Thr Val Leu Tyr Ser Lys Ala Gly Gln Tyr Asp  
 610 615 620  
 40 Val Thr Leu Lys Ala Ile Ser Ala Ser Gly Glu Thr Val Lys Thr Lys  
 625 630 635  
 Glu Lys Tyr Ile Thr Val Lys Lys Ala Pro Val Pro Ala Pro Val Ala  
 645 650 655  
 Asp Phe Glu Gly Thr Pro Arg Lys Val Lys Lys Gly Glu Thr Val Thr  
 660 665 670  
 45 Phe Lys Asp Leu Ser Thr Asn Asn Pro Thr Ser Trp Leu Trp Val Phe  
 675 680 685  
 Glu Gly Gly Ser Pro Ala Thr Ser Thr Glu Gln Asn Pro Val Val Thr  
 690 695 700  
 50 Tyr Asn Glu Thr Gly Lys Tyr Asp Val Gln Leu Thr Ala Thr Asn Glu  
 705 710 715  
 Gly Gly Ser Asn Val Lys Lys Ala Glu Asp Tyr Ile Glu Val Ile Leu  
 725 730 735  
 Asp Asp Ser Val Glu Asp Ile Val Ala Gln Thr Gly Ile Val Ile Arg  
 740 745 750  
 55 Pro Gln Asn Gly Thr Lys Gln Ile Leu Ile Glu Ala Asn Ala Ala Ile  
 755 760 765  
 Lys Ala Ile Val Leu Tyr Asp Ile Asn Gly Arg Val Val Leu Lys Thr  
 770 775 780  
 60 Thr Pro Asn Gln Leu Arg Ser Thr Val Asp Leu Ser Ile Leu Pro Glu  
 785 790 795  
 Gly Ile Tyr Thr Ile Asn Ile Lys Thr Glu Lys Ser Ala Arg Thr Glu  
 805 810 815  
 Lys Ile His Ile Gly  
 820

(2) INFORMATION FOR SEQ ID NO:427

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 76 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

5 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427

10 Met Arg Leu Ile Lys Ala Phe Leu Val Gln Leu Leu Leu Pro Ile  
1 5 10 15  
Phe Phe Tyr Lys Arg Phe Ile Ser Pro Leu Thr Pro Pro Ser Cys Arg  
20 25 30  
15 Phe Thr Pro Ser Cys Ser Ser Tyr Ala Ile Glu Ala Leu Arg Lys Tyr  
35 40 45  
Gly Pro Gly Lys Gly Leu Leu Ser Ile Lys Arg Ile Leu Arg Cys  
50 55 60  
20 His Pro Trp Gly Gly Ser Gly Tyr Asp Pro Val Pro  
65 70 75

(2) INFORMATION FOR SEQ ID NO:428

(i) SEQUENCE CHARACTERISTICS:  
25 (A) LENGTH: 859 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

35 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...859

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429

40 Met Ala Tyr Asp Phe Thr Gln Thr Phe Arg Asn Ser Leu Glu Tyr Ser  
1 5 10 15  
Tyr Gln Glu Ala Thr Arg Leu Gly Val Val Ala Val Thr Gln Asp Met  
20 25 30  
45 Leu Val Leu Gly Ile Ile Arg Asp Gly Asp Asn Gly Ala Ile Asp Ile  
35 40 45  
Met Arg His Tyr Gly Ile Asn Leu Tyr Glu Leu Lys Arg Leu Ile Glu  
50 55 60  
Leu Glu Ala Ile Ala Glu Ser Leu Pro Ala Ser Pro Glu Gly Ser Pro  
65 70 75 80  
Ile Phe Thr Pro Ser Ala Arg Glu Ala Ile Asp Asp Ala Thr Asp Ile  
85 90 95  
55 Cys Ala Asp Met Glu Asp Glu Ala Val Ser Pro Val His Leu Leu  
100 105 110  
Ser Ile Leu Asn Ser Thr Gln Glu Ser Leu Val Gln Lys Ile Phe Met  
115 120 125  
Lys Gln Gly Ile Lys Tyr Asp Thr Ile Leu Ser Asp Tyr Phe Gly Gln  
130 135 140  
60 Arg Asn Pro Ser Glu Gly Lys Ser Pro Ser Glu Met Glu Ile Leu Asp  
145 150 155  
Gly Tyr Gln Asp Asn Asp Phe Asp Asp Glu Glu Asp Glu Ser Ser Pro  
165 170 175  
Pro Ser Gly Asn Ser Gly Thr Gly Gly Gly Ser Gly Asp Ala Pro Glu  
180 185 190  
65 Gln Asn Thr Gly Gly Gly Asp Thr Thr Thr Thr Arg Ser Gly Gly  
195 200 205  
Asp Thr Pro Ala Leu Asp Thr Phe Gly Thr Asp Ile Thr Ala Met Ala  
210 215 220  
70 Ala Ala Gly Lys Leu Asp Pro Val Val Gly Arg Glu Gln Glu Ile Glu  
225 230 235  
Arg Val Ile Gln Ile Leu Ser Arg Arg Lys Lys Asn Asn Pro Val Leu  
245 250 255  
75 Ile Gly Glu Pro Gly Val Gly Lys Ser Ala Ile Val Glu Gly Leu Ala  
260 265 270

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Glu Arg Ile Val Asn Arg Lys Val Ser Arg Ile Leu Phe Asp Lys Arg  
 275 280 285  
 Ile Ile Ser Leu Asp Leu Ala Gln Met Val Ala Gly Thr Lys Tyr Arg  
 290 295 300  
 5 Gly Gln Phe Glu Glu Arg Leu Lys Ala Val Leu Asp Glu Leu Lys Lys  
 305 310 315 320  
 Asn Pro Gln Ile Ile Leu Phe Ile Asp Gln Ile His Thr Ile Val Gly  
 325 330 335  
 10 Ala Gly Ser Ala Ala Gly Ser Met Asp Thr Ala Asn Met Leu Lys Pro  
 340 345 350  
 Ala Leu Ala Arg Gly Gln Val Gln Cys Ile Gly Ala Thr Thr Leu Asp  
 355 360 365  
 Glu Tyr Arg Lys Asn Ile Glu Lys Asp Gly Ala Leu Glu Arg Arg Phe  
 370 375 380  
 15 Gln Lys Val Pro Ile Ala Pro Ser Thr Ala Glu Glu Thr Leu Thr Ile  
 385 390 395 400  
 Leu Gln Asn Ile Lys Glu Lys Tyr Glu Asp Tyr His Gly Val Arg Tyr  
 405 410 415  
 20 Thr Asp Glu Ala Ile Lys Ala Ala Val Glu Leu Thr Asp Arg Tyr Val  
 420 425 430  
 Ser Asp Arg Phe Phe Pro Asp Lys Ala Ile Asp Ala Met Asp Glu Ala  
 435 440 445  
 Gly Ala Ser Val His Ile Thr Asn Val Val Ala Pro Lys Glu Ile Glu  
 450 455 460  
 25 Ile Leu Glu Ala Glu Leu Ala Ser Val Arg Glu Asn Lys Leu Ser Ala  
 465 470 475 480  
 Val Lys Ala Gln Asn Tyr Glu Leu Ala Ala Ser Phe Arg Asp Gln Glu  
 485 490 495  
 30 Arg Arg Thr Gln Gln Gln Ile Ala Glu Glu Lys Lys Lys Trp Glu Glu  
 500 505 510  
 Gln Met Ser Lys His Arg Glu Thr Val Asp Glu Asn Val Val Ala His  
 515 520 525  
 Val Val Ala Leu Met Thr Gly Val Pro Ala Glu Arg Leu Ser Thr Gly  
 530 535 540  
 35 Glu Gly Glu Arg Leu Arg Thr Met Ala Asp Asp Leu Lys Thr Lys Val  
 545 550 555 560  
 Val Gly Gln Asp Thr Ala Ile Glu Lys Met Val His Ala Ile Gln Arg  
 565 570 575  
 40 Asn Arg Leu Gly Leu Arg Asn Glu Lys Lys Pro Ile Gly Ser Phe Leu  
 580 585 590  
 Phe Leu Gly Pro Thr Gly Val Gly Lys Thr Tyr Leu Ala Lys Lys Leu  
 595 600 605  
 Ala Glu Tyr Leu Phe Glu Asp Glu Asn Ala Met Ile Arg Val Asp Met  
 610 615 620  
 45 Ser Glu Tyr Met Glu Lys Phe Ser Val Ser Arg Leu Val Gly Ala Pro  
 625 630 635 640  
 Pro Gly Tyr Val Gly Tyr Glu Glu Gly Gly Gln Leu Thr Glu Arg Val  
 645 650 655  
 50 Arg Arg Lys Pro Tyr Ser Val Val Leu Asp Glu Ile Glu Lys Ala  
 660 665 670  
 His Ala Asp Val Phe Asn Leu Leu Leu Gln Val Met Asp Glu Gly Gln  
 675 680 685  
 Leu Thr Asp Ser Leu Gly Arg Arg Val Asn Phe Lys Asn Thr Val Ile  
 690 695 700  
 55 Ile Ile Thr Ser Asn Val Gly Thr Arg Gln Leu Lys Asp Phe Gly Gln  
 705 710 715 720  
 Gly Ile Gly Phe Arg Ser Glu Lys Asp Glu Glu Ala Asn Lys Glu His  
 725 730 735  
 60 Ser Arg Ser Val Ile Gln Lys Ala Leu Asn Lys Thr Phe Ser Pro Glu  
 740 745 750  
 Phe Leu Asn Arg Leu Asp Asp Ile Ile Leu Phe Asp Gln Leu Gly Lys  
 755 760 765  
 Thr Glu Ile Arg Arg Met Val Asp Ile Glu Leu Lys Ala Val Leu Ala  
 770 775 780  
 65 Arg Ile His Arg Ala Gly Tyr Asp Leu Val Leu Thr Asp Glu Ala Lys  
 785 790 795 800  
 Asp Val Ile Ala Thr Lys Gly Tyr Asp Leu Gln Tyr Gly Ala Arg Pro  
 805 810 815  
 70 Leu Lys Arg Thr Leu Gln Asn Glu Val Glu Asp Arg Leu Thr Asp Leu  
 820 825 830  
 Ile Leu Ser Gly Gln Ile Glu Lys Gly Gln Thr Leu Thr Leu Ser Ala  
 835 840 845  
 Arg Asp Gly Glu Ile Ile Val Gln Glu Gln Ala  
 850 855

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(2) INFORMATION FOR SEQ ID NO:429

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 417 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(iv) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429

Met Asn Tyr Leu Tyr Ile Leu Ile Thr Leu Leu Leu Ser Gly Phe Phe  
 1 5 10 15  
 Ser Gly Ala Glu Ile Ala Phe Leu Ser Ser Asp Lys Leu Arg Leu Glu  
 20 25 30  
 Leu Asp Arg Asn Arg Gly Asp Leu Thr Gly Arg Ala Leu Asn Leu Leu  
 35 40 45  
 Tyr Arg His Pro Asp Gln Leu Val Thr Thr Leu Leu Val Gly Asn Asn  
 50 55 60  
 Ile Val Leu Val Val Tyr Gly Leu Leu Met Ala Gly Leu Leu Ala Ala  
 65 70 75 80  
 Pro Leu Ala Gln Trp Ile Asp Asn Asp Ala Met Ile Val Val Leu Gln  
 85 90 95  
 Ser Val Leu Ser Thr Ile Ile Ile Leu Phe Thr Gly Glu Phe Leu Pro  
 100 105 110  
 Lys Ala Ile Phe Lys Thr Asn Ala Asn Met Met Met Arg Val Phe Ala  
 115 120 125  
 Leu Pro Ile Val Ala Ile Tyr Tyr Leu Leu Tyr Pro Leu Ser Lys Leu  
 130 135 140  
 Phe Thr Gly Leu Ser Arg Ser Phe Ile Arg Leu Val Asp Lys Asn Tyr  
 145 150 155 160  
 Val Pro Thr Thr Val Gly Leu Gly Arg Val Asp Leu Asp His Tyr Leu  
 165 170 175  
 Ala Glu Asn Met Ser Gly Glu Asn Glu Gln Asn Asp Leu Thr Thr Glu  
 180 185 190  
 Val Lys Ile Ile Gln Asn Ala Leu Asp Phe Ser Gly Ile Gln Val Arg  
 195 200 205  
 Asp Cys Met Ile Pro Arg Asn Glu Met Ile Ala Cys Glu Leu Gln Thr  
 210 215 220  
 Asp Ile Glu Val Leu Lys Thr Thr Phe Ile Asp Thr Gly Leu Ser Lys  
 225 230 235 240  
 Ile Ile Ile Tyr Arg Gln Asn Ile Asp Asp Val Val Gly Tyr Ile His  
 245 250 255  
 Ser Ser Glu Met Phe Arg Gly Gln Asp Trp Gln Lys Arg Ile Asn Thr  
 260 265 270  
 Thr Val Phe Val Pro Glu Ser Met Tyr Ala Asn Lys Leu Met Arg Leu  
 275 280 285  
 Leu Met Gln Arg Lys Lys Ser Ile Ala Ile Val Ile Asp Glu Leu Gly  
 290 295 300  
 Gly Thr Ala Gly Met Val Thr Leu Glu Asp Leu Val Glu Glu Ile Phe  
 305 310 315 320  
 Gly Asp Ile Glu Asp Glu His Asp Thr Arg Lys Ile Ile Ala Lys Gln  
 325 330 335  
 Leu Gly Pro His Thr Tyr Leu Val Ser Gly Arg Met Glu Ile Asp Asp  
 340 345 350  
 Val Asn Glu Arg Phe Gly Leu Ser Leu Pro Glu Ser Asp Asp Tyr Leu  
 355 360 365  
 Thr Val Ala Gly Phe Ile Leu Asn Ser His Gln Asn Ile Pro Gln Ala  
 370 375 380  
 Asn Glu Val Val Glu Ile Ala Pro Tyr Thr Phe Thr Ile Leu Arg Ser  
 385 390 395 400  
 Ser Ser Thr Lys Ile Glu Leu Val Lys Met Ser Ile Asp Asp Gln Ser  
 405 410 415  
 Asn

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## (2) INFORMATION FOR SEQ ID NO:430

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 293 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...293
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:430

Met Lys Gln Asn Tyr Phe Lys Arg Val Cys Ser Leu Leu Trp Leu Val  
 1 5 10 15  
 Leu Pro Met Leu Ile Met Pro Leu Glu Val Ala Ala Gln Glu Ile Ile  
 20 25 30  
 Pro Asn Glu Glu Val Leu Glu Ser Leu Thr Phe Val Ala Pro Val Glu  
 35 40 45  
 Glu Thr Asp Ala Ile Glu Ala Glu Val Glu Ala Leu Gln Glu Ile Val  
 50 55 60  
 Ala Thr Glu Glu Ile Ala Glu Gln Ala Val Arg Ser Tyr Thr Tyr Thr  
 65 70 75 80  
 Val Tyr Arg Asp Gly Val Lys Ile Ala Ser Gly Leu Thr Glu Pro Thr  
 85 90 95  
 Phe Leu Asp Glu Asp Val Pro Ala Gly Glu His Thr Tyr Cys Val Glu  
 100 105 110  
 Val Gln Tyr Gln Gly Gly Val Ser Asp Lys Val Cys Val Asp Val Glu  
 115 120 125  
 Val Lys Asp Phe Lys Pro Val Thr Asn Leu Thr Gly Thr Ala Ser Asn  
 130 135 140  
 Asp Glu Val Ser Leu Asp Trp Asp Gly Val Glu Glu Lys Ala Glu Glu  
 145 150 155 160  
 Pro Ala Ser Asp Lys Ala Val Ser Tyr Asn Val Tyr Lys Asn Gly Thr  
 165 170 175  
 Leu Ile Gly Asn Thr Ala Glu Thr His Tyr Val Glu Thr Gly Val Ala  
 180 185 190  
 Asn Gly Thr Tyr Ile Tyr Glu Val Glu Val Lys Tyr Pro Asp Gly Val  
 195 200 205  
 Ser Pro Lys Val Ala Val Thr Val Thr Val Thr Asn Ser Ser Leu Ser  
 210 215 220  
 Asn Val Asp Gly Gln Ala Pro Tyr Thr Leu Arg Val Glu Gly Lys Lys  
 225 230 235 240  
 Ile Ile Ala Glu Ala His Gly Met Ile Thr Leu Tyr Asp Ile Asn Gly  
 245 250 255  
 Arg Thr Val Ala Val Ala Pro Asn Arg Leu Glu Tyr Met Ala Gln Thr  
 260 265 270  
 Gly Phe Tyr Ala Val Arg Phe Asp Val Gly Asn Lys His His Val Ser  
 275 280 285  
 Lys Ile Gln Val Arg  
 290

## (2) INFORMATION FOR SEQ ID NO:431

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 312 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature



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(B) LOCATION 1...312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431

```

5 Met Ile Pro Leu Ser Glu Ser Phe Glu Ser Gly Ile Pro Ala Ile Trp
  1      5      10      15
Lys Thr Ile Asp Ala Asp Gly Asp Gly Tyr Asn Trp Met His Leu Thr
  20      25      30
Asn Phe Thr Gly Gln Ser Gly Leu Cys Val Ser Ser Ala Ser Tyr Ile
10 Gly Gly Val Gly Ala Leu Thr Pro Asp Asn Tyr Leu Ile Thr Pro Glu
  35      40      45      50
Leu Lys Leu Pro Thr Asp Ala Leu Val Glu Ile Ile Tyr Trp Val Cys
  55      60      65
Thr Gln Asp Leu Thr Ala Pro Ser Glu His Tyr Ala Val Tyr Ser Ser
15 Ser Thr Gly Asn Asn Ala Ala Asp Phe Val Asn Leu Leu Tyr Glu Glu
  70      75      80      85
Thr Leu Thr Ala Lys Arg Ile Gln Ser Pro Glu Leu Ile Arg Gly Asn
  90      95      100
Arg Thr Gln Gly Val Trp Tyr Gln Arg Lys Val Val Leu Pro Asn Asp
20 Thr Lys Tyr Val Ala Phe Arg His Phe Asn Ser Thr Asp Asn Phe Trp
  105      110      115      120
Leu Asn Leu Asp Glu Val Ser Ile Leu Tyr Thr Pro Leu Pro Arg Arg
  125      130      135      140
Ala Pro Cys Pro His Pro Gly Gly Tyr Thr Tyr Ser Val Phe Arg Arg
25 Gly Gln Lys Ile Ala Ser Gly Leu Ser Ala Leu Ala Tyr Ile Asp Thr
  145      150      155      160
Asp Val Pro Tyr Gly Thr Gln Asp Tyr Cys Val Gln Val Asn Tyr Leu
  165      170      175      180
Gln Gly Asp Ser Tyr Lys Val Cys Lys Asn Ile Val Val Ala Asn Ser
30 Ala Asn Ile Tyr Gly Ala Asp Lys Pro Phe Ala Leu Thr Val Val Gly
  185      190      195      200
Lys Thr Ile Val Ala Ser Ala Phe Lys Gly Glu Ile Thr Leu Tyr Asp
  205      210      215      220
Ile Arg Gly Arg Leu Ile Ala Ser Gly Cys Asp Thr Leu Arg Tyr Lys
35 Ala Glu Asn Gly Phe Tyr Leu Ile Lys Ile Gln Val Asn Gly Thr Val
  225      230      235      240
Tyr Thr Glu Lys Ile Gln Ile Gln
  245      250      255      260
305      310

```

(2) INFORMATION FOR SEQ ID NO:432

(1) SEQUENCE CHARACTERISTICS:

```

50 (A) LENGTH: 843 amino acids
    (B) TYPE: amino acid
    (D) TOPOLOGY: linear

```

(ii) MOLECULE TYPE: protein

55 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

60 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

```

65 (A) NAME/KEY: misc feature
    (B) LOCATION 1...843

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432

```

65 Met Lys Lys Ser Phe Leu Leu Ala Ile Val Met Leu Phe Gly Ile Ala
  1      5      10      15
Met Gln Gly His Ser Ala Pro Val Thr Lys Glu Arg Ala Leu Ser Leu
  20      25      30
Ala Arg Leu Ala Leu Arg Gln Val Ser Leu Arg Met Gly Gln Thr Ala
70 Val Ser Asp Lys Ile Ser Ile Asp Tyr Val Tyr Arg Gln Gly Asp Ala
  35      40      45      50
Glu Arg Gly Ile Thr Ser Gln Glu Glu Gly Ser Pro Ala Tyr Phe Tyr
75 65      70      75      80

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Val Ala Asn Arg Gly Asn Asn Glu Gly Tyr Ala Leu Val Ala Ala Asp  
 85 90 95  
 Asp Arg Ile Pro Thr Ile Leu Ala Tyr Ser Pro Ile Gly Arg Phe Asp  
 100 105 110  
 5 Met Asp Ser Met Pro Asp Asn Leu Arg Met Trp Leu Gln Ile Tyr Asp  
 115 120 125  
 Gln Glu Ile Gly Leu Ile Leu Ser Gly Lys Ala Gln Leu Asn Glu Glu  
 130 135 140  
 10 Ile Leu Arg Thr Glu Gly Val Pro Ala Glu Val His Ala Leu Met Asp  
 145 150 155 160  
 Asn Gly His Phe Ala Asn Asp Pro Met Arg Trp Asn Gln Gly Tyr Pro  
 165 170 175  
 Trp Asn Asn Lys Glu Pro Leu Leu Pro Asn Gly Asn His Ala Tyr Thr  
 180 185 190  
 15 Gly Cys Val Ala Thr Ala Ala Ala Gln Ile Met Arg Tyr His Ser Trp  
 195 200 205  
 Pro Leu Gln Gly Glu Gly Ser Phe Asp Tyr His Ala Gly Ser Leu Val  
 210 215 220  
 20 Gly Asn Trp Ser Gly Thr Phe Gly Glu Met Tyr Asp Trp Ile Asn Met  
 225 230 235 240  
 Pro Gly Asn Pro Asp Leu Asp Asn Leu Thr Gln Ser Gln Val Asp Ala  
 245 250 255  
 Tyr Ala Thr Leu Met Arg Asp Val Ser Ala Ser Val Ser Met Ser Phe  
 260 265 270  
 25 Tyr Glu Asn Gly Ser Gly Thr Tyr Ser Val Tyr Val Val Gly Ala Leu  
 275 280 285  
 Arg Asn Asn Phe Arg Tyr Lys Arg Ser Leu Gln Leu His Val Arg Ala  
 290 295 300  
 30 Leu Tyr Thr Ser Gln Glu Trp His Asp Met Ile Arg Gly Glu Leu Ala  
 305 310 315 320  
 Ser Gly Arg Pro Val Tyr Tyr Ala Gly Asn Asn Gln Ser Ile Gly His  
 325 330 335  
 Ala Phe Val Cys Asp Gly Tyr Ala Ser Asp Gly Thr Phe His Phe Asn  
 340 345 350  
 35 Trp Gly Trp Gly Gly Val Ser Asn Gly Phe Tyr Lys Leu Thr Leu Leu  
 355 360 365  
 Ser Pro Thr Ser Leu Gly Ile Gly Gly Glu Gly Ile Gly Phe Thr Ile  
 370 375 380  
 40 Tyr Gln Glu Ile Ile Thr Gly Ile Glu Pro Ala Lys Thr Pro Ala Glu  
 385 390 395 400  
 Ala Gly Thr Asp Ala Leu Pro Ile Leu Ala Leu Lys Asp Ile Glu Ala  
 405 410 415  
 Glu Tyr Lys Ser Glu Ser Gly Leu Asn Val Gly Tyr Ser Ile Tyr Asn  
 420 425 430  
 45 Thr Gly Glu Glu Gln Ser Asn Leu Asp Leu Gly Tyr Arg Leu Asn Lys  
 435 440 445  
 Ala Asp Gly Glu Val Ile Glu Val Lys Thr Ser Ser Ile Asn Ile Ser  
 450 455 460  
 50 Trp Tyr Gly Tyr Gly Glu His Pro Glu Ser Phe Ser Leu Ala Pro Asn  
 465 470 475 480  
 Gln Leu Ser Gln Gly Ile Asn Thr Ile Thr Leu Leu Tyr Arg Arg Thr  
 485 490 495  
 Gly Thr Glu Gln Trp Glu Pro Val Arg His Ala Gln Gly Gly Tyr Val  
 500 505 510  
 55 Asn Ser Ile Lys Val Asn Thr Thr Asp Pro Asn Asn Val Val Val Thr  
 515 520 525  
 Val Asp Asn Asn Glu Gly Lys Leu Ser Ile Val Pro Asn Ser Phe Val  
 530 535 540  
 60 Ala Asp Leu Asn Ser Tyr Glu His Ser Thr Ile Thr Val Gln Phe Asn  
 545 550 555 560  
 Ser Asp Ser Pro Asp Glu Ile Arg Thr Pro Val Ala Phe Ala Leu Ser  
 565 570 575  
 Thr Gly Ala Thr Ala Asp Asp Val Ile Ser Leu Gly Trp Val Met Ala  
 580 585 590  
 65 Glu Val Pro Gly Gly Ser Ser Asn Tyr Pro Val Val Trp Ser Lys Asp  
 595 600 605  
 Val Leu Thr Leu Ser Glu Gly Asp Tyr Thr Leu Trp Tyr Arg Phe Ser  
 610 615 620  
 70 Ile Asn Asn Gln Lys Asp Glu Trp Lys Lys Ile Gly Ser Val Ser Val  
 625 630 635 640  
 Lys Thr Pro Thr Glu Tyr Thr His Pro Leu Phe Glu Val Gly His Asn  
 645 650 655  
 Gln Thr Ser Thr Tyr Thr Leu Asp Met Ala His Asn Arg Val Leu Pro  
 660 665 670  
 75 Asp Phe Thr Leu Lys Asn Leu Gly Leu Pro Phe Asn Gly Glu Leu Val



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Leu Ile Ser Leu Asp Thr Val Arg Ser Asn Ala Arg Ala Leu Asp Leu  
 85 90 95  
 Arg Tyr Glu Asp Glu Leu His Arg Val Ile Ile His Gly Ile Leu His  
 100 105 110  
 5 Leu Cys Gly Leu Lys Asp Lys Ser Lys Lys Asp Glu Ala Gln Met Arg  
 115 120 125  
 Ala Ala Glu Glu Lys Ala Leu Val Met Leu Arg Glu Thr Ile Gly Ser  
 130 135 140  
 10 Glu Leu Ser Leu Leu His Thr  
 145 150

## (2) INFORMATION FOR SEQ ID NO:437

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 391 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...391  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:437

Met Lys Val Lys Tyr Leu Met Leu Thr Leu Val Gly Ala Ile Ala Leu  
 1 5 10 15  
 35 Asn Ala Ser Ala Gln Glu Asn Thr Val Pro Ala Thr Gly Gln Leu Pro  
 20 25 30  
 Ala Lys Asn Val Ala Phe Ala Arg Asn Lys Ala Gly Ser Asn Trp Phe  
 35 40 45  
 Val Thr Leu Gln Gly Gly Val Ala Ala Gln Phe Leu Asn Asp Asn Asn  
 50 55 60  
 40 Asn Lys Asp Leu Met Asp Arg Leu Gly Ala Ile Gly Ser Leu Ser Val  
 65 70 75 80  
 Gly Lys Tyr His Ser Pro Phe Phe Ala Thr Arg Leu Gln Ile Asn Gly  
 85 90 95  
 45 Gly Gln Ala His Thr Phe Leu Gly Lys Asn Gly Glu Gln Glu Ile Asn  
 100 105 110  
 Thr Asn Phe Gly Ala Ala His Phe Asp Phe Met Phe Asp Val Val Asn  
 115 120 125  
 Tyr Phe Ala Pro Tyr Arg Glu Asn Arg Phe Phe His Leu Ile Pro Trp  
 130 135 140  
 50 Val Gly Val Gly Tyr Gln His Lys Phe Ile Gly Ser Glu Trp Ser Lys  
 145 150 155 160  
 Asp Asn Val Glu Ser Leu Thr Ala Asn Val Gly Val Met Met Ala Phe  
 165 170 175  
 55 Arg Leu Gly Lys Arg Val Asp Phe Val Ile Glu Ala Gln Ala Ala His  
 180 185 190  
 Ser Asn Leu Asn Leu Ser Arg Ala Tyr Asn Ala Lys Lys Thr Pro Val  
 195 200 205  
 Phe Glu Asp Pro Ala Gly Arg Tyr Tyr Asn Gly Phe Gln Gly Met Ala  
 210 215 220  
 60 Thr Ala Gly Leu Asn Phe Arg Leu Gly Ala Val Gly Phe Asn Ala Ile  
 225 230 235 240  
 Unk Pro Met Asp Tyr Ala Leu Ile Asn Asp Leu Asn Gly Gln Ile Asn  
 245 250 255  
 65 Arg Leu Arg Ser Glu Val Glu Glu Leu Ser Lys Arg Pro Val Ser Cys  
 260 265 270  
 Pro Glu Cys Pro Glu Val Thr Pro Val Thr Lys Thr Glu Asn Ile Leu  
 275 280 285  
 Thr Glu Lys Ala Val Leu Phe Arg Phe Asp Ser His Val Val Asp Lys  
 290 295 300  
 70 Asp Gln Leu Ile Asn Leu Tyr Asp Val Ala Gln Phe Val Lys Glu Thr  
 305 310 315 320  
 Asn Glu Pro Ile Thr Val Val Gly Tyr Ala Asp Pro Thr Gly Asn Thr  
 325 330 335  
 75 Gln Tyr Asn Glu Lys Leu Ser Glu Arg Arg Ala Lys Ala Val Val Asp  
 340 345 350

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Val Leu Thr Gly Lys Tyr Gly Val Pro Ser Glu Leu Ile Ser Val Glu  
 355 360 365  
 Trp Lys Gly Asp Ser Thr Gln Pro Phe Ser Lys Lys Ala Trp Asn Arg  
 370 375 380  
 5 Val Val Ile Val Arg Ser Lys  
 385 390

(2) INFORMATION FOR SEQ ID NO:438

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 385 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...385

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:438

Met Thr Tyr Arg Ile Met Lys Ala Lys Ser Leu Leu Leu Ala Leu Ala  
 1 5 10 15  
 30 Gly Leu Ala Cys Thr Phe Ser Ala Thr Ala Gln Glu Ala Thr Thr Gln  
 20 25 30  
 Asn Lys Ala Gly Met His Thr Ala Phe Gln Arg Asp Lys Ala Ser Asp  
 35 35 40 45  
 His Trp Phe Ile Asp Ile Ala Gly Gly Ala Gly Met Ala Leu Ser Gly  
 50 55 60  
 Trp Asn Asn Asp Val Asp Phe Val Asp Arg Leu Ser Ile Val Pro Thr  
 65 70 75 80  
 Phe Gly Ile Gly Lys Trp His Glu Pro Tyr Phe Gly Thr Arg Leu Gln  
 85 90 95  
 40 Phe Thr Gly Phe Asp Ile Tyr Gly Phe Pro Gln Gly Ser Lys Glu Arg  
 100 105 110  
 Asn His Asn Tyr Phe Gly Asn Ala His Leu Asp Phe Met Phe Asp Leu  
 115 120 125  
 Thr Asn Tyr Phe Gly Val Tyr Arg Pro Asn Arg Val Phe His Ile Ile  
 130 135 140  
 45 Pro Trp Ala Gly Ile Gly Phe Gly Tyr Lys Phe His Ser Glu Asn Ala  
 145 150 155 160  
 Asn Gly Glu Lys Val Gly Ser Lys Asp Asp Met Thr Gly Thr Val Asn  
 165 170 175  
 50 Val Gly Leu Met Leu Lys Phe Arg Leu Ser Arg Val Val Asp Phe Asn  
 180 185 190  
 Ile Glu Gly Gln Ala Phe Ala Gly Lys Met Asn Phe Ile Gly Thr Lys  
 195 200 205  
 Arg Gly Lys Ala Asp Phe Pro Val Met Ala Thr Ala Gly Leu Thr Phe  
 210 215 220  
 55 Asn Leu Gly Lys Thr Glu Trp Thr Glu Ile Val Pro Met Asp Tyr Ala  
 225 230 235 240  
 Leu Val Asn Asp Leu Asn Asn Gln Ile Asn Ser Leu Arg Gly Gln Val  
 245 250 255  
 60 Glu Glu Leu Ser Arg Arg Pro Val Ser Cys Pro Glu Cys Pro Glu Pro  
 260 265 270  
 Thr Gln Pro Thr Val Thr Arg Val Val Val Asp Asn Val Val Tyr Phe  
 275 280 285  
 Arg Ile Asn Ser Ala Lys Ile Asp Arg Asn Gln Glu Ile Asn Val Tyr  
 290 295 300  
 65 Asn Thr Ala Glu Tyr Ala Lys Thr Asn Asn Ala Pro Ile Lys Val Val  
 305 310 315 320  
 Gly Tyr Ala Asp Glu Lys Thr Gly Thr Ala Ala Tyr Asn Met Lys Leu  
 325 330 335  
 70 Ser Glu Arg Arg Ala Lys Ala Val Ala Lys Met Leu Glu Lys Tyr Gly  
 340 345 350  
 Val Ser Ala Asp Arg Ile Thr Ile Glu Trp Lys Gly Ser Ser Glu Gln  
 355 360 365  
 75 Ile Tyr Glu Glu Asn Ala Trp Asn Arg Ile Val Val Met Thr Ala Ala  
 370 375 380

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Glu  
385

## 5 (2) INFORMATION FOR SEQ ID NO:439

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 190 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

15 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

20 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439

25 Met Glu Phe Phe Met Leu Phe Ile Ala Ala Val Phe Val Asn Asn Val  
 1 5 10 15  
 Val Leu Ser Gln Phe Leu Gly Ile Cys Pro Phe Leu Gly Val Ser Lys  
 20 25 30  
 Lys Val Asp Thr Ser Ile Gly Met Gly Ala Ala Val Thr Phe Val Leu  
 35 40 45  
 30 Ala Leu Ala Thr Leu Val Thr Phe Leu Ile Gln Lys Phe Val Leu Asp  
 50 55 60  
 Arg Phe Gly Leu Gly Phe Met Gln Thr Ile Ala Phe Ile Leu Val Ile  
 65 70 75 80  
 35 Ala Ala Leu Val Gln Met Val Glu Ile Ile Leu Lys Lys Val Ser Pro  
 85 90 95  
 Pro Leu Tyr Gln Ala Leu Gly Val Phe Leu Pro Leu Ile Thr Thr Asn  
 100 105 110  
 Cys Cys Val Leu Gly Val Ala Ile Leu Val Ile Gln Lys Asp Tyr Thr  
 115 120 125  
 40 Leu Leu Gln Ser Phe Val Tyr Ala Ile Ser Thr Ala Ile Gly Phe Thr  
 130 135 140  
 Leu Ala Met Val Thr Phe Ala Gly Ile Arg Glu Gln Leu Asp Met Thr  
 145 150 155 160  
 45 Asn Leu Pro Lys Ala Met Lys Gly Ile Pro Ser Ala Leu Leu Ala Ala  
 165 170 175  
 Gly Ile Leu Ala Met Ala Phe Met Gly Phe Ser Gly Ile Ala  
 180 185 190

## 50 (2) INFORMATION FOR SEQ ID NO:440

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 186 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

60 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

65 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440

70 Met Leu Phe Ile Ala Ala Val Phe Val Asn Asn Val Val Leu Ser Gln  
 1 5 10 15  
 Phe Leu Gly Ile Cys Pro Phe Leu Gly Val Ser Lys Lys Val Asp Thr  
 20 25 30  
 Ser Ile Gly Met Gly Ala Ala Val Thr Phe Val Leu Ala Leu Ala Thr  
 35 40 45  
 75 Leu Val Thr Phe Leu Ile Gln Lys Phe Val Leu Asp Arg Phe Gly Leu



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50 55 60  
 Gly Phe Met Gln Thr Ile Ala Phe Ile Leu Val Ile Ala Ala Leu Val  
 65 70 75 80  
 Gln Met Val Glu Ile Ile Leu Lys Lys Val Ser Pro Pro Leu Tyr Gln  
 85 90 95  
 5 Ala Leu Gly Val Phe Leu Pro Leu Ile Thr Thr Asn Cys Cys Val Leu  
 100 105 110  
 Gly Val Ala Ile Leu Val Ile Gln Lys Asp Tyr Thr Leu Leu Gln Ser  
 115 120 125  
 10 Phe Val Tyr Ala Ile Ser Thr Thr Ala Ile Gly Phe Thr Leu Ala Met Val  
 130 135 140  
 Thr Phe Ala Gly Ile Arg Glu Gln Leu Asp Met Thr Asn Leu Pro Lys  
 145 150 155 160  
 15 Ala Met Lys Gly Ile Pro Ser Ala Leu Leu Ala Ala Gly Ile Leu Ala  
 165 170 175  
 Met Ala Phe Met Gly Phe Ser Gly Ile Ala  
 180 185

(2) INFORMATION FOR SEQ ID NO:441

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 833 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441

40 Met Lys Gln Leu Asn Ile Ile Ser Phe Ile Ile Ala Phe Leu Phe Leu  
 1 5 10 15  
 Gly Thr Ser Ala Ser Ala Gln Gln Ser Gly Gly Ser Val Thr Gly Thr  
 20 25 30  
 Val Val Asp Lys Ser Ser Lys Glu Pro Ile Ala Tyr Val Gln Val Phe  
 35 40 45  
 45 Val Lys Gly Thr Thr Leu Gly Thr Ser Thr Asp Ala Asn Gly Asn Tyr  
 50 55 60  
 Ser Ile Lys Gly Ile Pro Ser Gly Asn Gln Thr Ile Val Ala Arg Leu  
 65 70 75 80  
 50 Met Gly Tyr Ser Thr Cys Glu Glu Lys Val His Ile Glu Lys Gly Gly  
 85 90 95  
 Ser Arg His Val Asp Leu Tyr Leu Thr Glu Glu Ile Leu Ser Leu Asp  
 100 105 110  
 Gly Val Val Val Ser Ala Asn Arg Asn Glu Thr Phe Arg Arg Gln Ala  
 115 120 125  
 55 Pro Ser Leu Val Thr Val Leu Ser Pro Glu Leu Phe Leu Lys Thr Asn  
 130 135 140  
 Ser Thr Asn Leu Ser Gln Gly Leu Lys Phe Gln Pro Gly Leu Arg Val  
 145 150 155 160  
 60 Glu Asp Asn Cys Gln Asn Cys Gly Phe Asn Gln Val Arg Ile Asn Gly  
 165 170 175  
 Leu Glu Gly Ala Tyr Ser Gln Ile Leu Ile Asp Ser His Pro Ile Phe  
 180 185 190  
 Ser Ser Leu Ala Gly Val Tyr Gly Leu Glu Gln Met Pro Ala Asn Met  
 195 200 205  
 65 Ile Glu Arg Val Glu Val Ile Arg Gly Gly Gly Ser Ala Leu Phe Gly  
 210 215 220  
 Ser Asn Ala Val Gly Gly Val Ile Asn Val Ile Thr Lys Glu Pro Leu  
 225 230 235 240  
 70 Arg Asn Ser Ala Glu Ile Ser His Ser Thr Met Thr Phe Asp His Ala  
 245 250 255  
 Lys Gly Trp Gly Ser Phe Gln Asn Thr Thr Gln Phe Asn Gly Ser Met  
 260 265 270  
 Leu Thr Glu Asp Arg Lys Ala Gly Val Met Val Phe Gly Gln His Asn  
 275 280 285  
 75 Tyr Arg Pro Gly Gln Asp Ile Asp Gly Asp Asn Phe Thr Glu Leu Pro

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290 295 300  
 Asn Leu Arg Asn Arg Ser Leu Gly Phe Arg Ser Tyr Tyr Lys Thr Gly  
 305 310 315 320  
 Leu Tyr Ser Lys Ala Thr Leu Glu Tyr His Ser Met Gln Glu Tyr Arg  
 325 330 335  
 Arg Gly Gly Asp Arg Leu Asp Asn Pro Pro Phe Glu Ala Gln Ile Ala  
 340 345 350  
 Glu Tyr Leu Gln His Tyr Ile Asn Gly Gly Ser Phe Lys Phe Asp Gln  
 355 360 365  
 10 Gly Phe Ser Gly Gly Lys Asp Phe Phe Ser Leu Tyr Ala Ser Ala Gln  
 370 375 380  
 Asp Val Gln Arg Arg Ser Tyr Tyr Gly Gly Gly Asp Tyr Thr Glu Asn  
 385 390 395 400  
 Leu Leu Asn Gly Ala Val Gln Ser Gly Ser Thr Glu Ser Asp Glu Tyr  
 405 410 415  
 15 Asn Asp Ala Phe Thr Ala Leu Thr Ser Tyr Gly Thr Thr Lys Gly Phe  
 420 425 430  
 Asp Leu Gln Gly Gly Gly Met Tyr Arg His Thr Phe Gly Glu Asn Trp  
 435 440 445  
 20 Asp Phe Thr Gly Gly Leu Glu Tyr Ile Tyr Gly Gln Leu Asp Asp Arg  
 450 455 460  
 Ser Gly Tyr Arg Pro Ser Lys Ile Asp Gln Asn Thr Ser Thr Phe Ser  
 465 470 475 480  
 25 Gln Tyr Asp Gln Leu Glu Tyr Lys Thr Glu Lys Leu Ser Ala Leu Ile  
 485 490 495  
 Gly Ala Arg Ile Asp Tyr Val Leu Leu Asn Gln Asp Gly Lys Arg Tyr  
 500 505 510  
 Ile Asp Pro Leu Phe Ile Phe Ser Pro Arg Ala Asn Val Arg Tyr Asn  
 515 520 525  
 30 Pro Asn Lys Asn Leu Ser Phe Arg Leu Ser Tyr Ser Glu Gly Phe Arg  
 530 535 540  
 Ala Pro Gln Tyr Phe Asp Glu Asp Leu His Val Glu Leu Ala Gly Gly  
 545 550 555 560  
 35 Thr Pro Ile Ser Arg Val Leu Ser Pro Asn Leu Lys Glu Glu Arg Ser  
 565 570 575  
 Arg Ser Ile Ser Ala Ser Phe Asp Tyr Tyr His Arg Ala Asp Glu Trp  
 580 585 590  
 Gln Phe Asn Ile Met Gly Glu Ala Phe Ser Thr Phe Ile Ser Asn Gln  
 595 600 605  
 40 Phe Lys Pro Ser Asp Lys Val Glu Thr Thr Ser Asp Gly Lys Glu Trp  
 610 615 620  
 Ile Ile Arg Thr Ile Tyr Asn Asp Lys Asp Gly Val Ser Lys Val Tyr  
 625 630 635 640  
 45 Gly Val Asn Leu Glu Gly Arg Ile Ala Tyr Asn Lys Ser Phe Asp Leu  
 645 650 655  
 Gln Leu Gly Gly Thr Trp Gln Arg Ser Arg Tyr Gly Ser Ile Tyr Thr  
 660 665 670  
 Ala Val Glu Ala Asp Lys Thr Thr Gly Gln Ala Glu Ile Ser Val Lys  
 675 680 685  
 50 Asp Tyr Val Arg Thr Pro Asn Leu Tyr Gly Tyr Phe Val Ala Thr Val  
 690 695 700  
 Arg Pro Thr Glu His Phe Ala Ile Asn Leu Ser Gly Thr Phe Thr Gly  
 705 710 715 720  
 55 Lys Met Asp Val Val His Glu Ala Tyr Glu Gly Asp Ile Pro Ala Glu  
 725 730 735  
 His Ile Ala Pro Asp Gly Ser Phe Asp Phe Glu Met Asn Gly Gln Gln  
 740 745 750  
 Phe Lys Gly Leu Ala Glu Gly His Ala Lys Leu Val Lys Thr Pro Ala  
 755 760 765  
 60 Phe Ala Asp Ile Asp Leu Lys Leu Ser His Asp Phe His Leu Ala Ser  
 770 775 780  
 Thr Met Thr Leu Glu Leu Asn Ala Gly Ile Gln Asn Ile Phe Asn Ser  
 785 790 795 800  
 Tyr Gln Lys Asp Thr Asp Lys Gly Pro Gly Arg Ala Ser Thr Tyr Val  
 805 810 815  
 65 Tyr Gly Pro Met Gln Pro Arg Arg Ile Phe Val Gly Thr Lys Ile Asn  
 820 825 830  
 Phe

70

(2) INFORMATION FOR SEQ ID NO:442

75

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 891 amino acids  
 (B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

10 (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442

15 Met Tyr Lys Lys Ile Ile Ala Val Ala Ala Leu Phe Cys Ala Ser Ile  
1 5 10 15  
Gly Ile Leu Lys Gly Gln Ser Ser Asp Leu Thr Pro Gln Asp Thr Ile  
20 25 30  
Tyr Ser Pro Glu Ile Ser Tyr Ala Lys Pro Ile His Lys Thr Ile Ala  
35 40 45  
Ser Ile Glu Ile Glu Gly Met Arg Ser Phe Asp Asp Phe Val Leu Arg  
50 55 60  
Asn Leu Ser Gly Leu Ala Val Gly Asp Glu Val Ile Pro Gly Asp  
25 65 70 75 80  
Ala Met Ser Ala Ala Val Asn Arg Ile Met Arg Gln Gly Tyr Phe Ser  
85 90 95  
Asn Val Arg Ile Ile Ala Asp Lys Tyr Val Gly Asn Lys Val Tyr Leu  
100 105 110  
30 Lys Ile Ile Val Thr Glu Arg Pro Arg Ile Ser Lys Val Thr Phe Ser  
115 120 125  
Gly Val Lys Lys Ser Glu Arg Glu Asp Leu Glu Met Lys Ile Gly Leu  
130 135 140  
Arg Glu Gly Ile Gln Met Thr Arg Asn Asn Glu Asp Lys Val Arg Gln  
35 145 150 155 160  
Ile Val Gln Lys Tyr Phe Ser Glu Lys Gly Tyr Arg Asp Ala Ser Ile  
165 170 175  
Arg Ile Thr Gln Glu Pro Asp Leu Ser Lys Asp Gly Phe Val Asn Val  
180 185 190  
40 Leu Ile Ser Ile Glu Lys Lys Ser Lys Thr Lys Val Asn Glu Ile Tyr  
195 200 205  
Phe Ser Gly Asn Lys Ala Leu Ser Asn His Lys Leu Arg Met Ala Met  
210 215 220  
45 Lys Asn Thr Asn Ala Lys Phe Ser Leu Arg Lys His Ile Arg Ser Ser  
225 230 235 240  
Phe Leu Lys Leu Phe Ser Thr His Lys Phe Val Glu Glu Ser Tyr Arg  
245 250 255  
Glu Asp Leu Val Arg Leu Ile Glu Lys Tyr Gln Glu Tyr Gly Tyr Arg  
260 265 270  
50 Asp Ala Glu Ile Leu Thr Asp Ser Val Val Lys Ala Pro Asp Gly Lys  
275 280 285  
Arg Val Asp Ile Tyr Leu Asn Ile Glu Glu Gly Gln Lys Tyr Tyr Ile  
290 295 300  
Lys Asp Val Asn Phe Val Gly Asn Ser Gln Tyr Pro Ser Glu Tyr Leu  
305 310 315 320  
55 Glu Arg Val Leu Gly Ile Lys Ser Gly Asp Val Tyr Asn Gln Arg Arg  
325 330 335  
Leu Ala Lys Arg Leu Asn Glu Asp Glu Asp Ala Val Gly Asn Leu Tyr  
340 345 350  
60 Tyr Asn Asn Gly Tyr Ile Phe Ala Trp Val Asp Pro Val Glu Thr Asn  
355 360 365  
Val Val Gly Asp Ser Val Ser Leu Asp Ile Arg Ile Ala Glu Gly Lys  
370 375 380  
Gln Ala Asn Ile Asn Lys Val Ile Ile Lys Gly Asn Thr Val Val Tyr  
385 390 395 400  
65 Glu Asp Val Val Arg Arg Glu Leu Tyr Thr Lys Pro Gly Gln Leu Phe  
405 410 415  
Ser Arg Glu Asp Ile Ile Asn Ser Ile Arg Leu Ile Asn Gln Leu Gly  
420 425 430  
70 His Phe Asp Ala Glu Lys Ser Ile Pro Arg Pro Ile Pro Asn Pro Glu  
435 440 445  
Thr Gly Thr Val Asp Ile Glu Tyr Asp Leu Val Pro Arg Ser Ser Asp  
450 455 460  
75 Gln Leu Glu Leu Ser Val Gly Trp Ser Gln Ser Gly Leu Leu Phe Arg  
465 470 475 480

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Gly Ala Ile Lys Phe Thr Asn Phe Ser Val Gly Asn Leu Leu His Pro  
 485 490 495  
 Ser Met Tyr Lys Lys Gly Ile Ile Pro Gln Gly Asp Gly Gln Thr Leu  
 500 505 510  
 5 Ser Leu Ser Ala Gln Thr Asn Gly Lys Tyr Tyr Gln Gln Tyr Ser Val  
 515 520 525  
 Thr Phe Met Asp Pro Trp Phe Gly Gly Lys Arg Pro Asp Met Phe Ser  
 530 535 540  
 10 Phe Ser Ala Phe Tyr Ser Lys Thr Thr Ala Ile Asp Ser Lys Phe Tyr  
 545 550 555 560  
 Asn Ser Asn Ala Gly Asn Tyr Tyr Asn Ala Tyr Tyr Asn Ser Tyr Tyr  
 565 570 575  
 Asn Asn Tyr Asn Ser Tyr Tyr Asn Gly Met Ser Asn Tyr Thr Gly Asp  
 580 585 590  
 15 Leu Tyr Thr Gln Ala Ser Asp Pro Asp Arg Ser Leu Gln Met Leu Gly  
 595 600 605  
 Thr Ser Ile Gly Tyr Gly Lys Arg Leu Thr Trp Pro Asp Asn Trp Phe  
 610 615 620  
 20 Gln Ile Tyr Thr Ser Leu Asn Tyr Thr Tyr Tyr Arg Leu Arg Asn Trp  
 625 630 635 640  
 Ser Tyr Asn Thr Phe Gln Asn Phe His His Gly Ser Ala Asn Asp Leu  
 645 650 655  
 Asn Leu Glu Leu Arg Leu Ser Arg Thr Ser Ile Asp Asn Pro Ile Tyr  
 660 665 670  
 25 Thr Arg Ser Gly Ser Asp Phe Met Val Ser Val Ala Ala Thr Leu Pro  
 675 680 685  
 Tyr Ser Leu Trp Asp Asn His Asp Tyr Ala Ser Gln Asn Leu Ser Val  
 690 695 700  
 30 Ser Asp Arg Tyr Arg Phe Ile Glu Tyr His Lys Trp Lys Phe Arg Gly  
 705 710 715 720  
 Arg Val Phe Thr Pro Leu Leu Asn Pro Ala Thr His Lys Tyr Thr Pro  
 725 730 735  
 Val Leu Met Ser Arg Val Glu Gly Ala Val Leu Gly Ser Tyr Asn Ser  
 740 745 750  
 35 Asn Lys Lys Ser Pro Phe Gly Thr Phe Tyr Met Gly Gly Asp Gly Met  
 755 760 765  
 Ser Ser Tyr Tyr Gly Gly Tyr Met Asn Glu Thr Ile Gly Leu Arg Gly  
 770 775 780  
 40 Tyr Lys Asn Gly Ser Ile Ala Gly Asn Asn Tyr Asp Tyr Ala Tyr Ala  
 785 790 795 800  
 Tyr Met Arg Leu Thr Met Glu Leu Arg Phe Pro Ile Leu Phe Glu Asn  
 805 810 815  
 Ser Phe Asn Ala Trp Leu Leu Ala Phe Ala Glu Ala Gly Asn Ala Trp  
 820 825 830  
 45 Arg Ser Ile Asp Asn Tyr Asn Pro Phe Asn Leu Lys Arg Ser Ala Gly  
 835 840 845  
 Val Gly Leu Arg Val Thr Leu Pro Met Val Gly Met Leu Gly Ile Asp  
 850 855 860  
 50 Trp Gly Tyr Gly Phe Asp Arg Pro Asp Asn Ser Leu Gln Arg Gly Gly  
 865 870 875 880  
 Ser Asn Val His Phe Val Leu Gly Gln Glu Phe  
 885 890

(2) INFORMATION FOR SEQ ID NO:443

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 1...174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443

Met Asn Gly Asp Met Lys Arg Phe Leu Ile Leu Ile Gly Phe Ala Leu  
 1 5 10 15

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Ala Val Ala Phe Ser Gly Phe Ser Gln Lys Phe Ala Leu Val Asp Met  
 20 25 30  
 Glu Tyr Ile Leu Arg Asn Ile Pro Asp Tyr Glu Met Met Asn Glu Gln  
 35 40 45  
 5 Leu Glu Gln Val Ser Lys Lys Trp Gln Asn Glu Ile Glu Ala Leu Glu  
 50 55 60  
 Asn Glu Ala Gln Ser Met Tyr Lys Lys Tyr Gln Ser Asp Leu Val Phe  
 65 70 75 80  
 10 Leu Ser Ala Ala Gln Lys Lys Thr Gln Glu Ala Ile Val Lys Lys  
 85 90 95  
 Glu Gln Gln Ala Ser Glu Leu Lys Arg Lys Tyr Phe Gly Pro Glu Gly  
 100 105 110  
 Glu Leu Tyr Lys Lys Arg Ser Asp Leu Met Lys Pro Ile Gln Asp Glu  
 115 120 125  
 15 Ile Trp Asn Ala Ile Lys Glu Ile Ala Lys Arg Asn Asn Tyr Gln Met  
 130 135 140  
 Val Leu Asp Arg Gly Thr Ser Gly Ile Ile Phe Ala Ser Pro Ser Ile  
 145 150 155 160  
 20 Asp Ile Ser Asp Leu Val Leu Ser Lys Met Gly Phe Ser Lys  
 165 170

(2) INFORMATION FOR SEQ ID NO:444

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 170 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...170
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:444

Met Lys Arg Phe Leu Ile Leu Ile Gly Phe Ala Leu Ala Val Ala Phe  
 1 5 10 15  
 45 Ser Gly Phe Ser Gln Lys Phe Ala Leu Val Asp Met Glu Tyr Ile Leu  
 20 25 30  
 Arg Asn Ile Pro Asp Tyr Glu Met Met Asn Glu Gln Leu Glu Gln Val  
 35 40 45  
 Ser Lys Lys Trp Gln Asn Glu Ile Glu Ala Leu Glu Asn Glu Ala Gln  
 50 55 60  
 Ser Met Tyr Lys Lys Tyr Gln Ser Asp Leu Val Phe Leu Ser Ala Ala  
 65 70 75 80  
 Gln Lys Lys Thr Gln Glu Glu Ala Ile Val Lys Lys Glu Gln Gln Ala  
 85 90 95  
 55 Ser Glu Leu Lys Arg Lys Tyr Phe Gly Pro Glu Gly Glu Leu Tyr Lys  
 100 105 110  
 Lys Arg Ser Asp Leu Met Lys Pro Ile Gln Asp Glu Ile Trp Asn Ala  
 115 120 125  
 Ile Lys Glu Ile Ala Lys Arg Asn Asn Tyr Gln Met Val Leu Asp Arg  
 130 135 140  
 60 Gly Thr Ser Gly Ile Ile Phe Ala Ser Pro Ser Ile Asp Ile Ser Asp  
 145 150 155 160  
 Leu Val Leu Ser Lys Met Gly Phe Ser Lys  
 165 170

(2) INFORMATION FOR SEQ ID NO:445

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 163 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

5 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445

```

10 Met Lys Lys Phe Phe Leu Met Leu Leu Met Ala Leu Pro Leu Ser Leu
    1      5      10      15
    Leu Ala Gln Lys Val Ala Val Val Asn Thr Glu Glu Ile Ile Ser Lys
        20      25      30
15 Met Pro Glu Gln Val Ala Ala Thr Lys Gln Leu Asn Glu Leu Ala Glu
    35      40      45
    Lys Tyr Arg Leu Asp Leu Lys Ser Met Asp Asp Glu Phe Ala Lys Lys
    50      55      60
    Thr Glu Glu Phe Val Lys Glu Lys Asp Ser Leu Leu Glu Asn Ile Arg
    65      70      75      80
20 Asn Arg Arg Gln Gln Glu Leu Gln Asp Ile Gln Thr Arg Tyr Gln Gln
    85      90      95
    Ser Tyr Gln Thr Met Gln Glu Asp Leu Gln Lys Arg Gln Gln Gln Leu
    100      105      110
    Phe Ala Pro Ile Gln Gln Lys Val Ala Asp Ala Ile Lys Lys Val Gly
    115      120      125
25 Asp Glu Glu Asn Cys Ala Tyr Ile Met Glu Ala Gly Met Met Leu Tyr
    130      135      140
    Thr Gly Ala Thr Ala Ile Asp Leu Thr Ala Lys Val Lys Ala Lys Leu
    145      150      155      160
30 Gly Ile Lys

```

(2) INFORMATION FOR SEQ ID NO:446

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 827 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

45 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...827

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:446

```

Met Lys Glu Ala Ile Pro Arg Lys Asn Lys Tyr Ile Lys Leu Asn Gly
1      5      10      15
55 Ile Tyr Arg Leu Ser Phe Ile Leu Leu Cys Cys Leu Leu Cys Ser Gln
    20      25      30
    Ala Ala Met Ala Gln Gly Val Arg Val Ser Gly Tyr Val Leu Asp Arg
    35      40      45
60 Gly Glu Lys Pro Ile Pro Phe Ala Gly Val Lys Val Arg Gly Thr Gly
    50      55      60
    Thr Gly Ala Thr Thr Asn Leu Lys Gly Tyr Tyr Glu Phe Arg Met Lys
    65      70      75      80
    Ala Thr Thr Asp Ser Ile Thr Ile Glu Phe Ser Ser Met Gly Tyr Gln
    85      90      95
65 Gly Val Ser Arg Ser Phe Pro Ser Leu Thr Lys Asp Thr Arg Leu Asn
    100      105      110
    Val Arg Leu Ala Glu Ala Glu Met Glu Leu Ser Ser Val Thr Val Gln
    115      120      125
70 Ala Thr Lys Arg Arg Leu Asn Thr Met Glu Arg Val Asn Thr Arg Asp
    130      135      140
    Leu Arg Val Asn Ala Gly Pro Thr Gly Gly Val Glu Ser Leu Ile Ser
    145      150      155      160
    Thr Tyr Ala Gly Val Thr Gln Asn Asn Glu Leu Ser Ser Gln Tyr Ser
    165      170      175
75 Val Arg Gly Gly Ser Tyr Asp Glu Asn Met Val Tyr Val Asn Gly Val

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[illegible]

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Leu Phe Asn Leu Phe Asp Met Thr Asn Val Asn Ser Tyr Tyr Trp Val  
 785 790 795 800  
 Ser Asp Ala Tyr Gln Gln Gln Tyr Ala Val Pro Asn Tyr Leu Thr Arg  
 805 810 815  
 5 Arg Gln Phe Asn Leu Arg Leu Leu Val Glu Phe  
 820 825

(2) INFORMATION FOR SEQ ID NO:447

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 672 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...672
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:447

Met Tyr Ser Gly His His Lys Ile His Tyr Pro Phe Leu Ile Leu Leu  
 1 5 10 15  
 30 Val Cys Leu Ala Phe Ala Ala Cys Lys Ser Val Lys Leu Lys Asp Ala  
 20 25 30  
 Glu Lys Ala His Asp Arg Gln Glu Tyr Thr Lys Ala Ala Asp Met Tyr  
 35 35 40 45  
 Asn Thr Leu Tyr Arg Arg Thr Arg Arg Lys Gln Val Glu Met Lys Ala  
 50 50 55 60  
 Tyr Thr Ala Phe Arg Ser Gly Glu Asn Tyr Arg Ala Ala Gly Arg Gln  
 65 70 75 80  
 Ala Lys Ala Leu Arg Gly Tyr Leu Asn Ala Arg Arg Tyr Gly Tyr Pro  
 85 90 95  
 40 Asp Ser Val Val Leu Leu Arg Leu Ala Gln Thr Tyr Gln Gln Gly Gly  
 100 105 110  
 Asn Tyr Lys Glu Ala Glu Val Leu Phe Arg Gly Tyr Leu Glu Ala Tyr  
 115 120 125  
 Pro Lys Ser Tyr Phe Ala Ala Ile Gly Leu Glu Gly Cys Leu Phe Ala  
 130 135 140  
 45 Arg Gln Gln Lys Glu Tyr Pro Thr Arg Tyr Arg Ile Arg Arg Ala Ala  
 145 150 155 160  
 Glu Trp Asn Ser Ala Arg Gly Asp Phe Gly Pro Ala Tyr Ala Pro Asp  
 165 170 175  
 50 Ala Ser Ala Leu Tyr Phe Thr Ser Ser Arg Ser Lys Asp Asp Gly Leu  
 180 185 190  
 Asp Asn Ser Ser Ile Thr Gly Leu Lys Pro Asn Asp Ile Tyr Ile Ile  
 195 200 205  
 Lys Arg Asp Ala Gln Gly Arg Trp Gly Arg Pro Asp Ser Val Ser Gly  
 210 215 220  
 55 Gly Ile Asn Thr Pro Trp Asp Glu Gly Val Pro Thr Ile Thr Pro Asp  
 225 230 235 240  
 Gly Ser Thr Ile Tyr Tyr Thr Leu Ala Gln Gln Gly Ala Asp Tyr Asp  
 245 250 255  
 60 Arg Thr Val Gln Ile Tyr Ser Ala Ala Arg Ser Gly Glu Gly Gly Trp  
 260 265 270  
 Ser Asn Gly Ser Leu Val Asp Ile Met Arg Asp Ser Leu Arg Met Ala  
 275 280 285  
 65 Ala His Pro Ser Met Ser Ala Ser Gly Asp Tyr Leu Tyr Phe Val Ser  
 290 295 300  
 Asn Ile Gly Gly Ser Tyr Gly Gly Lys Asp Ile Tyr Arg Val Lys Val  
 305 310 315 320  
 Ser Asp Arg Ser Tyr Gly Ser Pro Glu Asn Leu Gly Pro Asp Ile Asn  
 325 330 335  
 70 Thr Pro Gly Asp Glu Met Phe Pro Phe Ile Asp Gly Asp Ser Thr Leu  
 340 345 350  
 Phe Phe Ala Ser Asp Gly His Ala Gly Leu Gly Gly Leu Asp Ile Phe  
 355 360 365  
 75 Lys Ala Thr Leu Asp Ser Thr Gly Gln Trp His Val Val Asn Met Gly  
 370 375 380



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Gln Pro Val Asn Ser Ser Ala Asp Asp Phe Gly Leu Ala Val Glu Pro  
 385 390 395 400  
 Lys Gly Lys Asn Lys Glu Glu Ala Leu Pro Asp Asn Gly Val Lys Gly  
 405 410 415  
 5 Val Phe Cys Ser Asn Arg Gly Asp Ala Arg Gly Trp Pro His Leu Phe  
 420 425 430  
 His Phe Glu Leu Pro Ala Ile Tyr Thr Glu Ile Gln Gly Tyr Val Met  
 435 440 445  
 10 Asp Arg Glu Glu Asn Pro Ile Ala Gly Ala Thr Val Arg Ile Val Gly  
 450 455 460  
 Glu Arg Gly Pro Val Gly Gln Gly Phe Val Thr Thr Arg Asp Asp Gly  
 465 470 475 480  
 Ser Tyr Lys Met Ser Val Gln Gly Asp Thr Arg Tyr Val Met Leu Ala  
 485 490 495  
 15 Gly Ala Ser Gly Tyr Leu Asn Gln Tyr Val Glu Leu Lys Thr Asp Thr  
 500 505 510  
 Ala Lys Gln Ser Glu Thr Tyr Tyr Val Asp Phe Phe Leu Ala Ser Arg  
 515 520 525  
 20 Glu Lys Ala Glu Gly Leu Gln Asn Ile Phe Tyr Asp Phe Asp Lys Ala  
 530 535 540  
 Thr Leu Arg Pro Glu Ser Met Lys Ser Leu Asp Glu Leu Ile Arg Ile  
 545 550 555 560  
 Leu Thr Asp Asn Pro Asp Ile Arg Ile Glu Leu Gly Ser His Ala Asp  
 565 570 575  
 25 Arg Lys Gly Pro Asp Ala Tyr Asn Leu Gly Leu Ser Asp Arg Arg Ala  
 580 585 590  
 Lys Ser Val Val Asp Tyr Leu Thr Ser Arg Gly Ile Ala Ala Asp Arg  
 595 600 605  
 30 Leu Thr Trp Lys Gly Tyr Gly Lys Ser Val Pro Lys Thr Val Thr Ala  
 610 615 620  
 Lys Ile Ala Glu Arg His Asp Phe Leu Lys Glu Gly Asp Val Leu Thr  
 625 630 635 640  
 Glu Glu Phe Val Ala Pro Leu Thr Glu Glu Gln Gln Ser Val Cys Asp  
 645 650 655  
 35 Gln Leu Asn Arg Arg Thr Glu Phe Arg Val Ile Glu Glu Glu Leu Arg  
 660 665 670

(2) INFORMATION FOR SEQ ID NO:448

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 708 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 50 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...708  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:448

Met Lys Lys Phe Phe Phe Ala Leu Leu Ser Ile Gly Ile Ser Ala Gln  
 1 5 10 15  
 60 Ala Phe Ala Lys Thr Asp Asn Val Pro Thr Asp Ser Leu Arg Val His  
 20 25 30  
 Asn Leu Gln Thr Val Thr Val Tyr Ser Thr Arg Thr Ala Val Pro Leu  
 35 40 45  
 65 Lys Lys Ile Pro Ala Lys Met Glu Leu Ile Ser Ser Arg Asn Ile Lys  
 50 55 60  
 Gln Ser Gly Phe Asn Asn Met Thr Asp Ile Leu Lys Thr Gln Ser Ser  
 65 70 75 80  
 Leu Asp Val Ile Gln Tyr Pro Gly Phe Ser Ser Asn Ile Gly Ile Arg  
 85 90 95  
 70 Gly Phe Lys Pro Ser Gly Lys Tyr Val Thr Val Leu Val Asn Gly Ile  
 100 105 110  
 Pro Ala Gly Thr Asp Asn Ile Ser Thr Leu Asn Thr Ser Asn Ile Glu  
 115 120 125  
 75 Gln Ile Glu Ile Leu Lys Gly Pro Phe Ser Ser Ile Tyr Gly Thr Asn  
 130 135 140

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(2) INFORMATION FOR SEQ ID NO: 449

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 462 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

10 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...462

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:449

20 Met Asn Arg Phe Ser Asn His Trp Pro Cys Ile Leu Val Gly Phe Val  
 1 5 10 15  
 Leu Trp Phe Val Ser Ala Ser Arg Thr Val Ala Gln Asn Ala Ser Glu  
 20 25 30  
 Thr Thr Val Ser Tyr Asp Thr Asp Thr Ala Val Leu Ser Glu Ala Asp  
 35 40 45  
 25 Val Leu Arg Ile Ala Leu Ser Glu Asn Ala Thr Val Lys Val Ala Asp  
 50 55 60  
 Met Asp Val Arg Lys Gln Glu Tyr Ala Arg Arg Ala Ala Arg Ala Asp  
 65 70 75 80  
 30 Leu Phe Pro Lys Val Asp Leu Asn Gly Val Tyr Ser His Thr Leu Lys  
 85 90 95  
 Lys Gln Val Leu Tyr Ile Asp Met Pro Gly Phe Ser Ser Ser Glu Gly  
 100 105 110  
 Ile Glu Met Gly Arg Thr His Asn Thr Gln Gly Gly Val Asn Val Ser  
 115 120 125  
 35 Met Pro Leu Val Ser Ala Gln Leu Trp Lys Ser Ile Ala Met Thr Gly  
 130 135 140  
 Glu Gln Leu Asp Leu Ala Leu Glu Lys Ala Arg Ser Ser Arg Ile Asp  
 145 150 155 160  
 40 Leu Val Ala Glu Val Lys Lys Ala Tyr Leu Ser Val Leu Leu Ala Glu  
 165 170 175 180  
 Asp Ser Tyr Gly Val Phe Lys Arg Ser Tyr Asp Asn Ala Leu Ala Asn  
 185 190 195  
 Tyr Lys Asn Ile Ser Asp Lys Phe Asp Arg Gly Leu Val Ala Glu Tyr  
 200 205 210  
 45 Asp Lys Ile Arg Ala Asn Val Gln Val Arg Asn Ile Glu Pro Asn Leu  
 215 220 225  
 Leu Gln Ala Gln Asn Ser Val Ala Leu Ala Leu Trp Gln Leu Lys Val  
 230 235 240  
 50 Leu Met Ser Met Glu Val Glu Thr Pro Ile Arg Leu Ser Gly Ser Leu  
 245 250 255  
 Ser Asp Tyr Lys Glu Gln Val Tyr Thr Gly Tyr Phe Ala Ala Asp Thr  
 260 265 270  
 Leu Ile Ser Asn Asn Ser Ser Leu Arg Gln Leu Asp Ile Gln Arg Arg  
 275 280 285  
 55 Leu Ala Val Ser Ala Asp Lys Leu Asn Lys Tyr Ser Phe Leu Pro Thr  
 290 295 300  
 Leu Asn Leu Gly Gly Gln Tyr Thr Tyr Ser Leu Asn Ser Asn Asp Ile  
 305 310 315 320  
 60 Lys Phe Trp Gly Glu Gly Gln Arg Trp Thr Pro Phe Ser Thr Ile Ser  
 325 330 335  
 Leu Ser Leu Tyr Ile Pro Ile Phe Asn Gly Gly Lys Arg Leu Tyr Asn  
 340 345 350  
 Val Lys Gln Ser Ala Leu Ser Ile Arg Gln Ile Asp Leu Gln Arg Arg  
 355 360 365  
 65 His Ile Glu Gln Ser Ile Arg Met Gly Ile Lys Asn Gln Asn Asp Arg  
 370 375 380  
 Leu Arg Thr Cys Met Gln Arg Phe Val Ala Ser Glu Glu Ala Val Arg  
 385 390 395 400  
 70 Ser Ala Glu Lys Gly Tyr Gln Ile Ala Glu Lys Arg-Tyr Gln Thr Gly  
 405 410 415  
 Glu Gly Thr Leu Val Glu Leu Asn Asp Ala Asp Val Ala Leu Leu Gln  
 420 425 430  
 Ala Arg Leu Asn Tyr Asn Gln Ala Ile Phe Asp Phe Met Thr Ala Lys  
 435 440 445  
 75 Ala Glu Leu Asp Lys Met Asn Gly Met Gly Ile Pro Glu Gln

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450 455 460

(2) INFORMATION FOR SEQ ID NO:450

5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 492 amino acids  
(R) TYPE: amino acid  
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: YES  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

15 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...492

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:450

Met Trp Gly Asp Ser His Gly Val Ala Pro Asn Gln Val Arg Arg Thr  
1 5 10 15  
25 Leu Val Lys Val Ala Leu Ser Glu Ser Leu Pro Pro Gly Ala Lys Gln  
20 25 30  
Ile Arg Ile Gly Phe Ser Leu Pro Lys Glu Thr Glu Glu Lys Val Thr  
35 40 45  
30 Ala Leu Tyr Leu Leu Val Ser Asp Ser Leu Ala Val Arg Asp Leu Pro  
50 55 60  
Asp Tyr Lys Gly Arg Val Ser Tyr Asp Ser Phe Pro Ile Ser Lys Glu  
65 70 75 80  
Asp Arg Thr Thr Ala Leu Ser Ala Asp Ser Val Ala Gly Arg Arg Phe  
85 90 95  
35 Phe Tyr Leu Ala Ala Asp Ile Gly Pro Val Ala Ser Phe Ser Arg Ser  
100 105 110  
Asp Thr Leu Thr Ala Arg Val Glu Glu Val Ala Val Asp Gly Arg Pro  
115 120 125  
40 Leu Pro Leu Lys Glu Leu Ser Pro Ala Ser Arg Arg Leu Tyr Arg Gly  
130 135 140  
Tyr Glu Ala Leu Phe Val Pro Gly Asp Gly Ser Arg Asn Tyr Arg  
145 150 155 160  
Ile Pro Ala Ile Leu Lys Thr Ala Asn Gly Thr Leu Ile Ala Met Ala  
165 170 175  
45 Asp Arg Arg Lys Tyr Asn Gln Thr Asp Leu Pro Glu Asp Ile Asp Ile  
180 185 190  
Val Met Arg Arg Ser Thr Asp Gly Lys Ser Trp Ser Asp Pro Arg  
195 200 205  
50 Ile Ile Val Gln Gly Glu Gly Arg Asn His Gly Phe Gly Asp Val Ala  
210 215 220  
Leu Val Gln Thr Gln Ala Gly Lys Leu Leu Met Ile Phe Val Gly Gly  
225 230 235 240  
Val Gly Leu Trp Gln Ser Thr Pro Asp Arg Pro Gln Arg Thr Tyr Ile  
245 250 255  
55 Ser Glu Ser Arg Asp Glu Gly Leu Thr Trp Ser Pro Pro Arg Asp Ile  
260 265 270  
Thr His Phe Ile Phe Gly Lys Asp Cys Ala Asp Pro Gly Arg Ser Arg  
275 280 285  
60 Trp Leu Ala Ser Phe Cys Ala Ser Gly Gln Gly Leu Val Leu Pro Ser  
290 295 300  
Gly Arg Ile Thr Phe Val Ala Ala Ile Arg Glu Ser Gly Gln Glu Tyr  
305 310 315 320  
Val Leu Asn Asn Tyr Val Leu Tyr Ser Asp Asp Glu Gly Asp Thr Trp  
325 330 335  
65 Gln Leu Ser Asp Cys Ala Tyr Arg Arg Gly Asp Glu Ala Lys Leu Ser  
340 345 350  
Leu Met Pro Asp Gly Arg Val Leu Met Ser Ile Arg Asn Gln Gly Arg  
355 360 365  
70 Gln Glu Ser Arg Gln Arg Phe Phe Ala Leu Ser Ser Asp Asp Gly Leu  
370 375 380  
Thr Trp Glu Arg Ala Lys Gln Phe Glu Gly Ile His Asp Pro Gly Cys  
385 390 395 400  
Asn Gly Ala Met Leu Gln Val Lys Arg Asn Gly Arg Asp Gln Val Leu  
405 410 415  
75 His Ser Leu Pro Leu Gly Pro Asp Gly Arg Arg Asp Gly Ala Val Tyr

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420 425 430  
 Leu Phe Asp His Val Ser Gly Arg Trp Ser Ala Pro Val Val Val Asn  
 435 440 445  
 5 Ser Gly Ser Ser Ala Tyr Ser Asp Met Thr Leu Leu Ala Asp Gly Thr  
 450 455 460  
 Ile Gly Tyr Phe Val Glu Glu Gly Asp Glu Ile Ser Leu Val Phe Ile  
 465 470 475 480  
 Arg Phe Val Leu Asp Asp Leu Phe Asp Val Arg Gln  
 485 490

10

(2) INFORMATION FOR SEQ ID NO:451

15

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 245 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: protein

20

(iii) HYPOTHETICAL: YES

25

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

25

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...245

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451

Met Lys Lys Glu Lys Leu Trp Ile Ala Ile Val Ala Gly Leu Ala Phe  
 1 5 10 15  
 Val Leu Gly Leu Tyr Ala Leu Gly Arg Ser Val Ala Gln Leu Arg Arg  
 20 25 30  
 35 Ser Gln Pro Ser Val Thr Val Thr Gly Met Ala Glu Arg Asn Phe Lys  
 35 40 45  
 Ser Asp Leu Ile Val Trp Thr Ala Ser Tyr Gln Leu Gln Met Met Asp  
 50 55 60  
 40 Leu Glu Ser Ala Tyr Lys Ala Leu Lys Glu Lys Gln Ile Leu Val Ala  
 65 70 75 80  
 Asp Tyr Leu Lys Asn Lys Gln Leu Pro Asp Ser Ser Tyr Ile Phe Ser  
 85 90 95  
 Ser Val Ala Ile Ser Lys Glu Tyr Asn Tyr Tyr Tyr Asp Pro Arg Gln  
 100 105 110  
 45 Glu Gln Asn Val Arg Thr Phe Ala Gly Tyr Leu Leu Ser Gln Thr Val  
 115 120 125  
 Thr Val Thr Ser Gln Asp Ile Glu His Val Glu Lys Ile Ser Arg Asp  
 130 135 140  
 50 Ile Thr Glu Leu Ile Asn Gln Gly Val Glu Ile Thr Ser Asp Arg Pro  
 145 150 155 160  
 Ala Tyr Tyr Tyr Thr Lys Leu Asn Asp Leu Lys Val Glu Met Leu Arg  
 165 170 175  
 Asn Ala Ser Glu Asp Ala Phe Asn Arg Ala Ser Val Ile Ala Glu Gly  
 180 185 190  
 55 Ser Gly Ser Ser Val Gly Lys Met Leu Ser Ser Ser Met Gly Val Phe  
 195 200 205  
 Gln Ile Val Gly Leu Asn Ser Asn Glu Asp Tyr Ser Trp Gly Gly Ser  
 210 215 220  
 60 Phe Asn Thr Ser Ser Lys Met Lys Thr Ala Ser Ile Thr Val Lys Ala  
 225 230 235 240  
 Ser Phe Ala Leu Lys  
 245

65

(2) INFORMATION FOR SEQ ID NO:452

70

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 276 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

70

(ii) MOLECULE TYPE: protein

75

(iii) HYPOTHETICAL: YES

75

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452

10 Met Lys Lys Thr Ile Ala Ile Ile Ala Ser Ala Leu Leu Ala Leu Gly  
 1 5 10 15  
 Ala Val Gly Cys Lys Lys Asn Ala Asp Thr Thr Ala Val Ser Glu Lys  
 20 25 30  
 Asp Ser Ile Ala Leu Ser Met Gly Ile Leu Tyr Gly Gln Asp Phe Ala  
 35 40 45  
 15 Asn Gln Phe Glu Met Ser Arg Leu Gln Gly Gln Pro Ile Asp Ser Val  
 50 55 60  
 Ala Phe Leu Asp Gly Phe Lys Tyr Gly Ile Asp Thr Thr Arg Phe Ser  
 65 70 75 80  
 Tyr Asn Leu Gly Ala Ile Tyr Ala Ser Asn Ile Ala Arg Gln Leu Ala  
 85 90 95  
 20 His Asp Ser Ile Asp Ile Asp Lys Phe Tyr Ala Ala Met Arg Ala Ala  
 100 105 110  
 Leu Leu Lys Asp Thr Val Ser Ile Ala Met Lys Pro Ala Asp Ala Gln  
 115 120 125  
 25 Ala Phe Met Gln Arg Ile Gln Ala Lys Lys Gln Arg Glu Asn Asn Met  
 130 135 140  
 Lys Gln Phe Gly Gln Asn Ile Glu Lys Gly Asn Glu Tyr Ile Asp Thr  
 145 150 155 160  
 Phe Lys Lys Glu Asp Gly Val Thr Val Thr Thr Thr Gly Leu Ala Tyr  
 165 170 175  
 30 Lys Thr Leu Gln Glu Gly Thr Gly Ala Thr Pro Ser Leu Ala Asp Thr  
 180 185 190  
 Val Arg Val Lys Tyr Val Gly Thr Leu Val Asp Gly Lys Glu Phe Asp  
 195 200 205  
 35 Lys Asn Glu Glu Gly Ile Glu Phe Ala Val Thr Gly Val Ile Lys Gly  
 210 215 220  
 Trp Thr Glu Met Leu Gln Leu Met Lys Val Gly Gln Lys Val Arg Val  
 225 230 235 240  
 40 Val Ile Pro Gln Glu Leu Ala Tyr Gly Glu Thr Gly Asn Tyr Thr Ile  
 245 250 255  
 Glu Pro Phe Ser Thr Leu Thr Phe Glu Met Glu Leu Ile Gly Ile Lys  
 260 265 270  
 Pro Gly Lys Lys  
 275

(2) INFORMATION FOR SEQ ID NO:453

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 775 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453

65 Met Lys Val Leu Arg Gln Val Phe Leu Pro Ile Leu Phe Val Leu Leu  
 1 5 10 15  
 Thr Gly Ala Cys Ser Thr Thr Lys Asn Leu Pro Glu Gly Glu Gln Leu  
 20 25 30  
 70 Tyr Ile Gly Met Gly Lys Thr Gln Ile Leu Arg Gln Asp Lys Ser His  
 35 40 45  
 Ala Gly Gln Gln Ala Leu Thr Glu Val Glu Ser Thr Leu Lys Val Thr  
 50 55 60  
 75 Pro Asn Gly Ala Ile Phe Gly Ser Ala Ser Ala Ser Leu Pro Lys Ile  
 65 70 75 80

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Pro Phe Gly Leu Trp Leu Tyr Asn Ser Phe Val Gly Asp Ser Thr Val  
85 90 95  
Ile Ser Lys Trp Ile Phe Asp Lys Phe Ala Ala Lys Pro Val Phe Ile  
100 105 110  
5 Ser Gln Val Lys Ser Asp Ser Arg Ala Lys Val Ala Thr Asn Ile Leu  
115 120 125  
Arg Glu His Gly Tyr Phe Asp Ala Lys Val Lys Ser Ser Val Thr Thr  
130 135 140  
10 Leu Lys Lys Asp Ser Leu Lys Ala Lys Ile Ser Tyr Thr Val Asp Met  
145 150 155 160  
Ala Ser Pro Tyr His Tyr Asp Ser Ile Ile Pro Leu Pro Ile Ser Thr  
165 170 175  
Phe Pro Asp Ser Ile Leu Ala Tyr Arg Gln Thr Pro Ser Leu Ile Arg  
180 185 190  
15 Lys Gly Asp Gln Phe Asn Leu Ala Lys Leu His Glu Glu Arg Gln Thr  
195 200 205  
Ile Ser Ala Leu Leu Arg Asp Asn Gly Tyr Tyr Tyr Phe Arg Pro Gln  
210 215 220  
20 Asp Ile Ile Tyr Glu Ala Asp Thr Leu Leu Val Arg Gly Ala Val Cys  
225 230 235 240  
Leu Arg Ala Lys Leu Ser Glu Asp Thr Pro Pro Gln Ala Met Arg Pro  
245 250 255  
Trp Arg Ile Gly Lys Arg Thr Ala Val Leu Leu Gly Met Asn Gly Glu  
260 265 270  
25 Ser Pro Thr Asp Ser Leu Glu Val Glu Asp Met Lys Val Leu Tyr Tyr  
275 280 285  
Arg Lys Met Pro Val Arg Pro Lys Ile Leu Ala Lys Arg Phe Arg Phe  
290 295 300  
30 Phe Ser Gly Asn Leu Tyr Arg Gln Lys Asp Asp Glu Thr Thr Arg Lys  
305 310 315 320  
Ser Leu Ala Arg Leu Gly Ala Phe Ser Val Ile Asp Leu Asn Phe Leu  
325 330 335  
Gln Arg Asp Ser Ile Ser Gly Leu Leu Asp Val Arg Leu Leu Thr Thr  
340 345 350  
35 Leu Asp Lys Pro Trp Asp Ala Ser Leu Glu Thr Leu Phe Thr Ser Lys  
355 360 365  
Ser Asn Asp Phe Ile Gly Pro Gly Leu Asn Phe Ala Leu Ala Arg Arg  
370 375 380  
40 Asn Val Phe Gly Gly Gly Glu Asn Leu Ser Trp Asn Ile Gly Gly Ser  
385 390 395 400  
Tyr Glu Trp Glu Thr Gly Asn Arg Pro Glu Asn Ser Ser Asn Arg Leu  
405 410 415  
Ile Asp Ile Asn Ser Tyr Asn Met Asn Thr Ala Val Asn Leu Ser Phe  
420 425 430  
45 Pro Ser Ile Val Phe Pro Gly Leu Leu Asp Lys Tyr Tyr Tyr Pro  
435 440 445  
Thr Thr Thr Thr Phe Gln Ala Ser Ala Thr Ala Leu Asn Arg Ala His  
450 455 460  
50 Tyr Phe Ser Met Tyr Ser Phe Gly Phe Ser Thr Thr Tyr Glu Phe Gln  
465 470 475 480  
Pro Ser Lys Glu His Arg His Ala Ile Phe Pro Leu Lys Leu Asn Tyr  
485 490 495  
Asn Leu Leu Gly His Gln Thr Glu Thr Phe Gln Ala Ile Thr Ala Asn  
500 505 510  
55 Asn Pro Pro Leu Leu Ser Leu Gln Ser Gln Phe Leu Ala Gln Met  
515 520 525  
Gly Tyr Ile Tyr Thr Phe Asn Lys Ser Val Ser Glu Lys Ser Pro His  
530 535 540  
His Leu Trp Met Gln Phe Gly Leu Ser Glu Ala Gly Asn Leu Leu Asn  
545 550 555 560  
60 Leu Ile Tyr Leu Ala Ala Gly Lys Lys Tyr Ser Asp Thr Lys Asn Phe  
565 570 575  
Val Gly Val Pro Phe Ser Gln Phe Ile Lys Ala Thr Gly Glu Leu Arg  
580 585 590  
65 Tyr Ser Tyr Thr Ile Asp Arg Asn Gln Ser Leu Ala Thr Arg Phe Gly  
595 600 605  
Thr Gly Val Ile Tyr Ser Tyr Gly Asn Met Arg Val Ala Pro Tyr Ser  
610 615 620  
70 Glu Gln Phe Tyr Val Gly Gly Ala Asn Ser Ile Arg Ala Phe Thr Val  
625 630 635 640  
Arg Ser Ile Gly Pro Gly Arg Phe Asn Pro Asp Ser Asp Asn Gln Tyr  
645 650 655  
Ser Tyr Leu Asp Gln Val Gly Glu Phe Lys Leu Glu Ala Asn Val Glu  
660 665 670  
75 Tyr Arg Gly Lys Leu Phe Gly Asp Leu His Ala Ala Val Phe Leu Asp

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675 680 685  
 Ala Gly Asn Val Trp Leu Leu Arg Glu Asp Ser Ser Arg Pro Gly Gly  
 690 695 700  
 5 Ala Leu Ser Glu Val Gly Ser Val Ser Asn Phe Leu Asn Ser Ile Ala  
 705 710 715 720  
 Leu Gly Thr Gly Val Gly Leu Arg Tyr Asp Leu Ala Phe Leu Val Val  
 725 730 735  
 Arg Val Asp Val Gly Phe Gly Leu His Leu Pro Tyr Asn Thr Gly Lys  
 740 745 750  
 10 Lys Gly Tyr Tyr Asn Ile Pro Arg Phe Lys Asp Ala Ile Gly Phe His  
 755 760 765  
 Leu Ala Val Gly Tyr Pro Phe  
 770 775  
 15 (2) INFORMATION FOR SEQ ID NO:454  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 774 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 20 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 25 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (E) LOCATION 1...774  
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:454  
 35 Met Ser Ser His Ser Val Arg Tyr Leu Ile Gly Ile Ala Gly Cys Leu  
 1 5 10 15  
 Leu Leu Met Leu Ala Ser Ser Cys Ser Val Thr Arg Tyr Val Pro Asp  
 20 25 30  
 40 Gly Ser Arg Leu Leu Asp Arg Val Thr Ile Ala Ser Glu Thr Gly Ser  
 35 40 45  
 Ile Ala Leu Pro Glu Asp Ile Arg Asp Tyr Thr Leu Gln Gln Pro Asn  
 50 55 60  
 Tyr Arg Leu Phe Gly Met Thr Arg Trp Leu Leu Arg Val Tyr Ser Ser  
 65 70 75 80  
 45 Ser Asn Pro Asn Ser Asn Ser Trp Trp Asn Arg Ser Leu Arg Lys Met  
 85 90 95  
 Gly Glu Pro Pro Val Leu Ile Asp Ser Val Leu Thr Asp Arg Thr Ala  
 100 105 110  
 50 Asn Arg Leu Ala Lys Ala Met Ala Gly Asp Gly Phe Leu Asp Ala Thr  
 115 120 125  
 Ala Arg Ala Val Val Asp Thr Gly Leu Tyr Lys Lys Ala Arg Ile Thr  
 130 135 140  
 Tyr Leu Ile Gln Pro Gly Ser Arg Tyr Tyr Ile Arg Asn Met Ala Leu  
 145 150 155 160  
 55 Asp Val Lys Asn Pro Leu Leu Pro Pro Val Ala Leu Gly Asn Ser Leu  
 165 170 175  
 Pro Ser Ala Tyr Lys Val Gly Ile Ser Glu Gly Ser Pro Leu Ser Pro  
 180 185 190  
 60 Ile Val Leu Asp Glu Glu Arg Lys Ala Ile Ala Arg His Met Arg Asn  
 195 200 205  
 Asn Gly Phe Trp Lys Phe Ser Ala Glu Asp Val Tyr Tyr Glu Ala Asp  
 210 215 220  
 Thr Thr Val Ser Gly Gly Ser Gly Thr Lys Ser Ala Asp Leu Lys Leu  
 225 230 235 240  
 65 Val Val Asn Gly Ile Gly Arg Tyr Pro Tyr Arg Ile Gly Arg Val Phe  
 245 250 255  
 Phe His Ala Asp Tyr Asp Pro Leu Glu Ser Asp Phe Arg Val Gln Glu  
 260 265 270  
 70 Leu Pro Arg Ile Asp Ser Ile Ser Arg Gly Asp Tyr Thr Val Tyr Tyr  
 275 280 285  
 Gly Ser Arg Gly Arg Tyr Ile Arg Ala Ser Ala Leu Thr Arg Ser Val  
 290 295 300  
 Ser Val Thr Pro Gly Ala Phe Phe Cys Glu Asp Asp Val Glu Arg Ser  
 305 310 315 320  
 75 Tyr Ile Lys Leu Asn Ala Leu Pro Ile Val Arg Asn Val Asn Ile Arg

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5 Phe Val Glu His 325 Asn Gly Lys Asp Glu Ile Ala Leu Ala Asp Ser Ser  
 340 345 350  
 Arg Leu Val Asp Cys Tyr Ile Leu Thr Val Pro Ala Lys Ser Lys Ser  
 355 360 365  
 Phe Glu Ala Glu Val Leu Gly Thr Asn Ser Ala Gly Asp Phe Gly Ala  
 370 375 380  
 Ala Leu Ser Leu Gly Phe Thr Asp Arg Asn Leu Phe Arg Gly Ala Glu  
 385 390 395 400  
 10 Met Phe Asn Ile Lys Leu Lys Gly Ala Tyr Glu Ala Ile Arg Lys Gly  
 405 410 415  
 Ser His Ser Phe Met Glu Tyr Gly Val Glu Ser Ser Leu Arg Phe Pro  
 420 425 430  
 15 Arg Leu Leu Phe Pro Phe Ile Ser Asp Glu Thr Arg Arg Arg Leu Arg  
 435 440 445  
 Ala Ser Thr Glu Trp Lys Ile Gly Tyr Asn Tyr Gln Thr Arg Pro Glu  
 450 455 460  
 Phe Asp Arg Val Ile Leu Ser Ala Gln Leu Asn Tyr Ser Trp Gln Thr  
 465 470 475 480  
 20 Tyr Leu His Asn Arg Leu Arg His Thr Ile Arg Leu Leu Asp Val Asp  
 485 490 495  
 Tyr Leu His Leu Pro Tyr Ile Asp Pro Asp Phe Ala Gln Ser Leu Pro  
 500 505 510  
 25 Pro Thr Thr Ala Leu Tyr Asn Tyr Thr Glu Gln Phe Ile Leu Gly Ser  
 515 520 525  
 Ala Tyr Ile Leu Asn Tyr Thr Thr Ala Ser Ser Met Glu Arg Thr Val  
 530 535 540  
 Ser Asn Pro Phe Thr Ala Arg Phe Ser Ile Gln Thr Ala Gly Asn Leu  
 545 550 555 560  
 30 Leu Gln Ala Ile Ser Tyr Leu Thr Asp Ser Pro Lys Asp Glu His Gly  
 565 570 575  
 Leu Tyr Lys Met Phe Gly Leu His Tyr Ala Gln Phe Val Lys Leu Asp  
 580 585 590  
 35 Leu Asp Leu Ala Lys Thr Val Leu Leu Glu Lys Asp Asn Thr Leu Ala  
 595 600 605  
 Leu His Leu Gly Phe Gly Leu Ala Phe Pro Tyr Gly Asn Ala Arg His  
 610 615 620  
 Ile Pro Phe Glu Leu Arg Tyr Phe Ala Gly Gly Ser Asn Ser Val Arg  
 625 630 635 640  
 40 Gly Trp Ser Val Arg Thr Leu Gly Pro Gly Ser Met Lys Met Thr Pro  
 645 650 655  
 Asp Lys Thr Phe Phe Asp Gln Met Gly Asp Ile Arg Leu Asp Leu Asn  
 660 665 670  
 45 Val Glu Tyr Arg Thr Lys Leu Phe Trp Lys Phe Arg Ala Ala Phe  
 675 680 685  
 Val Asp Ala Gly Asn Val Trp Thr Ile Lys Glu Tyr Glu Asn Gln Glu  
 690 695 700  
 Asp Gly Leu Phe Arg Phe Asp Arg Phe Tyr Lys Glu Ile Ala Leu Ala  
 705 710 715 720  
 50 Tyr Gly Leu Gly Leu Arg Leu Asp Phe Asp Tyr Phe Leu Val Arg Leu  
 725 730 735  
 Asp Ala Gly Leu Lys Ala Tyr Asp Pro Gln Gln Thr Gly Arg Tyr Lys  
 740 745 750  
 55 Trp Ala Ile Thr Arg Pro Asn Leu Ser Ser Asn Phe Ala Trp His Ile  
 755 760 765  
 Ala Val Gly Tyr Pro Phe  
 770

(2) INFORMATION FOR SEQ ID NO:455

60

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 867 amino acids  
 (B) TYPE: amino acid  
 (C) TOPOLOGY: linear

65

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

70

- (iv) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

75

- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...867

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(x1) SEQUENCE DESCRIPTION: SEQ ID NO:455

5	Met	Arg	Lys	Arg	Ile	Leu	Gln	Leu	Phe	Leu	Thr	Ala	Leu	Leu	Leu	Ala
	1				5					10					15	
	Leu	Gly	Ser	Ser	Leu	Ala	Ile	Ala	Gln	Thr	Val	Val	Thr	Gly	Lys	Val
			20						25					30		
	Ile	Asp	Ser	Glu	Thr	Ser	Glu	Pro	Leu	Ile	Gly	Val	Ser	Val	Ser	Thr
			35					40						45		
10	Gly	Gln	Gly	Ala	Ser	Leu	Arg	Gly	Val	Thr	Thr	Asp	Met	Asp	Gly	Gly
		50					55					60				
	Phe	Arg	Phe	Glu	Val	Pro	Ala	Lys	Ser	Val	Leu	Thr	Phe	Arg	Cys	Val
		65			70					75					80	
	Gly	Tyr	Ala	Thr	Val	Thr	Arg	Ser	Ile	Gly	Arg	Gly	Ser	Gln	Glu	Asp
15					85					90				95		
	Leu	Gly	Thr	Ile	Leu	Leu	Asp	Pro	Gln	Ala	Ile	Gly	Leu	Asp	Glu	Ile
					100					105				110		
	Gln	Val	Ile	Ala	Ser	Val	Val	Pro	Lys	Asp	Arg	Met	Thr	Pro	Val	Pro
		115						120					125			
20	Val	Ser	Asn	Ile	Arg	Val	Ala	Asp	Ile	Gln	Ala	Ala	Ser	Leu	Asn	Val
		130					135					140				
	Glu	Phe	Pro	Glu	Leu	Val	Lys	Ser	Thr	Pro	Ser	Thr	Tyr	Thr	Thr	Lys
		145				150					155				160	
	Gly	Ser	Gly	Gly	Phe	Gly	Asp	Gly	Arg	Thr	Asn	Val	Arg	Gly	Phe	Asp
25					165					170				175		
	Thr	Tyr	Asn	Phe	Gly	Val	Leu	Ile	Asn	Gly	Val	Pro	Val	Asn	Gly	Met
			180						185					190		
	Glu	Asp	Gly	Lys	Val	Tyr	Trp	Ser	Asn	Trp	Ser	Gly	Leu	Met	Asn	Gln
		195						200					205			
30	Ala	Ser	Thr	Ile	Gln	Ile	Gln	Arg	Gly	Leu	Gly	Ala	Ser	Lys	Leu	Gly
		210					215					220				
	Ile	Ser	Ser	Val	Gly	Gly	Thr	Met	Asn	Ile	Ile	Thr	Lys	Thr	Thr	Asp
		225					230					235			240	
	Ala	Asn	Thr	Gly	Gly	Ser	Ala	Tyr	Val	Gly	Met	Gly	Asn	Asp	Gly	Leu
35					245					250				255		
	His	Lys	Glu	Ser	Phe	Ser	Ile	Ser	Thr	Gly	Met	Asn	Asp	Gly	Trp	Ala
					260				265					270		
	Ile	Thr	Ile	Ala	Gly	Ser	His	Met	Thr	Gly	Leu	Gly	Tyr	Val	Lys	Gly
		275					280						285			
40	Leu	Lys	Gly	Arg	Ala	Phe	Ser	Tyr	Phe	Phe	Asn	Val	Ser	Lys	Lys	Phe
		290					295					300				
	Asn	Glu	Arg	His	Thr	Leu	Ser	Leu	Thr	Gly	Phe	Gly	Ala	Pro	Gln	Trp
		305				310					315				320	
	His	Asn	Gln	Arg	Ser	Ser	Lys	Tyr	Ser	Val	Ala	Asp	Tyr	Asp	Lys	Tyr
45					325					330				335		
	Gly	Ile	Arg	His	Asn	Gln	Ser	Phe	Gly	Tyr	Leu	Arg	Gly	Glu	Leu	Thr
		340						345					350			
	Pro	Thr	Ala	Tyr	Ala	Tyr	Asn	Thr	Tyr	His	Lys	Pro	Gln	Phe	Ser	Leu
		355						360					365			
50	Asn	His	Phe	Trp	Lys	Met	Asp	Glu	Asn	Thr	Ser	Leu	Tyr	Thr	Ala	Unk
		370					375					380				
	Tyr	Ala	Ser	Leu	Ala	Thr	Gly	Gly	Arg	Arg	Ala	Tyr	Gly	Lys	Asn	
		385				390				395				400		
	Ser	Lys	Trp	Val	Leu	Ile	Asn	Tyr	Asn	Thr	Gly	Gln	Pro	Tyr	Glu	Gln
55					405					410				415		
	Thr	Lys	Val	Thr	Pro	Asp	Gly	Leu	Ile	Asp	Tyr	Asp	Ala	Val	Leu	Ala
				420					425					430		
	Ala	Asn	Ala	Ala	Ala	Ser	Asn	Gly	Ser	Glu	Ala	Ile	Phe	Ala	Leu	Gly
		435						440					445			
60	Ser	Asn	Ser	His	Lys	Trp	Phe	Gly	Leu	Leu	Ser	Ser	Phe	Lys	Lys	Lys
		450					455					460				
	Leu	Asn	Ser	Ser	Leu	Thr	Leu	Thr	Ala	Gly	Tyr	Asp	Gly	Arg	Tyr	Tyr
		465				470				475				480		
	Arg	Gly	Asp	His	Tyr	Asp	Lys	Ile	Thr	Asp	Leu	Leu	Gly	Gly	Ser	Tyr
65					485					490				495		
	Tyr	Ile	Glu	Asp	Pro	Lys	Thr	Lys	Leu	Ala	Tyr	His	Ala	Glu	Gly	Gln
				500					505					510		
	Gln	Leu	Lys	Val	Gly	Asp	Ile	Val	Asn	Arg	Asp	Tyr	Thr	Gly	Glu	Ile
		515						520					525			
70	Met	Trp	His	Gly	Leu	Phe	Ala	Gln	Met	Glu	His	Ser	Ser	Glu	Trp	Ile
		530					535					540				
	Asp	Ala	Phe	Val	Ser	Gly	Ser	Ile	Asn	Tyr	Glu	Leu	Tyr	Arg	Asn	His
		545				550				555				560		
	Asn	Tyr	Gly	Gly	Ser	Lys	Ser	Thr	Gly	Tyr	Leu	Pro	Gly	Val	Ser	Pro
75					565					570				575		

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Trp Lys Ser Phe Leu Pro Trp Ser Gly Lys Ala Gly Leu Ser Tyr Lys  
 590 585 590  
 Phe Ala Gln Gly His Asn Val Phe Ala Asn Gly Gly Phe Phe Thr Arg  
 595 600 605  
 5 Ala Pro Leu Phe Gly Asn Ile Tyr Ala Ala Gly Ala Ile Ile Pro Asn  
 610 615 620  
 Asp Lys Ala Asn Met Glu Lys Val Leu Thr Gly Glu Val Gly Tyr Gly  
 625 630 635 640  
 10 Phe Thr Asn His Lys Asn Phe Glu Phe Asn Ile Asn Gly Tyr Tyr Thr  
 645 650 655  
 Lys Trp Met Asp Arg Val Thr Ser Lys Arg Ile Gly Asn Glu Tyr Val  
 660 665 670  
 Tyr Leu Asn Gly Val Asp Ala Val His Cys Gly Val Glu Ala Glu Val  
 675 680 685  
 15 Ser Tyr Arg Pro Ile Arg Gln Ile Asp Leu Arg Gly Met Phe Ser Leu  
 690 695 700  
 Gly Asp Trp Thr Trp Gln Asn Asn Val Ser Tyr Thr Ser Tyr Asp Glu  
 705 710 715 720  
 20 Ala Gly Asn Glu Thr Gly Gln Asp Ile Thr Tyr Ile Lys Gly Leu His  
 725 730 735  
 Val Gly Asp Ala Ala Gln Met Thr Ala Val Ser Ala Asp Ile Glu  
 740 745 750  
 Leu Phe Lys Gly Phe His Val Ile Gly Lys Tyr Asn Phe Leu Gly Lys  
 755 760 765  
 25 Asn Tyr Ala Gly Phe Asn Pro Ala Thr Arg Asn Ala Gln Gln Tyr Glu  
 770 775 780  
 Ala Asp Gly Lys Glu Ile Val Glu Ser Trp Lys Leu Pro Asp Val Gly  
 785 790 795 800  
 30 Leu Phe Asp Leu Ser Ala Ser Tyr Asn Phe Lys Leu Gly Ser Leu Ser  
 805 810 815  
 Thr Thr Phe Tyr Phe Asn Met Asp Asn Val Ala Asp Lys Arg Tyr Val  
 820 825 830  
 Ser Asp Ala Asp Asn Ile Ile Gly Lys Lys His Asp Glu Ala Ser  
 835 840 845  
 35 Ala Leu Val Trp Tyr Gly Phe Gly Arg Thr Trp Ser Thr Gly Ile Arg  
 850 855 860  
 Val Asn Phe  
 865  
 40 (2) INFORMATION FOR SEQ ID NO:456  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 431 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 50 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...431  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:456  
 60 Met Lys Phe Ser Ile Arg Leu Phe Leu Cys Ile Ile Phe Leu Leu Ser  
 1 5 10 15  
 Ala Phe Ile Leu Pro Ala Leu Gly Gln Lys Ser Lys Gln Val Gln Arg  
 20 25 30  
 65 Leu Glu Lys Gln Arg Lys Glu Ala Leu Lys Ala Ile Glu Lys Thr Asp  
 35 40 45  
 Arg Glu Leu Arg Asn Thr Lys Lys Asp Lys Gln Asp Lys Gln Lys His  
 50 55 60  
 Leu Asn Leu Leu Asn Lys Gln Val Ala Gln Arg Lys Gln Met Val Gln  
 65 70 75 80  
 70 Leu Leu Asp Asn Glu Val Lys Glu Leu Gln Ser Asp Ile Asp Ser Met  
 85 90 95  
 Thr Gly Val Cys His Gln Leu Ser Val Glu Glu Lys Ala Arg Ser Asp  
 100 105 110  
 75 Glu Tyr Ala Gln Ala Leu Gln Ser Met Gln Lys Arg Lys Arg Ser Leu  
 115 120 125

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Asp Arg Ile Leu Phe Ile Ser Ser Ala Lys Ser Phe Asp Glu Gly Met  
 130 135 140  
 Arg Arg Met Arg Phe Leu Glu Gln Tyr Ala Ser Ala Tyr Lys Leu Ala  
 145 150 155 160  
 5 Ser Val Arg Leu Arg Asp Thr Arg Ser Lys Leu Glu Thr Glu Arg Ala  
 165 170 175  
 Thr Val Glu Asp Ala Lys Lys Glu Lys Gly His Leu Leu Val Ile Arg  
 180 185 190  
 10 Glu Glu Glu Lys Lys Lys Leu Glu Gly Gln Gln Ala Glu Gln Arg Arg  
 195 200 205  
 Gln Val Gln Ala Leu Gly Ala Lys Lys Asp Leu Glu Ala Gln Leu  
 210 215 220  
 Arg Lys Gln Lys Lys Gln Ala Glu Ala Leu Asn Arg Lys Ile Glu Lys  
 225 230 235 240  
 15 Gln Ile Ala Lys Glu Ile Glu Ala Ala Glu Arg Arg Ala Arg Glu Glu  
 245 250 255  
 Arg Glu Arg Leu Ala Arg Glu Ala Lys Ala Lys Gly Lys Pro Val Pro  
 260 265 270  
 20 Ala Glu Pro Glu Arg Lys Ala Glu Thr Lys Gly Gly Tyr Ala Met Asp  
 275 280 285  
 Ala Ser Glu Arg Ala Leu Ser Gly Ser Phe Ala Gln Asn Lys Gly Arg  
 290 295 300  
 Leu Pro Gly Pro Val Arg Gly Arg Tyr Arg Ile Val Ser Asp Phe Gly  
 305 310 315 320  
 25 Val His Gln His Ser Glu Leu Lys Lys Val Gln Val Asn Asn Gly Gly  
 325 330 335  
 Ile Asp Ile Ala Val Ala Thr Gly Ser Asp Ala Thr Ser Val Phe Asp  
 340 345 350  
 30 Gly Val Val Ser Ser Val Phe Val Ile Pro Gly Tyr Asn Ser Ala Val  
 355 360 365  
 Met Val Arg His Gly Asn Tyr Ile Thr Val Tyr Ala Asn Leu Ser Lys  
 370 375 380  
 Val Tyr Val Asn Ser Gly Thr Arg Val Lys Thr Gly Gln Ala Leu Gly  
 385 390 395 400  
 35 Arg Ala Tyr Thr Asp Pro Ser Asn Asn Gln Thr Ile Ile His Phe Glu  
 405 410 415  
 Ile Trp Lys Glu Arg Ser Lys Gln Asn Pro Arg Leu Trp Leu Arg  
 420 425 430  
 40 (2) INFORMATION FOR SEQ ID NO:457  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 333 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 50 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...333  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:457  
 60 Met Lys Lys Tyr Leu Leu Tyr Ala Ser Leu Leu Thr Ser Val Leu Leu  
 1 5 10 15  
 Phe Ser Cys Ser Lys Asn Asn Pro Asn Glu Pro Val Glu Asp Arg Ser  
 20 25 30  
 65 Ile Glu Ile Ser Ile Arg Val Asp Phe Thr Lys Thr Gly Glu Ala  
 35 40 45  
 Val Arg Tyr Glu Arg Asn Gln Gly Ser Ala Ala Glu Arg Leu Ile Thr  
 50 55 60  
 Asn Leu Tyr Leu Leu Leu Phe Asp Gln Ser Gly Ala Asn Pro Ala Lys  
 65 70 75 80  
 70 Tyr Tyr Ile Thr Gly Asn Thr Phe Thr Gly Gly Thr Trp Leu Pro Asp  
 85 90 95  
 Asp Met Lys Val Lys Leu Asp Met Thr Gln Ser Glu Ala Gly Glu Arg  
 100 105 110  
 75 Lys Val Tyr Val Val Ala Asn Val Asp Asn Ala Val Lys Thr Ala Leu  
 115 120 125

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Asp Ala Val Ala Asn Glu Ser Asp Leu Gln Thr Val Lys Arg Thr Thr  
 130 135 140  
 Ala Met Pro Trp Ser Thr Asp Ile Ala Ser Pro Phe Leu Met Ser Gly  
 145 150 155 160  
 5 Asn Lys Thr His Asp Phe Leu Ala Asn Arg Leu Leu Asp Asn Val Pro  
 165 170 175  
 Leu Val Arg Ala Ile Ala Lys Val Glu Leu Asn Ile Ser Leu Ser Glu  
 180 185 190  
 10 Lys Phe Gln Ile Val Pro Ile Ile Val Asn Gly Ser Leu Ser Glu Phe  
 195 200 205  
 Lys Phe Arg Tyr Val Asn Phe Asp Lys Glu Thr Tyr Val Val Lys Pro  
 210 215 220  
 Thr Thr Lys Pro Asp Asn Leu Ile Ser Ser Ala Asn Gly Val Trp Pro  
 225 230 235 240  
 15 Gln Ile Thr Asp Trp Thr Val Trp Gly Ala Ser Leu Asn Thr Ser Pro  
 245 250 255  
 Ala Pro Asp Ala Gly Thr Gly Tyr Thr Leu Asp Ala Asn Gly Lys Val  
 260 265 270  
 20 Thr Ala Leu Arg Ile Val Thr Tyr Leu Asn Glu Arg Asp Ser Lys Gly  
 275 280 285  
 Ala Thr Val Glu Val Ala Leu Pro Arg Val Asp Asp Gly Thr Leu Pro  
 290 295 300  
 Pro Pro Glu Phe Gly Pro Glu Leu Tyr Arg Leu Pro Leu Pro Asp Lys  
 305 310 315 320  
 25 Ile Leu Arg Asn His Trp Tyr Lys Tyr Glu Val Glu Ile  
 325 330

(2) INFORMATION FOR SEQ ID NO:458

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 315 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 35 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 40 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...315  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:458

Met Ile Arg Thr Ile Leu Ser Arg Tyr Val Ser Ser Asn Phe Trp Ser  
 1 5 10 15  
 50 Arg Gly Ala Thr Phe Phe Phe Thr Ile Phe Pro Ala Phe Ile Leu Ala  
 20 25 30  
 Ala Thr Ala Leu Pro Ala Cys Gly Gly Thr Ala Ser Gly Ser Asp  
 35 40 45  
 55 Arg Thr Leu Ala Val Thr Ile Glu Pro Gln Lys Tyr Phe Ile Glu Ser  
 50 55 60  
 Ile Ala Asp Lys Ser Val Gln Val Val Ala Leu Val Pro Ala Gly Ser  
 65 70 75 80  
 Asn Pro Glu Glu Tyr Asp Pro Ser Pro Thr Val Met Lys Arg Leu Ser  
 85 90 95  
 60 Glu Ala Asp Ala Tyr Phe Tyr Ile Gly Gly Leu Gly Phe Glu Gln Arg  
 100 105 110  
 Asn Leu Ala Ala Ile Arg Asp Asn Asn Pro Lys Leu Pro Leu Phe Glu  
 115 120 125  
 65 Met Gly Lys Ala Leu Ala Asp Ala Gly Ser Ala Asp Leu His Gly Ser  
 130 135 140  
 Cys Thr Asp His Ser His Thr Asp Leu His Ala His Asp Pro His Tyr  
 145 150 155 160  
 Trp Ser Ser Val Val Gly Ala Lys Ala Leu Ser Arg Ala Ala Tyr Asp  
 165 170 175  
 70 Ala Leu Val Glu Leu Tyr Pro Asn Glu Lys Asp Lys Trp Asp Lys Gly  
 180 185 190  
 His Asp Arg Leu Asn Gly Arg Ile Asp Ser Val Lys Arg Leu Val Asp  
 195 200 205  
 75 Thr Met Phe Ala Asn Gly Lys Ala Asp Lys Ala Phe Val Ile Tyr His  
 210 215 220

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Pro Ser Leu Ser Phe Phe Ala Gln Glu Phe Gly Leu Arg Gln Ile Val  
 225 230 235 240  
 Ile Glu Glu Asp Gly Lys Glu Pro Thr Ala Ala His Leu Arg Arg Val  
 245 250 255  
 5 Ile Asp Gln Ala Arg Ala Asp Gly Val Arg Ile Val Phe Ile Gln Pro  
 260 265 270  
 Glu Phe Glu Thr Arg Gln Ala Glu Asp Ile Ala Arg Glu Ile Gly Ala  
 275 280 285  
 10 Arg Pro Val Arg Ile Asn Pro Leu Arg Ser Ser Trp Glu Glu Glu Ile  
 290 295 300  
 Leu His Ile Ala Arg Ala Leu Ala His Glu Arg  
 305 310 315

## (2) INFORMATION FOR SEQ ID NO:459

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...848

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:459

Met Ile Gly Lys Lys Ile Phe Phe Ile Leu Leu Ala Leu Ile Ala Phe  
 1 5 10 15  
 Ser Gly Leu Asn Ala Ala Thr Asp Thr Glu Phe Lys Tyr Pro Thr Asp  
 20 25 30  
 Ala Asn Ile Ile Gly His Val Lys Asp Ser Lys Thr Gly Glu His Leu  
 35 40 45  
 40 Val Gly Ile Thr Ile Ala Ile Lys Gly Thr Thr Phe Gly Thr Ser Thr  
 50 55 60  
 Asp Ala Thr Gly His Tyr Tyr Leu Arg Asn Leu Arg Pro Gly Glu Ile  
 65 70 75 80  
 45 Thr Leu Ile Met Arg Gly Met Gly Tyr Lys Ser Gln Glu Arg Val Val  
 85 90 95  
 Arg Val Glu Lys Asp Lys Thr Ile Glu Val Asn Phe Glu Ala Glu Glu  
 100 105 110  
 Asp Ala Ile Asn Leu Asp Glu Val Val Ile Ser Ala Asn Arg Glu Leu  
 115 120 125  
 50 Thr Leu Arg Arg Leu Ala Pro Thr Leu Val Asn Val Leu Asn Glu Lys  
 130 135 140  
 Val Phe Ser Gln Val Asn Ala Ser Asn Leu Ala Gln Gly Leu Ser Phe  
 145 150 155 160  
 55 Gln Pro Gly Val Arg Val Glu Asn Asn Cys Gln Asn Cys Gly Phe Asn  
 165 170 175  
 Gln Val Arg Ile Asn Gly Leu Asp Gly Arg Tyr Ala Gln Ile Leu Ile  
 180 185 190  
 Asp Ser Arg Pro Ile Met Ser Ala Leu Ala Gly Val Tyr Gly Leu Glu  
 195 200 205  
 60 Gln Ile Pro Ala Asn Met Ile Glu Arg Val Glu Val Val Arg Gly Gly  
 210 215 220  
 Gly Ser Ala Leu Tyr Gly Ser Ser Ala Ile Ala Gly Val Val Asn Ile  
 225 230 235 240  
 65 Ile Thr Lys Glu Pro Ser His Asn Ser Phe Thr Phe Asn Glu Ser Leu  
 245 250 255  
 Ser Phe Thr Gly Phe Ser Lys Leu Asp Asn Asn Thr Asn Phe Asn Ala  
 260 265 270  
 Ser Ile Val Ser Asp Asp Asn Arg Ala Gly Ala Met Val Phe Gly Gln  
 275 280 285  
 70 Ala Arg Tyr Arg Asn His Trp Asp Ala Asn Asn Asp Gly Tyr Ser Glu  
 290 295 300  
 Leu Gly Lys Ile Asp Ala Arg Ser Leu Gly Ala His Ser Tyr Leu Arg  
 305 310 315 320  
 75 Leu Ser Asp Tyr Ser Lys Leu Thr Gly Glu Phe His Thr Ile Ser Glu  
 325 330 335

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Phe Arg Arg Gly Gly Asp Arg Ile Asp Leu Pro Pro His Val Val Gly  
 340 345 350  
 Val Ala Glu Gln Thr Asp His Ser Val Phe Ser Gly Asn Leu Lys Tyr  
 355 360 365  
 5 Asp Leu Phe Ser Ser Asn Tyr Lys His His Phe Gln Ala Tyr Thr Ser  
 370 375 380  
 Gly Gln Ile Val Asn Arg Lys Ser Tyr Tyr Gly Gly Ile Gly Glu Ile  
 385 390 395 400  
 10 Asp Val Asn Gly His Pro Gly Gly Thr Glu Gly Tyr Pro Ile Pro Gln  
 405 410 415  
 Asp Gln Tyr Gly Asn Asn Tyr Gly Val Thr Lys Gly Lys Thr Tyr Met  
 420 425 430  
 Gly Gly Ile Gln Tyr Ser Tyr Asp Leu Asp Lys Phe Leu Leu Met Pro  
 435 440 445  
 15 Ser Gln Leu Leu Phe Gly Ala Glu Tyr Thr Arg Asp Glu Leu Asn Asp  
 450 455 460  
 Val Met Pro Ile Leu Ser Trp Gln Thr Gly Glu Asp Ala Asn Gly Asn  
 465 470 475 480  
 20 Thr Ile Pro Leu Tyr Pro Glu Leu Asp Gln Asn Ile Asn Asn Tyr Ser  
 485 490 495  
 Leu Phe Gly Gln Asn Glu Trp Lys Asn Asp Arg Trp Ser Ile Leu Val  
 500 505 510  
 Gly Ala Arg Leu Asp Lys His Ser Glu Val Lys Asp Met Ile Leu Ser  
 515 520 525  
 25 Pro Arg Thr Thr Leu Arg Phe Asn Val Asn Pro Asp Ile Asn Leu Arg  
 530 535 540  
 Ala Thr Tyr Ala Lys Gly Phe Arg Ala Pro Gln Val Phe Asp Glu Asp  
 545 550 555 560  
 30 Leu His Val Gly Val Val Gly Gly Glu Ala Gln Lys Val Phe Asn Asp  
 565 570 575  
 Pro Asn Leu Lys Pro Glu Ile Ser His Ala Phe Ser Leu Ser Ala Asp  
 580 585 590  
 Met Tyr His Arg Phe Gly Asn Val Gln Thr Asn Phe Leu Val Glu Gly  
 595 600 605  
 35 Phe Tyr Thr Arg Leu Leu Asp Val Phe Thr Asn Glu Glu Gln Pro Asp  
 610 615 620  
 Gln His Asp Gly Ile Lys Arg Tyr Thr Arg Ile Asn Gly Ser Gly Ala  
 625 630 635 640  
 40 Lys Val Phe Gly Leu Asn Leu Glu Gly Lys Val Ala Tyr Lys Ser Phe  
 645 650 655  
 Gln Leu Gln Ala Gly Leu Thr Leu Ala Ser Asn Lys Tyr Asp Glu Ala  
 660 665 670  
 Gln Glu Trp Gly Leu Asn Thr Val Lys Asp Thr Asn Gly Ala Phe Val  
 675 680 685  
 45 Thr Glu Ala Asn Ala Asn Gly Gln Gln Glu Tyr Lys Asn Glu Ser Met  
 690 695 700  
 Thr Asp Thr Gln Ile Thr Arg Thr Pro Ser Val Tyr Gly Tyr Phe Thr  
 705 710 715 720  
 50 Leu Ala Tyr Asn Pro Ala His Ser Trp Asn Ile Ala Leu Thr Gly Ala  
 725 730 735  
 Tyr Thr Gly Gln Met Tyr Val Pro His Ala Ile Glu Tyr Gly Val Lys  
 740 745 750  
 Ser Ala Glu Leu Asp Ile Met Gln Asn Asn Pro Glu Ile Thr Asp Glu  
 755 760 765  
 55 Thr Gly Lys Ala Pro Arg Ile Asp Glu Leu Lys Lys Thr Pro Ala Phe  
 770 775 780  
 Phe Asp Leu Gly Leu Lys Val Gly Tyr Asp Phe His Val Phe Gln Ala  
 785 790 795 800  
 60 Thr Glu Val Gln Leu Tyr Val Gly Met Asn Asn Ile Phe Asn Ser Phe  
 805 810 815  
 Gln Lys Asp Phe Asp Arg Gly Ala Ala Arg Asp Ser Gly Tyr Ile Tyr  
 820 825 830  
 Gly Pro Thr Gln Pro Arg Thr Gly Tyr Met Gly Leu Val Val Lys Phe  
 835 840 845

(2) INFORMATION FOR SEQ ID NO:460

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

5 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460

10 Met Thr Val Lys Arg Ala Val Arg Ile Ala Leu Leu Thr Leu Ile Gly  
1 5 10 15  
Ile Leu Phe Ser Ser Pro Ser Leu Val Arg Ala Gln Ser Leu Phe Ser  
20 25 30  
15 Thr Glu His Val Leu Gln Leu Tyr Asn Lys Ile Leu Tyr Gly Glu Ser  
35 40 45  
Ala Ala Asp Thr Val Ala Glu Lys Thr Ala Gly Glu Ser Ala Phe Pro  
50 55 60  
Phe Ile Asp Lys Leu Ile Asn Leu Gly Arg Thr Phe Leu Gly Lys Pro  
65 70 75 80  
20 Tyr Arg Tyr Arg Gly Pro Ser Pro Trp Pro Met Asp Cys Ser Gly Tyr  
85 90 95  
Val Ser Tyr Leu Tyr Ser Lys Phe Asp Ile Lys Leu Pro Arg Gly Ala  
100 105 110  
25 Ala Ala Gln Ser Gln Tyr Thr Asn Pro Ile Glu Arg Glu Asp Val Arg  
115 120 125  
Pro Gly Asp Leu Leu Phe Phe Lys Gly Arg Asn Ala Arg Ser Asn Arg  
130 135 140  
30 Ile Gly His Val Ala Leu Val Val Ser Val Asp Glu Asp Asp Ile Thr  
145 150 155 160  
Met Met His Ser Arg Asn Ser Arg Gly Ile Val Ile Glu Lys Leu Asn  
165 170 175  
Arg Ser Ala Tyr Phe Ser Arg Arg Leu Val Ser Tyr Gly Arg Val Pro  
180 185 190  
35 Gly Ala Lys Arg Val Ile Pro Arg Lys Ser  
195 200

(2) INFORMATION FOR SEQ ID NO:461

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 455 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
50 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...455

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:461

60 Met Lys Arg Thr Ile Leu Leu Thr Ala Leu Thr Val Leu Ser Ser Leu  
1 5 10 15  
Ser Leu Leu Arg Ala Gln Asn Glu Ser Glu Ala Ser Thr Asn Pro Met  
20 25 30  
Ser Gly Leu Ser Leu Glu Asp Cys Ile Arg Ile Ala Lys Glu Arg Asn  
35 40 45  
65 Leu Asn Leu Arg Arg Gln Glu Ile Glu Gln Glu Asn Arg Ile Ile Ser  
50 55 60  
Leu Asp Ala Ala Arg His Ser Phe Leu Pro Ser Val Asn Ala Gly Ile  
65 70 75 80  
Gly His Asn Tyr Ser Phe Gly Arg Ser Lys Asp Lys Thr Gly Val Thr  
85 90 95  
70 Val Asp Arg Ser Ser Met Asn Thr Asn Leu Ser Ile Gly Ala Ser Val  
100 105 110  
Glu Val Phe Ser Gly Thr Arg Arg Leu His Asp Leu Lys Gln Gln Lys  
115 120 125  
75 Tyr Asn Val Glu Asp Gly Ile Ala Arg Leu Gln Lys Ala Arg Glu Asp  
130 135 140



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Leu Ser Leu Gln Ile Ala Ala Leu Tyr Ile Asn Leu Leu Phe Arg Gln  
 145 150 155 160  
 Glu Met Thr Arg Thr Ala Glu Thr Gln Leu Ala Leu Ile Arg Glu Gln  
 165 170 175  
 5 Arg Asn Arg Thr Ala Glu Met Val Arg Val Gly Lys Trp Ala Glu Gly  
 180 185 190  
 Lys Leu Leu Asp Ile Asn Ala Gln Met Ala Lys Asp Glu Gln Leu Leu  
 195 200 205  
 10 Val Gln Tyr Arg Ser Glu Glu Glu Leu Ala Arg Leu Asp Leu Gly Gln  
 210 215 220  
 Ala Leu Glu Leu Glu His Pro Glu Ser Ile Ala Val Lys Ala Pro Asp  
 225 230 235 240  
 Thr Asp Val Leu Val Ala Glu Arg Leu Gly Ser Leu Leu Ala Pro Glu  
 245 250 255  
 15 Glu Ile Tyr Arg Thr Ala Leu Gly Leu Lys Pro Ala Leu His Ser Ser  
 260 265 270  
 Glu Leu Gln Ile Ala Ser Ala Arg Glu Gly Leu Ala Ser Ala Arg Ala  
 275 280 285  
 20 Ala Tyr Phe Pro Thr Leu Ser Leu Ser Ala Gly Tyr Ser Asn Gly Tyr  
 290 295 300  
 Phe Arg Asp Leu Gly Lys Glu Tyr Ala Ala Ile Asn Pro Ser Phe Ser  
 305 310 315 320  
 Glu Gln Trp Lys Asn Asn Gly Ser Tyr Ser Ile Gly Leu Ser Leu Asn  
 325 330 335  
 25 Ile Pro Ile Phe Ser Ala Met Gln Thr Gln Asp Arg Val Arg Ser Ser  
 340 345 350  
 Arg Leu Gln Ile Arg Ser Ser Glu Leu Arg Leu Val Glu Glu Lys Lys  
 355 360 365  
 30 Ala Leu Tyr Lys Glu Ile Arg Gln Ala Tyr Ser Asn Ala Val Ala Ala  
 370 375 380  
 Asp Lys Ala Ile Ala Ala Ala Glu Asn Ser Lys Ala Ala Thr Leu Lys  
 385 390 395 400  
 Ala Tyr Glu Tyr Ala Arg Asp Ser Phe Glu Ala Gly Arg Leu Ser Ala  
 405 410 415  
 35 Tyr Glu Tyr Ala Glu Ala Lys Thr Lys Tyr Ala Leu Ser Gln Val Glu  
 420 425 430  
 Glu Leu Arg Ala Lys Tyr Asp Phe Ile Tyr Lys Ala Lys Val Leu Asp  
 435 440 445  
 40 Phe Tyr Gln Gly Lys Asp Phe  
 450 455

(2) INFORMATION FOR SEQ ID NO:462

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 444 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...444  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:462

Met Arg Phe Gln His Tyr Leu Ile Cys Thr Ala Ala Val Ala Ala Leu  
 1 5 10 15  
 65 Ala Ala Asn Pro Leu Thr Gly Gln Ser Asn Met Thr Leu Glu Cys  
 20 25 30  
 Ile Asp Tyr Ala Arg Arg His Ser Ser Ala Val Ala Leu Ser Ala Ala  
 35 40 45  
 Glu Leu Glu Gln Ser Lys Ala Asp Tyr Leu Gln Ala Val Gly Asn Phe  
 50 55 60  
 70 Leu Pro Arg Val Ser Ala Gly Thr Gly Ala Ser Trp Asn Phe Gly Arg  
 65 70 75 80  
 Gly Leu Asp Ala Glu Thr Asn Thr Tyr Thr Asp Ile Asn Ser Phe Asn  
 85 90 95  
 75 Asn Ser Tyr Ser Ile His Ala Thr Met Thr Leu Phe Asp Gly Leu Gln  
 100 105 110

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Ser Val Tyr Arg Leu Arg Met Ala His Ala Arg Arg Glu Ala Ser Arg
115 120 125
Leu Ser Val Arg Glu Gln Gln Glu Leu Ala Ala Leu Gly Thr Thr Glu
130 135 140
5 Ala Tyr Tyr Asp Leu Val Tyr Ala Arg Gln Met Gln Glu Leu Ala Met
145 150 155 160
Gln Lys Tyr Glu Glu Ser Ser Arg Leu His Arg Gln Thr Ala Arg Met
165 170 175
10 Glu Glu Leu Gly Met Lys Ser Arg Pro Asp Val Leu Glu Met Gln Ser
180 185 190
Arg Met Ala Gly Asp Arg Leu Ala Leu Thr Gln Ala Asp Asn Gln Cys
195 200 205
Ile Ile Ala Leu Ile Arg Leu Lys Glu Lys Met Asn Phe Pro Ile Asp
210 215 220
15 Asp Glu Leu Val Val Asp Asp Met Pro Ala Asp Ser Leu Ser Ala Asp
225 230 235 240
Met Ala Glu Ser Asp Ser Ser Ala Gly Val Phe Ala Arg Ala Ala His
245 250 255
20 His His Pro Val Leu Leu Arg Ala Lys Leu Asp Glu Gln Ala Ala Thr
260 265 270
Asp Arg Leu Arg Ala Ala Arg Gly Ala Phe Leu Pro Ser Val Ser Val
275 280 285
Ser Gly Gly Trp Asn Thr Gly Phe Ser Arg Phe Leu Asn Gly Ser Asp
290 295 300
25 Tyr Thr Pro Phe Ser Glu Gln Phe Arg Asn Arg Arg Gly Glu Tyr Val
305 310 315 320
Ser Leu Asn Leu Ser Ile Pro Ile Phe Ser Gly Phe Ser Leu Val Ser
325 330 335
30 His Leu Arg Gln Ala Arg Ala Glu Arg Arg Ala Ala Ile Val Arg Arg
340 345 350
Gly Glu Ala Glu Arg Arg Leu Tyr Ser Glu Ile Ala Gln Ala Met Ala
355 360 365
Asp Arg Asp Ala Ala Leu Ala Ser Tyr Arg Gln Ala Lys Glu His Thr
370 375 380
35 Asp Ala Met Gln Thr Ala Tyr Glu Ala Val Leu Gln Arg Tyr Glu Glu
385 390 395 400
Gly Leu Asn Thr Ala Ile Asp Leu Thr Thr Gln Ala Asn Arg Leu Leu
405 410 415
40 Asp Ala Arg Val Gln Arg Leu Arg Ala Ala Met Thr Tyr Arg Leu Lys
420 425 430
Cys Lys Leu Ile Ala Tyr Tyr Gly Cys Leu Ser Asp
435 440

```

## (2) INFORMATION FOR SEQ ID NO:463

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 940 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 55 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...940
- 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:463

```

Met Asn Lys Phe Tyr Lys Ser Leu Leu Gln Ser Gly Leu Ala Ala Phe
1 5 10 15
Val Ser Met Ala Thr Ala Leu Thr Ala Ser Ala Gln Ile Ser Phe Gly
20 25 30
Gly Glu Pro Leu Ser Phe Ser Ser Arg Ser Ala Gly Thr His Ser Phe
35 40 45
70 Asp Asp Ala Met Thr Ile Arg Leu Thr Pro Asp Phe Asn Pro Glu Asp
50 55 60
Leu Ile Ala Gln Ser Arg Trp Gln Ser Gln Arg Asp Gly Arg Pro Val
65 70 75 80
Arg Ile Gly Gln Val Ile Pro Val Asp Val Asp Phe Ala Ser Lys Ala
85 90 95

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Ser His Ile Ser Ser Ile Gly Asp Val Asp Val Tyr Arg Leu Gln Phe  
 100 105 110  
 Lys Leu Glu Gly Ala Lys Ala Ile Thr Leu Tyr Tyr Asp Ala Phe Asn  
 115 120 125  
 5 Ile Pro Glu Gly Gly Arg Leu Tyr Ile Tyr Thr Pro Asp His Glu Ile  
 130 135 140  
 Val Leu Gly Ala Tyr Thr Asn Ala Thr His Arg Arg Asn Gly Ala Phe  
 145 150 155 160  
 10 Ala Thr Glu Pro Val Pro Gly Ser Glu Leu Ile Met Asp Tyr Glu Val  
 165 170 175  
 Ser Arg Gly Gly Thr Leu Pro Asp Ile Lys Ile Ser Gly Ala Gly Tyr  
 180 185 190  
 Ile Phe Asp Lys Val Gly Gly Arg Pro Val Thr Asp Asn His Tyr Gly  
 195 200 205  
 15 Ile Gly Glu Asp Asp Ser Asp Ser Asp Cys Glu Ile Asn Ile Asn Cys  
 210 215 220  
 Pro Glu Gly Ala Asp Trp Gln Ala Glu Lys Asn Gly Val Val Gln Met  
 225 230 235 240  
 20 Ile Met Val Lys Gly Gln Tyr Ile Ser Met Cys Ser Gly Asn Leu Leu  
 245 250 255  
 Asn Asn Thr Lys Gly Asp Phe Thr Pro Leu Ile Ile Ser Ala Gly His  
 260 265 270  
 Cys Ala Ser Ile Thr Thr Asn Phe Gly Val Thr Gln Ser Glu Leu Asp  
 275 280 285  
 25 Lys Trp Ile Phe Thr Phe His Tyr Glu Lys Arg Gly Cys Ser Asn Gly  
 290 295 300  
 Thr Leu Ala Ile Phe Arg Gly Asn Ser Ile Ile Gly Ala Ser Met Lys  
 305 310 315 320  
 30 Ala Phe Leu Pro Ile Lys Gly Lys Ser Asp Gly Leu Leu Leu Gln Leu  
 325 330 335  
 Asn Asp Glu Val Pro Leu Arg Tyr Arg Val Tyr Tyr Asn Gly Trp Asp  
 340 345 350  
 Ser Thr Pro Asp Ile Pro Ser Ser Gly Ala Gly Ile His His Pro Ala  
 355 360 365  
 35 Gly Asp Ala Met Lys Ile Ser Ile Leu Lys Lys Thr Pro Ala Leu Asn  
 370 375 380  
 Thr Trp Ile Ser Ser Ser Gly Ser Gly Gly Thr Asp Asp His Phe Tyr  
 385 390 395 400  
 40 Phe Lys Tyr Asp Gln Gly Gly Thr Glu Gly Gly Ser Ser Gly Ser Ser  
 405 410 415  
 Leu Phe Asn Gln Asn Lys His Val Val Gly Thr Leu Thr Gly Gly Ala  
 420 425 430  
 Gly Asn Cys Gly Gly Thr Glu Phe Tyr Gly Arg Leu Asn Ser His Trp  
 435 440 445  
 45 Asn Glu Tyr Ala Ser Asp Gly Asn Thr Ser Arg Met Asp Ile Tyr Leu  
 450 455 460  
 Asp Pro Gln Asn Asn Gly Gln Thr Thr Ile Leu Asn Gly Thr Tyr Arg  
 465 470 475 480  
 50 Asp Gly Tyr Lys Pro Leu Pro Ser Val Pro Arg Leu Leu Leu Gln Ser  
 485 490 495  
 Thr Gly Asp Gln Val Glu Leu Asn Trp Thr Ala Val Pro Ala Asp Gln  
 500 505 510  
 Tyr Pro Ser Ser Tyr Gln Val Glu Tyr His Ile Phe Arg Asn Gly Lys  
 515 520 525  
 55 Glu Ile Ala Thr Thr Lys Glu Leu Ser Tyr Ser Asp Ala Ile Asp Glu  
 530 535 540  
 Ser Ile Ile Gly Ser Gly Ile Ile Arg Tyr Glu Val Ser Ala Arg Phe  
 545 550 555 560  
 60 Ile Tyr Pro Ser Pro Leu Asp Gly Val Glu Ser Tyr Lys Asp Thr Asp  
 565 570 575  
 Lys Thr Ser Ala Asp Leu Ala Ile Gly Asp Ile Gln Thr Lys Leu Lys  
 580 585 590  
 Pro Asp Val Thr Pro Leu Pro Gly Gly Gly Val Ser Leu Ser Trp Lys  
 595 600 605  
 65 Val Pro Phe Leu Ser Gln Leu Val Ser Arg Phe Gly Glu Ser Pro Asn  
 610 615 620  
 Pro Val Phe Lys Thr Phe Glu Val Pro Tyr Val Ser Ala Ala Ala Ala  
 625 630 635 640  
 70 Gln Thr Pro Asn Pro Pro Val Gly Val Val Ile Ala Asp Lys Phe Met  
 645 650 655  
 Ala Gly Thr Tyr Pro Glu Lys Ala Ala Ile Ala Ala Val Tyr Val Met  
 660 665 670  
 Pro Ser Ala Pro Asp Ser Thr Phe His Leu Phe Leu Lys Ser Asn Thr  
 675 680 685  
 75 Asn Arg Arg Leu Gln Lys Val Thr Thr Pro Ser Asp Trp Gln Ala Gly



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180 185 190  
 Val Val Gly Asn Ile Gln Ala Lys Phe Arg Asn Ser Val Thr Lys Gly  
 195 200 205  
 Phe Leu Thr Thr Glu Ala Gln Glu Ile Pro Ala Ala Ala Ser Tyr Lys  
 210 215 220  
 5 Thr Ser Glu Tyr Leu Asp Ile Ala Glu Ser Ala Pro Ala Asn Ser Ile  
 225 230 235 240  
 His Phe Tyr Ser Tyr Tyr Asn Lys Trp Thr Leu Ser Thr Pro Glu Lys  
 245 250 255  
 10 Arg Pro Glu Phe Phe Ile Met Val Lys Phe Lys Lys Thr Gly Gln Pro  
 260 265 270  
 Asp Asn Thr Ala Lys Pro Tyr Tyr Tyr Arg Val Pro Leu Glu Ser Gln  
 275 280 285  
 Asp Asn Gln Val Lys Ser Asn Val Leu Tyr Asn Leu Asn Val Lys Ile  
 290 295 300  
 15 Glu Ile Leu Gly Ser Leu Gln Glu Pro Glu Ala Val Ser Val Asn Gly  
 305 310 315 320  
 Thr Leu Ala Ile Glu Glu Trp Ile Leu His Gln Asp Ala Phe Asn Leu  
 325 330 335  
 20 Pro Ala Thr Asn Tyr Leu Ile Val Glu Gln His Glu Ile Phe Met Asn  
 340 345 350  
 Asn Val Asn Thr Tyr Ser Val Lys Tyr Gln Thr Ser Gln Lys Pro Ile  
 355 360 365  
 25 Ser Ile Ser Ile Gln Ser Val Thr Phe Ser Tyr Val Ser Ser Asp Gly  
 370 375 380  
 Thr Gln His Asn Asp Leu Val Ala Ser Ser Ser Asp Gln Tyr Pro Thr  
 385 390 395 400  
 Ile Thr Ser Asp Asn Thr Ser Ile Ile Ile Thr Ser Lys Ile Pro Val  
 405 410 415  
 30 Asn Asn Val Pro Lys Lys Ile Val Phe Glu Val Thr Asn Gly Val Ala  
 420 425 430  
 Gly Leu Lys Glu Thr Val Thr Val Leu Gln Tyr Pro Ala Gln Phe Ile  
 435 440 445  
 35 Val Asn Thr Leu Gly Thr Ala Ser Ala Trp Arg Pro Asp Gly Ser Leu  
 450 455 460  
 Ala Pro Gly Leu Asn Asn Lys Ala Ile Tyr His Val Val Val Leu Val  
 465 470 475 480  
 Pro Pro Glu Asn Leu Phe Glu Asp Gly Thr Gln Thr Ile Ile Gly Tyr  
 485 490 495  
 40 Pro Pro Thr Glu Thr Ile Ser Phe His Lys Lys Glu Asn Asn Thr Tyr  
 500 505 510  
 Pro Ile Val Trp Ser Asp Thr Asn Thr Thr Lys Gln Asp Leu Glu Thr  
 515 520 525  
 Ser Arg Met Ile Ser Pro Ser Phe Glu Leu Ala Ser Gln Leu Gly Ala  
 530 535 540  
 45 Thr Leu Pro Met Pro Tyr Leu Glu Tyr Trp Pro Gly Thr Ser Tyr Leu  
 545 550 555 560  
 Leu Asp Tyr Ser Gly Asn Tyr Asn Asn Lys Arg Tyr Ala Leu Phe Asn  
 565 570 575  
 50 Cys Ala Phe Tyr Trp Glu Lys Arg Lys Val Asn Asn Glu Glu Ile Lys  
 580 585 590  
 Phe Asp Asp Trp Arg Leu Pro Thr Glu Ala Glu Ile Lys Leu Ile Asp  
 595 600 605  
 55 Lys Leu Gln His Asn Glu Gln Ser Ala Val Gln Ala Ile Met Thr Gly  
 610 615 620  
 Asn Tyr Tyr Trp Asp Ser Tyr Ser Ala Asn Gly Ser Tyr Lys Met Gln  
 625 630 635 640  
 Gly Gly Gly Gly Gln Gly Asn Ser Ser Lys Ala Tyr Val Arg Cys Val  
 645 650 655  
 60 Arg Asp Val Lys Lys Pro Ile Arg Asp Lys Lys Ser Gly Lys  
 660 665 670

(2) INFORMATION FOR SEQ ID NO:465

- 65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1282 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 70 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 75 (A) ORGANISM: Porphyromonas gingivalis

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(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1282

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465

```

Met Arg Lys Ile Leu Ser Phe Leu Met Met Cys Ser Leu His Leu Gly
1      5      10      15
10  Leu Gln Ser Gln Thr Trp His Gly Asp Pro Asp Ser Val Ala Ala Leu
    20      25      30
    Pro Ser Ile Gly Ile Gln Glu Ser Ser Cys Thr Arg Ile Thr Phe Glu
    35      40      45
    Val Val Phe Pro Gly Phe Tyr Ser Val Glu Lys Arg Glu Gly Asn Gln
    50      55      60
15  Val Phe Gln Arg Ile Ser Met Pro Gly Cys Gly Ser Phe Gly Asn Leu
    65      70      75
    Gly Glu Ala Glu Leu Pro Val Leu Lys Lys Met Ile Ala Val Pro Glu
    85      90      95
20  Phe Ser Thr Ala Asn Val Ala Val Lys Ile Lys Glu Thr Glu Thr Phe
    100     105     110
    Asp Asn Tyr Asn Ile Tyr Pro Asn Pro Thr Tyr Val Val Glu Glu Leu
    115     120     125
25  Pro Glu Gly Gly Thr Tyr Leu Val Glu Ala Phe Ala Ile Asn Asn Asp
    130     135     140
    Tyr Tyr Ser Gln Asn Val Ser Leu Pro Ser Thr His Tyr Val Tyr Ser
    145     150     155
    Gln Asp Gly Tyr Phe Arg Ser Gln Arg Phe Ile Glu Val Thr Leu Tyr
    165     170     175
30  Pro Phe Arg Tyr Asn Pro Val Arg Gln Glu Ile Leu Phe Ala Lys Lys
    180     185     190
    Ile Glu Val Thr Ile Thr Phe Asp Asn Pro Gln Pro Pro Leu Gln Lys
    195     200     205
35  Asn Thr Gly Ile Phe Asn Lys Val Ala Ser Ser Ala Phe Ile Asn Tyr
    210     215     220
    Glu Ala Asp Gly Lys Ser Ala Ile Glu Asn Asp Met Val Phe Ser Arg
    225     230     235
    Gly Thr Thr Thr Tyr Ile Ser Gly Asn Val Ala Ser Asn Leu Pro Gln
    245     250     255
40  Asn Cys Asp Tyr Leu Val Ile Tyr Asp Asp Met Phe Asn Val Asn Gln
    260     265     270
    Gln Pro His Asp Glu Ile Lys Arg Leu Cys Glu His Arg Ala Phe Tyr
    275     280     285
45  Asn Gly Phe Asp Val Ala Ala Val Ser Ile Lys Asp Val Leu Asn Ser
    290     295     300
    Phe Pro Ser Asn Ala Thr Ser Tyr Ile Asn Glu Thr Lys Leu Lys Asn
    305     310     315
    Phe Ile Arg Ser Val Tyr Asn Gln Ser Asn Ala Lys Arg Thr Leu Asp
    325     330     335
50  Gly Lys Leu Gly Tyr Val Leu Leu Ile Gly Lys Pro Leu Ser Lys Tyr
    340     345     350
    Leu Ala Asp Thr Asp Asn Thr Lys Val Pro Thr Ser Phe Ile His Asn
    355     360     365
    Val Ser Leu Ile Pro Ser His Pro Thr Phe Gly Ser Ile Cys Ala Ser
    370     375     380
55  Asp Tyr Phe Phe Ser Cys Val Ser Pro Leu Asp Thr Val Gly Asp Leu
    385     390     395
    Phe Ile Gly Arg Phe Ser Val Thr Asn Ala His Glu Leu His Asn Leu
    405     410     415
60  Ile Glu Lys Thr Ile Asn Lys Glu Ile Ser Tyr Asn Pro Ile Ala His
    420     425     430
    Lys Asn Ile Leu Tyr Ala Glu Gly Lys Gly Cys Asp Ala Pro Ile Leu
    435     440     445
65  Arg Leu Phe Leu Lys Glu Ile Ala Ser Gly Tyr Thr Val Asn Ser Ile
    450     455     460
    Leu Lys Ser Asn Gln Val Ser Ala Ile Asp Ser Ile Phe Asp Cys Leu
    465     470     475
    Asn Asn Gly Ser His His Phe Tyr Phe Asn Thr His Gly Met Pro Thr
    485     490     495
70  Val Trp Gly Ile Gly Gln Gly Leu Asp Val Asn Thr Leu Thr Ala Arg
    500     505     510
    Leu Asn Asn Thr Ser Ser Gln Gly Leu Cys Thr Ser Leu Ser Cys Ser
    515     520     525
75  Ser Ala Val Ala Asp Ser Thr Ile Arg Ser Leu Gly Glu Val Leu Thr
    530     535     540

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SUBSTITUTE SHEET (Rule 26) (RO/AU)



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1140      1145      1150
Ile Leu Ser Cys Glu Gln Arg Lys Ser Leu Glu Ser His Gln Asn Val
1155      1160      1165
Lys Asn Tyr Leu Leu Ser Thr Leu Pro Glu Ser Thr Gly Thr Leu Leu
5 1170      1175      1180
Pro Pro Leu Glu Cys Asn Lys Ser Ser Leu Asp Lys Ser Lys Ile Ile
1185      1190      1195      1200
Ser Ile Ser Pro Asn Pro Ala Lys Ala Val Val Thr Ile Ile Tyr Tyr
1205      1210      1215
10 Thr Asp Asn Pro Ser Cys Ser Val Ile Lys Ile Tyr Gly Ile Asn Gly
1220      1225      1230
Ala Ser Ala Asp Ile Thr Gly Leu Pro Lys His Leu Ser Glu Gly Tyr
1235      1240      1245
Tyr Ser Ile Gln Phe Asn Thr Ser Asn Phe Asp Pro Gly Phe Tyr Leu
15 1250      1255      1260
Val Thr Leu Asn Val Asp Gln Lys Ile Ile Asp Thr Glu Lys Leu Arg
1265      1270      1275      1280
Ile Lys

```

20

(2) INFORMATION FOR SEQ ID NO:466

```

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1274 amino acids
25 (B) TYPE: amino acid
(D) TOPOLOGY: linear

```

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

```

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

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35 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1274

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466

```

40 Met Met Cys Ser Leu His Leu Gly Leu Gln Ser Gln Thr Trp His Gly
1 5 10 15
Asp Pro Asp Ser Val Ala Ala Leu Pro Ser Ile Gly Ile Gln Glu Ser
20 25 30
45 Ser Cys Thr Arg Ile Thr Phe Glu Val Val Phe Pro Gly Phe Tyr Ser
35 40 45
Val Glu Lys Arg Glu Gly Asn Gln Val Phe Gln Arg Ile Ser Met Pro
50 55 60
Gly Cys Gly Ser Phe Gly Asn Leu Gly Glu Ala Glu Leu Pro Val Leu
65 70 75 80
Lys Lys Met Ile Ala Val Pro Glu Phe Ser Thr Ala Asn Val Ala Val
85 90 95
Lys Ile Lys Glu Thr Glu Thr Phe Asp Asn Tyr Asn Ile Tyr Pro Asn
100 105 110
55 Pro Thr Tyr Val Val Glu Glu Leu Pro Glu Gly Gly Thr Tyr Leu Val
115 120 125
Glu Ala Phe Ala Ile Asn Asn Asp Tyr Tyr Ser Gln Asn Val Ser Leu
130 135 140
60 Pro Ser Thr His Tyr Val Tyr Ser Gln Asp Gly Tyr Phe Arg Ser Gln
145 150 155 160
Arg Phe Ile Glu Val Thr Leu Tyr Pro Phe Arg Tyr Asn Pro Val Arg
165 170 175
Gln Glu Ile Leu Phe Ala Lys Lys Ile Glu Val Thr Ile Thr Phe Asp
180 185 190
65 Asn Pro Gln Pro Pro Leu Gln Lys Asn Thr Gly Ile Phe Asn Lys Val
195 200 205
Ala Ser Ser Ala Phe Ile Asn Tyr Glu Ala Asp Gly Lys Ser Ala Ile
210 215 220
70 Glu Asn Asp Met Val Phe Ser Arg Gly Thr Thr Thr Tyr Ile Ser Gly
225 230 235 240
Asn Val Ala Ser Asn Leu Pro Gln Asn Cys Asp Tyr Leu Val Ile Tyr
245 250 255
Asp Asp Met Phe Asn Val Asn Gln Gln Pro His Asp Glu Ile Lys Arg
260 265 270
75 Leu Cys Glu His Arg Ala Phe Tyr Asn Gly Phe Asp Val Ala Ala Val

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		275				280				285				
		Ser	Ile	Lys	Asp	Val	Leu	Asn	Ser	Phe	Pro	Ser	Asn	Ala
		290											300	
		Ile	Asn	Glu	Thr	Lys	Leu	Lys	Asn	Phe	Ile	Arg	Ser	Val
5		305					310						315	
		Ser	Asn	Ala	Lys	Arg	Thr	Leu	Asp	Gly	Lys	Leu	Gly	Tyr
														320
														325
		Ile	Gly	Lys	Pro	Leu	Ser	Lys	Tyr	Leu	Ala	Asp	Thr	Asp
														330
10		Val	Pro	Thr	Ser	Phe	Ile	His	Asn	Val	Ser	Leu	Ile	Pro
														335
		Thr	Phe	Gly	Ser	Ile	Cys	Ala	Ser	Asp	Tyr	Phe	Phe	Ser
														340
15		Pro	Leu	Asp	Thr	Val	Gly	Asp	Leu	Phe	Ile	Gly	Arg	Phe
														345
		Asn	Ala	His	Glu	Leu	His	Asn	Leu	Ile	Glu	Lys	Thr	Ile
														350
		Ile	Ser	Tyr	Asn	Pro	Ile	Ala	His	Lys	Asn	Ile	Leu	Tyr
														355
20		Lys	Gly	Cys	Asp	Ala	Pro	Ile	Leu	Arg	Leu	Phe	Leu	Lys
														360
		Ser	Gly	Tyr	Thr	Val	Asn	Ser	Ile	Leu	Lys	Ser	Asn	Gln
														365
		Ile	Asp	Ser	Ile	Phe	Asp	Cys	Leu	Asn	Asn	Gly	Ser	His
														370
25		Phe	Asn	Thr	His	Gly	Met	Pro	Thr	Val	Trp	Gly	Ile	Gly
														375
		Asp	Val	Asn	Thr	Leu	Thr	Ala	Arg	Leu	Asn	Asn	Thr	Ser
														380
30		Leu	Cys	Thr	Ser	Leu	Ser	Cys	Ser	Ser	Ala	Val	Ala	Asp
														385
		Arg	Ser	Leu	Gly	Glu	Val	Leu	Thr	Thr	Tyr	Ala	Pro	Asn
														390
		Ser	Ala	Phe	Leu	Gly	Gly	Ser	Arg	Ala	Thr	Gln	Tyr	Ala
														395
35		Glu	Gly	Pro	Cys	Pro	Pro	Ser	Glu	Phe	Tyr	Glu	Tyr	Leu
														400
		Leu	Tyr	His	Asn	Leu	Ser	Thr	Val	Val	Gly	Glu	Met	Leu
														405
40		Ile	Ile	Asn	Thr	Asn	Ser	Val	Asp	Thr	Tyr	Ser	Lys	Phe
														410
		Leu	Leu	Gly	Asp	Pro	Ala	Leu	Asn	Ile	Met	Ala	His	Gly
														415
45		Ser	Asn	Cys	Ile	Thr	Leu	Pro	Asn	Asn	Thr	Ile	Ile	Ser
														420
		Thr	Ile	Lys	Asn	Gly	Gly	Cys	Leu	Lys	Ile	Pro	Glu	Lys
														425
		His	Phe	Thr	Asn	Asn	Gly	Ser	Ile	Gln	Val	Met	Ser	Gly
														430
50		Glu	Ile	Gly	Asn	Gln	Ala	Lys	Ile	Ser	Gly	Glu	Thr	Gly
														435
		Thr	Phe	Ile	Thr	Val	Tyr	Gly	Asp	Gly	Leu	Ala	Ile	Asn
														440
55		Glu	Ile	Asp	Asn	Ile	Asp	Arg	Leu	Asn	Leu	Phe	Ser	Thr
														445
		Met	Pro	Lys	Phe	His	Phe	Asp	Ser	Val	Lys	Phe	Asn	Ser
														450
		Tyr	Thr	Thr	Asn	Cys	Ile	Val	Glu	Ile	Ser	Asn	Cys	Glu
														455
60		Arg	Ser	Asp	Ile	Ile	Ser	Lys	Asn	Cys	Asp	Leu	Ser	Val
														460
		Met	Phe	Ser	Ser	Gly	Ile	Thr	Val	Phe	Lys	Pro	Met	Ala
														465
65		Ser	Ile	Thr	Gly	Leu	Ser	Thr	Lys	Ala	Lys	Ile	Thr	Asp
														470
		Phe	Ala	Thr	Gly	Asn	Phe	Ala	Tyr	His	Ile	Thr	Asn	Thr
														475
		Thr	Ala	Thr	Ser	Asn	Ala	Ala	Ile	Lys	Leu	Asp	Asn	Ile
														480
70		Tyr	Ile	Ser	Gly	Asn	Lys	Ile	Val	Asn	Cys	Asp	Glu	Ala
														485
		Asn	Asn	Ser	Gly	Asn	Arg	Thr	Asn	Arg	Leu	His	Asn	Ile
														490
		Val	Ile	Lys	Asn	Cys	Arg	Ile	Gly	Ser	Thr	Leu	Tyr	Asn
														495
75														500

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Ile Tyr Asn Arg Asn Lys Ile Ser Asn Asn His Ile Gly Val Arg Leu  
 885 890 895  
 Leu Asn Asn Ser Cys Phe Tyr Phe Asp Asn Ala Pro Val Ile Asn Glu  
 900 905 910  
 5 Glu Asp Lys Gln Thr Phe Ile Ser Asn Arg Thr Trp Gln Leu Tyr Ser  
 915 920 925  
 Ser Asn Gly Thr Phe Pro Leu Asn Phe His Tyr Asn Ser Leu Gln Gly  
 930 935 940  
 10 Gly Asp Thr Asp Thr Trp Ile Tyr Asn Asp Thr Tyr Thr Asn Arg Tyr  
 945 950 955 960  
 Ile Asp Val Ser Asn Asn His Trp Gly Asn Asn Asp Leu Phe Asp Pro  
 965 970 975  
 Asn Gln Val Phe Asn Thr Pro Asp Leu Phe Ile Trp Ile Pro Phe Trp  
 980 985 990  
 15 Asp Gly Leu Pro Asn Gly Arg Ser Gly Asn Ser Ser Ala Glu Ala Val  
 995 1000 1005  
 Glu Phe Gln Thr Ala Leu Asp Cys Ile Gly Asn Ser Asp Tyr Leu Ser  
 1010 1015 1020  
 20 Ala Lys Val Ala Leu Lys Met Met Val Glu Thr Tyr Pro Glu Ser Asp  
 1025 1030 1035 1040  
 Phe Ala Ile Ala Ala Leu Lys Glu Leu Phe Arg Ile Glu Lys Met Ser  
 1045 1050 1055  
 Gly Asn Asp Tyr Glu Gly Leu Lys Asp Tyr Phe Arg Ser Asn Pro Thr  
 1060 1065 1070  
 25 Ile Ile Ser Ser Gln Asn Leu Phe Pro Thr Ala Asp Phe Leu Ser Ala  
 1075 1080 1085  
 Arg Cys Asp Ile Val Cys Glu Asn Tyr Gln Ser Ala Ile Asp Trp Tyr  
 1090 1095 1100  
 30 Glu Asn Arg Leu Asn Ser Glu Ile Ser Tyr Gln Asp Ser Val Phe Ala  
 1105 1110 1115 1120  
 Val Ile Asp Leu Gly Asp Ile Tyr Trp Asn Met Gln Leu Asp Ser Leu  
 1125 1130 1135  
 Arg Gly Thr Gly Ile Asp Leu Asn Ile Leu Ser Cys Glu Gln Arg Lys  
 1140 1145 1150  
 35 Ser Leu Glu Ser His Gln Asn Val Lys Asn Tyr Leu Leu Ser Thr Leu  
 1155 1160 1165  
 Pro Glu Ser Thr Gly Thr Leu Leu Pro Pro Leu Glu Cys Asn Lys Ser  
 1170 1175 1180  
 40 Ser Leu Asp Lys Ser Lys Ile Ile Ser Ile Ser Pro Asn Pro Ala Lys  
 1185 1190 1195 1200  
 Ala Val Val Thr Ile Ile Tyr Tyr Thr Asp Asn Pro Ser Cys Ser Val  
 1205 1210 1215  
 Ile Lys Ile Tyr Gly Ile Asn Gly Ala Ser Ala Asp Ile Thr Gly Leu  
 1220 1225 1230  
 45 Pro Lys His Leu Ser Glu Gly Tyr Tyr Ser Ile Gln Phe Asn Thr Ser  
 1235 1240 1245  
 Asn Phe Asp Pro Gly Phe Tyr Leu Val Thr Leu Asn Val Asp Gln Lys  
 1250 1255 1260  
 50 Ile Ile Asp Thr Glu Lys Leu Arg Ile Lys  
 1265 1270

## (2) INFORMATION FOR SEQ ID NO:467

- 55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 925 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
  
 60 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 65 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...925  
 70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:467

Met Ala Ile Met Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile  
 1 5 10 15  
 75 Leu Leu Ser Trp Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser  
 20 25 30

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	Gly	Met	Asn	Ala	Ser	Cys	Leu	Ala	Ala	Pro	Ala	Gln	Pro	Asp	Thr	Ile
			35				40					45				
	Leu	Tyr	Glu	Ser	Phe	Glu	Asn	Gly	Pro	Val	Pro	Asn	Gly	Trp	Leu	Glu
			50				55					60				
5	Ile	Asp	Ala	Asp	Ala	Asp	Gly	Ala	Thr	Trp	Gly	Ser	Pro	Ser	Gly	Ser
			65				70					75				80
	Phe	Ser	Val	Pro	Tyr	Gly	His	Asn	Gly	Leu	Cys	Thr	Tyr	Ser	His	Ile
					85					90					95	
10	Arg	Ser	Gly	Ile	Ser	Thr	Ala	Gly	Asn	Tyr	Leu	Ile	Thr	Pro	Asn	Ile
					100					105					110	
	Glu	Gly	Ala	Lys	Arg	Val	Lys	Tyr	Trp	Val	Cys	Asn	Gln	Tyr	Ser	Thr
					115					120					125	
	Asn	Pro	Glu	His	Tyr	Ala	Val	Met	Val	Ser	Thr	Thr	Gly	Thr	Ala	Ile
					130					135					140	
15	Glu	Asp	Phe	Val	Leu	Leu	Phe	Asp	Asp	Ser	Ile	Thr	Gly	Lys	Pro	Thr
					145					150					155	160
	Pro	Leu	Val	Trp	Arg	Arg	Arg	Ile	Val	Asp	Leu	Pro	Glu	Gly	Thr	Lys
					165					170					175	
20	Tyr	Ile	Ala	Trp	Arg	His	Tyr	Lys	Val	Thr	Asp	Ser	His	Thr	Glu	Phe
					180					185					190	
	Leu	Lys	Leu	Asp	Asp	Val	Thr	Val	Tyr	Arg	Ser	Ile	Glu	Gly	Pro	Glu
					195					200					205	
	Pro	Ala	Thr	Asp	Phe	Thr	Val	Ile	Asn	Ile	Gly	Gln	Asn	Val	Gly	Arg
					210					215					220	
25	Leu	Thr	Trp	Asn	Tyr	Pro	Glu	Asp	Tyr	Gln	Pro	Glu	Gly	Lys	Gly	Asn
					225					230					235	240
	Glu	Glu	Leu	Gln	Leu	Ser	Gly	Tyr	Asn	Ile	Tyr	Ala	Asn	Gly	Thr	Leu
					245					250					255	
30	Leu	Ala	Gln	Ile	Lys	Asp	Val	Ser	Ile	Leu	Glu	Tyr	Val	Asp	Ser	Thr
					260					265					270	
	Tyr	Ser	Leu	Arg	Asp	Asn	Pro	Leu	Gln	Val	Glu	Tyr	Cys	Val	Thr	Ala
					275					280					285	
	Val	Tyr	Asp	Glu	Ser	Ile	Glu	Ser	Ser	Thr	Val	Cys	Gly	Thr	Leu	His
					290					295					300	
35	Tyr	Ala	Thr	Asp	Ala	Ile	Leu	Tyr	Glu	Asn	Phe	Glu	Asn	Gly	Pro	Val
					305					310					315	320
	Pro	Asn	Gly	Trp	Leu	Val	Ile	Asp	Ala	Asp	Gly	Asp	Gly	Phe	Ser	Trp
					325					330					335	
40	Gly	His	Tyr	Leu	Asn	Ala	Tyr	Asp	Ala	Phe	Pro	Gly	His	Asn	Gly	Gly
					340					345					350	
	His	Cys	Ser	Leu	Ser	Ala	Ser	Tyr	Val	Pro	Gly	Ile	Gly	Pro	Val	Thr
					355					360					365	
	Pro	Asp	Asn	Tyr	Leu	Ile	Thr	Pro	Lys	Val	Glu	Gly	Ala	Lys	Arg	Val
					370					375					380	
45	Lys	Tyr	Trp	Val	Ser	Thr	Gln	Asp	Ala	Asn	Trp	Ala	Ala	Glu	His	Tyr
					385					390					395	400
	Ala	Val	Met	Ala	Ser	Thr	Thr	Gly	Thr	Ala	Val	Gly	Asp	Phe	Val	Ile
					405					410					415	
50	Leu	Phe	Glu	Glu	Thr	Met	Thr	Ala	Lys	Pro	Thr	Gly	Ala	Trp	Tyr	Glu
					420					425					430	
	Arg	Thr	Ile	Asn	Leu	Pro	Glu	Gly	Thr	Lys	Tyr	Ile	Ala	Trp	Arg	His
					435					440					445	
	Tyr	Asn	Cys	Thr	Asp	Ile	Tyr	Phe	Leu	Lys	Leu	Asp	Asp	Ile	Thr	Val
					450					455					460	
55	Phe	Gly	Thr	Pro	Ala	Ser	Glu	Pro	Glu	Pro	Val	Thr	Asp	Phe	Val	Val
					465					470					475	480
	Ser	Leu	Ile	Glu	Asn	Asn	Lys	Gly	Arg	Leu	Lys	Trp	Asn	Tyr	Pro	Asn
					485					490					495	
60	Gly	Tyr	Glu	Pro	Asp	Lys	Thr	Asp	Asp	Lys	Asp	Pro	Leu	Gln	Leu	Ala
					500					505					510	
	Gly	Tyr	Asn	Ile	Tyr	Ala	Asn	Gly	Ser	Leu	Leu	Val	His	Ile	Gln	Asp
					515					520					525	
	Pro	Thr	Val	Leu	Glu	Tyr	Ile	Asp	Glu	Thr	Tyr	Ser	Ser	Arg	Asp	Asp
					530					535					540	
65	Gln	Val	Glu	Val	Glu	Tyr	Cys	Val	Thr	Ala	Val	Tyr	Asn	Asp	Asn	Ile
					545					550					555	560
	Glu	Ser	Gln	Ser	Val	Cys	Asp	Lys	Leu	Ile	Tyr	Asp	Ser	Gln	Ser	Asp
					565					570					575	
70	Ile	Ile	Leu	Tyr	Glu	Gly	Phe	Glu	Ala	Gly	Ser	Ile	Pro	Glu	Gly	Trp
					580					585					590	
	Leu	Leu	Ile	Asp	Ala	Asp	Gly	Asp	Asn	Val	Asn	Trp	Asp	Tyr	Tyr	Pro
					595					600					605	
	Trp	Thr	Met	Tyr	Gly	His	Asp	Ser	Glu	Lys	Cys	Ile	Ala	Ser	Pro	Ser
					610					615					620	
75	Tyr	Leu	Pro	Met	Ile	Gly	Val	Leu	Thr	Pro	Asp	Asn	Tyr	Leu	Val	Thr



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130 135 140  
 Val Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr Pro Leu Val  
 145 150 155 160  
 Trp Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys Tyr Ile Ala  
 165 170 175  
 5 Trp Arg His Tyr Lys Val Thr Asp Ser His Thr Glu Phe Leu Lys Leu  
 180 185 190  
 Asp Asp Val Thr Val Tyr Arg Ser Ile Glu Gly Pro Glu Pro Ala Thr  
 195 200 205  
 10 Asp Phe Thr Val Ile Asn Ile Gly Gln Asn Val Gly Arg Leu Thr Trp  
 210 215 220  
 Asn Tyr Pro Glu Asp Tyr Gln Pro Glu Gly Lys Gly Asn Glu Glu Leu  
 225 230 235 240  
 15 Gln Leu Ser Gly Tyr Asn Ile Tyr Ala Asn Gly Thr Leu Leu Ala Gln  
 245 250 255  
 Ile Lys Asp Val Ser Ile Leu Glu Tyr Val Asp Ser Thr Tyr Ser Leu  
 260 265 270  
 Arg Asp Asn Pro Leu Gln Val Glu Tyr Cys Val Thr Ala Val Tyr Asp  
 275 280 285  
 20 Glu Ser Ile Glu Ser Ser Thr Val Cys Gly Thr Leu His Tyr Ala Thr  
 290 295 300  
 Asp Ala Ile Leu Tyr Glu Asn Phe Glu Asn Gly Pro Val Pro Asn Gly  
 305 310 315 320  
 25 Trp Leu Val Ile Asp Ala Asp Gly Asp Gly Phe Ser Trp Gly His Tyr  
 325 330 335  
 Leu Asn Ala Tyr Asp Ala Phe Pro Gly His Asn Gly Gly His Cys Ser  
 340 345 350  
 Leu Ser Ala Ser Tyr Val Pro Gly Ile Gly Pro Val Thr Pro Asp Asn  
 355 360 365  
 30 Tyr Leu Ile Thr Pro Lys Val Glu Gly Ala Lys Arg Val Lys Tyr Trp  
 370 375 380  
 Val Ser Thr Gln Asp Ala Asn Trp Ala Ala Glu His Tyr Ala Val Met  
 385 390 395 400  
 35 Ala Ser Thr Thr Gly Thr Ala Val Gly Asp Phe Val Ile Leu Phe Glu  
 405 410 415  
 Glu Thr Met Thr Ala Lys Pro Thr Gly Ala Trp Tyr Glu Arg Thr Ile  
 420 425 430  
 Asn Leu Pro Glu Gly Thr Lys Tyr Ile Ala Trp Arg His Tyr Asn Cys  
 435 440 445  
 40 Thr Asp Ile Tyr Phe Leu Lys Leu Asp Asp Ile Thr Val Phe Gly Thr  
 450 455 460  
 Pro Ala Ser Glu Pro Glu Pro Val Thr Asp Phe Val Val Ser Leu Ile  
 465 470 475 480  
 45 Glu Asn Asn Lys Gly Arg Leu Lys Trp Asn Tyr Pro Asn Gly Tyr Glu  
 485 490 495  
 Pro Asp Lys Thr Asp Asp Lys Asp Pro Leu Gln Leu Ala Gly Tyr Asn  
 500 505 510  
 Ile Tyr Ala Asn Gly Ser Leu Leu Val His Ile Gln Asp Pro Thr Val  
 515 520 525  
 50 Leu Glu Tyr Ile Asp Glu Thr Tyr Ser Ser Arg Asp Asp Gln Val Glu  
 530 535 540  
 Val Glu Tyr Cys Val Thr Ala Val Tyr Asn Asp Asn Ile Glu Ser Gln  
 545 550 555 560  
 55 Ser Val Cys Asp Lys Leu Ile Tyr Asp Ser Gln Ser Asp Ile Ile Leu  
 565 570 575  
 Tyr Glu Gly Phe Glu Ala Gly Ser Ile Pro Glu Gly Trp Leu Leu Ile  
 580 585 590  
 Asp Ala Asp Gly Asp Asn Val Asn Trp Asp Tyr Tyr Pro Trp Thr Met  
 595 600 605  
 60 Tyr Gly His Asp Ser Glu Lys Cys Ile Ala Ser Pro Ser Tyr Leu Pro  
 610 615 620  
 Met Ile Gly Val Leu Thr Pro Asp Asn Tyr Leu Val Thr Pro Arg Leu  
 625 630 635 640  
 65 Glu Gly Ala Lys Leu Val Lys Tyr Trp Val Ser Ala Gln Asp Ala Val  
 645 650 655  
 Tyr Ser Ala Glu His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala  
 660 665 670  
 Val Glu Asp Phe Val Leu Leu Phe Glu Glu Thr Met Thr Ala Lys Ala  
 675 680 685  
 70 Asn Gly Ala Trp Tyr Glu Arg Thr Ile Thr Leu Pro Ala Gly Thr Lys  
 690 695 700  
 Tyr Ile Ala Trp Arg His Tyr Asp Cys Thr Asp Met Phe Phe Leu Leu  
 705 710 715 720  
 75 Leu Asp Asp Ile Thr Val Tyr Arg Ser Thr Glu Thr Val Pro Glu Pro  
 725 730 735

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Val Thr Asp Phe Val Val Ser Leu Ile Glu Asn Asn Lys Gly Arg Leu  
 740 745 750  
 Lys Trp Asn Tyr Pro Asn Gly Tyr Glu Pro Asp Lys Thr Asp Asp Lys  
 755 760 765  
 5 Lys Pro Leu Gln Leu Thr Gly Tyr Asn Ile Tyr Ala Asn Gly Ser Leu  
 770 775 780  
 Leu Val His Ile Gln Asp Pro Thr Val Leu Glu Tyr Ile Asp Glu Thr  
 785 790 795 800  
 10 Tyr Ser Ser Arg Asp Gly Gln Val Glu Met Glu Tyr Cys Val Thr Ala  
 805 810 815  
 Val Tyr Asn Asp Asn Ile Glu Ser Gln Ser Val Cys Asp Lys Leu Asn  
 820 825 830  
 Tyr Thr Ile Thr Ser Leu Asp Asn Ile Gln Ser Asp Thr Ser Leu Lys  
 835 840 845  
 15 Ile Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu Gly Leu Ser  
 850 855 860  
 Arg Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly Ile Cys Ile  
 865 870 875 880  
 20 Leu Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp Val Ser Arg  
 885 890 895  
 Leu Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly Asn Lys Thr  
 900 905 910  
 Thr Thr Glu Lys Val Glu Ile Lys Arg Pro  
 915 920

## (2) INFORMATION FOR SEQ ID NO:469

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 921 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (iv) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

## (ix) FEATURE:

(A) NAME/KEY: misc feature  
 (B) LOCATION 1...921

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:469

Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile Leu Leu Ser Trp  
 1 5 10 15  
 Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser Gly Met Asn Ala  
 20 25 30  
 50 Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile Leu Tyr Glu Ser  
 35 40 45  
 Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu Ile Asp Ala Asp  
 50 55 60  
 55 Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser Phe Ser Val Pro  
 65 70 75 80  
 Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile Arg Ser Gly Ile  
 85 90 95  
 Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile Glu Gly Ala Lys  
 100 105 110  
 60 Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr Asn Pro Glu His  
 115 120 125  
 Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile Glu Asp Phe Val  
 130 135 140  
 65 Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr Pro Leu Val Trp  
 145 150 155 160  
 Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys Tyr Ile Ala Trp  
 165 170 175  
 Arg His Tyr Lys Val Thr Asp Ser His Thr Glu Phe Leu Lys Leu Asp  
 180 185 190  
 70 Asp Val Thr Val Tyr Arg Ser Ile Glu Gly Pro Glu Pro Ala Thr Asp  
 195 200 205  
 Phe Thr Val Ile Asn Ile Gly Gln Asn Val Gly Arg Leu Thr Trp Asn  
 210 215 220  
 75 Tyr Pro Glu Asp Tyr Gln Pro Glu Gly Lys Gly Asn Glu Glu Leu Gln  
 225 230 235 240



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418/490

835 840 845  
 Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu Gly Leu Ser Arg  
 850 855 860  
 Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly Ile Cys Ile Leu  
 865 870 875 880  
 Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp Val Ser Arg Leu  
 885 890 895  
 Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly Asn Lys Thr Thr  
 900 905 910  
 Thr Glu Lys Val Glu Ile Lys Arg Pro  
 915 920

(2) INFORMATION FOR SEQ ID NO:470

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 593 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 20 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 25 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...593  
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:470

Met Asn Ser Ile Met Lys Tyr Gln Leu Tyr Thr Ala Val Ile Met Ala  
 1 5 10 15  
 35 Leu Ser Val Ser Ser Val Cys Gly Gln Thr Pro Arg Asn Thr Glu Thr  
 20 25 30  
 Lys Arg Pro Asp Thr Leu Arg Arg Glu Leu Thr Ile Val Asn Asp Gln  
 35 40 45  
 Thr Val Glu Met Glu His Ala Asp Pro Leu Pro Ala Ala Tyr Lys Ala  
 40 50 55 60  
 Ile Glu Pro Arg Leu Lys Pro Phe Arg Pro Glu Tyr Asn Lys Arg Thr  
 65 70 75 80  
 Phe Gly Phe Val Pro Glu Val Ser Ser Ser Gly Arg Asn Asn Leu Pro  
 85 90 95  
 45 Asn Ile Leu Pro Thr Glu Gly His Met Lys His Arg Gly Tyr Leu Asn  
 100 105 110  
 Ile Gly Ile Gly His Thr Leu Asn Gln Arg Met Asp Ala Gly Tyr Arg  
 115 120 125  
 50 Leu Ile Asp Ala Glu Gln Glu Arg Leu Asn Leu Phe Leu Ser Tyr Arg  
 130 135 140  
 Gly Met Lys Ser Ala Phe Asn Thr Gly Asp Phe Asp Gly Asp Arg Lys  
 145 150 155 160  
 Asp Arg Arg Met Met Ala Gly Val Asp Tyr Glu Gln Arg Arg Pro Ser  
 165 170 175  
 55 Phe Val Leu Ala Thr Gly Leu Tyr Tyr Ser Asn His Tyr Phe Asn Asn  
 180 185 190  
 Tyr Gly Arg Gly Ala Thr Thr Asn Val Gly Ser Ile Pro Gln Leu Ser  
 195 200 205  
 60 Thr Pro Val Thr Pro Gln Met Asp Asn Gly Thr His Asn Val Arg Val  
 210 215 220  
 Tyr Leu Gly Ala Lys Asn Asp Val Ile Asp Ala Arg Ile Asp Tyr Arg  
 225 230 235 240  
 Phe Phe Arg Ser Ile Pro Tyr Leu Gly Thr Asp Pro Met Lys Ala Leu  
 245 250 255  
 65 Thr Glu His Thr Pro Glu Leu Asn Val Thr Met Ser Asn Glu Leu Ser  
 260 265 270  
 Asp Asp Ile Lys Leu Gly Val Glu Val Arg Thr Gly Gly Leu Phe Phe  
 275 280 285  
 Ala Lys Asn Ser Glu Met Ile Gln Thr Gly Val Leu Ser Glu Thr Asp  
 290 295 300  
 70 Arg Asn Leu Tyr Tyr Val Glu Gly Ala Pro Thr Ile Gly Phe Val Gly  
 305 310 315 320  
 Asp Ser Asp Asn Met Gln Trp Asn Ile Gln Ala Gly Val Gly Ile Ser  
 325 330 335  
 75 Ser His Phe Gly Ala Lys Gly Arg Leu Phe Phe Trp Pro Lys Leu Asp

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419/490

340 345 350  
 Ala Ser Leu Ser Ile Phe Pro Ser Trp Arg Val Tyr Ala Lys Ala Phe  
 355 360 365  
 Gly Gly Val Ile Arg Asn Gly Leu Ala Asp Val Met Gln Glu Glu Met  
 370 375 380  
 5 Pro Tyr Leu Met Pro Asn Thr Ile Val Leu Pro Ser Arg Asn Ala Leu  
 385 390 395 400  
 Thr Ala Gln Leu Gly Val Lys Gly Asn Ile Ala Asp Val Val Arg Met  
 405 410 415  
 10 Glu Val Tyr Gly Asp Phe Ser Lys Leu Thr Gly Val Pro Phe Tyr Thr  
 420 425 430  
 Pro Thr Leu Pro Leu Tyr Asn Pro Ser Asp Leu Tyr Gln Tyr Asn Val  
 435 440 445  
 15 Ser Phe Leu Pro Ile Tyr Ala Asp Gly Ser Arg Trp Arg Ala Gly Gly  
 450 455 460  
 Lys Leu Glu Tyr Ser Tyr Arg Asp Met Leu Arg Phe Leu Val Asp Ala  
 465 470 475 480  
 Ser Tyr Gly Lys Trp Asn Leu Asp Gly Gly Leu Val Ala Ser Met Gln  
 485 490 495  
 20 Pro Asp Leu Ile Leu Lys Ala Glu Val Gly Val His Pro Ile Ala Pro  
 500 505 510  
 Leu Asp Val Arg Leu Arg Tyr Thr Gln Leu Asn Gly Arg Tyr Arg Tyr  
 515 520 525  
 25 Ser Phe Gly Ser Ala Gly Ser Glu Ala Leu Gly Ile Gly Asn Val His  
 530 535 540  
 Leu Leu Ser Ala Asp Val Ser Tyr Lys Leu Lys Lys Asn Leu Ser Leu  
 545 550 555 560  
 Tyr Leu Lys Ile Asp Asn Met Leu Ala Glu Thr Thr Glu Leu Ile Gly  
 565 570 575  
 30 Tyr Tyr Pro Met Gln Pro Phe His Cys Phe Ala Gly Phe Ser Trp Thr  
 580 585 590  
 Phe

35 (2) INFORMATION FOR SEQ ID NO:471

(1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 589 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

40 (11) MOLECULE TYPE: protein

45 (111) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

50 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471

55 Met Lys Tyr Gln Leu Tyr Thr Ala Val Ile Met Ala Leu Ser Val Ser  
 1 5 10 15  
 Ser Val Cys Gly Gln Thr Pro Arg Asn Thr Glu Thr Lys Arg Pro Asp  
 20 25 30  
 60 Thr Leu Arg Arg Glu Leu Thr Ile Val Asn Asp Gln Thr Val Glu Met  
 35 40 45  
 Glu His Ala Asp Pro Leu Pro Ala Ala Tyr Lys Ala Ile Glu Pro Arg  
 50 55 60  
 Leu Lys Pro Phe Arg Pro Glu Tyr Asn Lys Arg Thr Phe Gly Phe Val  
 65 70 75 80  
 65 Pro Glu Val Ser Ser Ser Gly Arg Asn Asn Leu Pro Asn Ile Leu Pro  
 85 90 95  
 Thr Glu Gly His Met Lys His Arg Gly Tyr Leu Asn Ile Gly Ile Gly  
 100 105 110  
 His Thr Leu Asn Gln Arg Met Asp Ala Gly Tyr Arg Leu Ile Asp Ala  
 115 120 125  
 70 Glu Gln Glu Arg Leu Asn Leu Phe Leu Ser Tyr Arg Gly Met Lys Ser  
 130 135 140  
 Ala Phe Asn Thr Gly Asp Phe Asp Gly Asp Arg Lys Asp Arg Arg Met  
 145 150 155 160  
 75 Met Ala Gly Val Asp Tyr Glu Gln Arg Arg Pro Ser Phe Val Leu Ala

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420/ 490

165 170 175  
 Thr Gly Leu Tyr Tyr Ser Asn His Tyr Phe Asn Asn Tyr Gly Arg Gly  
 180 185 190  
 Ala Thr Thr Asn Val Gly Ser Ile Pro Gln Leu Ser Thr Pro Val Thr  
 195 200 205  
 Pro Gln Met Asp Asn Gly Thr His Asn Val Arg Val Tyr Leu Gly Ala  
 210 215 220  
 Lys Asn Asp Val Ile Asp Ala Arg Ile Asp Tyr Arg Phe Phe Arg Ser  
 225 230 235 240  
 10 Ile Pro Tyr Leu Gly Thr Asp Pro Met Lys Ala Leu Thr Glu His Thr  
 245 250 255  
 Pro Glu Leu Asn Val Thr Met Ser Asn Glu Leu Ser Asp Asp Ile Lys  
 260 265 270  
 Leu Gly Val Glu Val Arg Thr Gly Gly Leu Phe Phe Ala Lys Asn Ser  
 275 280 285  
 15 Glu Met Ile Gln Thr Gly Val Leu Ser Glu Thr Asp Arg Asn Leu Tyr  
 290 295 300  
 Tyr Val Glu Gly Ala Pro Thr Ile Gly Phe Val Gly Asp Ser Asp Asn  
 305 310 315 320  
 20 Met Gln Trp Asn Ile Gln Ala Gly Val Gly Ile Ser Ser His Phe Gly  
 325 330 335  
 Ala Lys Gly Arg Leu Phe Phe Trp Pro Lys Leu Asp Ala Ser Leu Ser  
 340 345 350  
 25 Ile Phe Pro Ser Trp Arg Val Tyr Ala Lys Ala Phe Gly Gly Val Ile  
 355 360 365  
 Arg Asn Gly Leu Ala Asp Val Met Gln Glu Glu Met Pro Tyr Leu Met  
 370 375 380  
 Pro Asn Thr Ile Val Leu Pro Ser Arg Asn Ala Leu Thr Ala Gln Leu  
 385 390 395 400  
 30 Gly Val Lys Gly Asn Ile Ala Asp Val Val Arg Met Glu Val Tyr Gly  
 405 410 415  
 Asp Phe Ser Lys Leu Thr Gly Val Pro Phe Tyr Thr Pro Thr Leu Pro  
 420 425 430  
 35 Leu Tyr Asn Pro Ser Asp Leu Tyr Gln Tyr Asn Val Ser Phe Leu Pro  
 435 440 445  
 Ile Tyr Ala Asp Gly Ser Arg Trp Arg Ala Gly Gly Lys Leu Glu Tyr  
 450 455 460  
 Ser Tyr Arg Asp Met Leu Arg Phe Leu Val Asp Ala Ser Tyr Gly Lys  
 465 470 475 480  
 40 Trp Asn Leu Asp Gly Gly Leu Val Ala Ser Met Gln Pro Asp Leu Ile  
 485 490 495  
 Leu Lys Ala Glu Val Gly Val His Pro Ile Ala Pro Leu Asp Val Arg  
 500 505 510  
 45 Leu Arg Tyr Thr Gln Leu Asn Gly Arg Tyr Arg Tyr Ser Phe Gly Ser  
 515 520 525  
 Ala Gly Ser Glu Ala Leu Gly Ile Gly Asn Val His Leu Leu Ser Ala  
 530 535 540  
 Asp Val Ser Tyr Lys Leu Lys Lys Asn Leu Ser Leu Tyr Leu Lys Ile  
 545 550 555 560  
 50 Asp Asn Met Leu Ala Glu Thr Thr Glu Leu Ile Gly Tyr Tyr Pro Met  
 565 570 575  
 Gln Pro Phe His Cys Phe Ala Gly Phe Ser Trp Thr Phe  
 580 585

55 (2) INFORMATION FOR SEQ ID NO:472

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

65

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1...346

70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472

75

Met Met Glu Lys Cys Ile Phe Ala His Tyr Pro His Asn Leu Val Phe

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1      5      10      15
Met Ile Arg Lys His Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val
20      25      30
Phe Ser Ala Gly Ala Gln Gln Glu Lys Gln Val Phe His Phe Leu Asn
35      40      45
Leu Pro Ala Thr Ala Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr
50      55      60
Ile Val Asp Asp Asn Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu
65      70      75
10 Gly Tyr Glu Ser Gly Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met
85      90      95
Ser Gly Ser His Met Gly Asn Ala Cys Tyr Ala Ser Ser Val Gly Glu
100      105      110
Arg Gly Met Trp Gly Val Gly Met Arg Phe Leu Asn Tyr Gly Ser Met
115      120      125
15 Gln Gly Tyr Asp Gln Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser
130      135      140
Asp Ile Ala Val Gln Gly Phe Tyr Ser His Glu Leu Ser Asn His Phe
145      150      155
20 Arg Gly Gly Val Ser Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr
165      170      175
Ser Ser Phe Gly Leu Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp
180      185      190
25 Asp Lys Gly Tyr Ser Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln
195      200      205
Leu Lys Gly Tyr Asn Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln
210      215      220
Leu Gly Phe Ser Arg Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile
225      230      235
30 Thr Leu Phe Asn Leu Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg
245      250      255
Asp Leu Ser Lys Met Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala
260      265      270
35 Glu Phe Thr Pro Ser Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro
275      280      285
Gln Ile Ala Gln Asp Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly
290      295      300
Leu Ser Ala Gly Val Gly Phe Thr Ser Gly Val Val Arg Val Gly Val
305      310      315
40 Ser Ala Ala Thr Tyr His Pro Ala Ala Leu Ser Phe Met Cys Ser Val
325      330      335
Gly Ile Arg Leu Asp Asp Lys Ser Ile Phe
340      345

```

45 (2) INFORMATION FOR SEQ ID NO:473

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(ii) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 345 amino acids
(B) TYPE: amino acid
50 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

```

```

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

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(ix) FEATURE:
(A) NAME/KEY: misc feature
60 (D) LOCATION 1...345

```

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473

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65 Met Glu Lys Cys Ile Phe Ala His Tyr Pro His Asn Leu Val Phe Met
1      5      10      15
Ile Arg Lys His Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val Phe
20      25      30
Ser Ala Gly Ala Gln Gln Glu Lys Gln Val Phe His-Phe Leu Asn Leu
35      40      45
70 Pro Ala Thr Ala Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr Ile
50      55      60
Val Asp Asp Asn Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu Gly
65      70      75
75 Tyr Glu Ser Gly Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met Ser

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422/490

85 90 95  
 Gly Ser His Met Gly Asn Ala Cys Tyr Ala Ser Ser Val Gly Glu Arg  
 100 105 110  
 5 Gly Met Trp Gly Val Gly Met Arg Phe Leu Asn Tyr Gly Ser Met Gln  
 115 120 125  
 Gly Tyr Asp Gln Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser Asp  
 130 135 140  
 Ile Ala Val Gln Gly Phe Tyr Ser His Glu Leu Ser Asn His Phe Arg  
 145 150 155 160  
 10 Gly Gly Val Ser Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr Ser  
 165 170 175  
 Ser Phe Gly Leu Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp Asp  
 180 185 190  
 15 Lys Gly Tyr Ser Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln Leu  
 195 200 205  
 Lys Gly Tyr Asn Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln Leu  
 210 215 220  
 Gly Phe Ser Arg Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile Thr  
 225 230 235 240  
 20 Leu Phe Asn Leu Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg Asp  
 245 250 255  
 Leu Ser Lys Met Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala Glu  
 260 265 270  
 25 Phe Thr Pro Ser Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro Gln  
 275 280 285  
 Ile Ala Gln Asp Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly Leu  
 290 295 300  
 Ser Ala Gly Val Gly Phe Thr Ser Gly Val Val Arg Val Gly Val Ser  
 305 310 315 320  
 30 Ala Ala Thr Tyr His Pro Ala Ala Leu Ser Phe Met Cys Ser Val Gly  
 325 330 335  
 Ile Arg Leu Asp Asp Lys Ser Ile Phe  
 340 345

35 (2) INFORMATION FOR SEQ ID NO:474

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 330 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

45 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

50 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474

55 Met Ile Arg Lys His Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val  
 1 5 10 15  
 Phe Ser Ala Gly Ala Gln Gln Glu Lys Gln Val Phe His Phe Leu Asn  
 20 25 30  
 60 Leu Pro Ala Thr Ala Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr  
 35 40 45  
 Ile Val Asp Asp Asn Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu  
 50 55 60  
 Gly Tyr Glu Ser Gly Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met  
 65 70 75 80  
 Ser Gly Ser His Met Gly Asn Ala Cys Tyr Ala Ser Ser Val Gly Glu  
 85 90 95  
 Arg Gly Met Trp Gly Val Gly Met Arg Phe Leu Asn Tyr Gly Ser Met  
 100 105 110  
 70 Gln Gly Tyr Asp Gln Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser  
 115 120 125  
 Asp Ile Ala Val Gln Gly Phe Tyr Ser His Glu Leu Ser Asn His Phe  
 130 135 140  
 Arg Gly Gly Val Ser Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr  
 145 150 155 160  
 75 Ser Ser Phe Gly Leu Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp

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423/ 490

165 170 175  
 Asp Lys Gly Tyr Ser Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln  
 180 185 190  
 5 Leu Lys Gly Tyr Asn Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln  
 195 200 205  
 Leu Gly Phe Ser Arg Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile  
 210 215 220  
 Thr Leu Phe Asn Leu Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg  
 225 230 235  
 10 Asp Leu Ser Lys Met Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala  
 245 250 255  
 Glu Phe Thr Pro Ser Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro  
 260 265 270  
 15 Gln Ile Ala Gln Asp Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly  
 275 280 285  
 Leu Ser Ala Gly Val Gly Phe Thr Ser Gly Val Val Arg Val Gly Val  
 290 295 300  
 Ser Ala Ala Thr Tyr His Pro Ala Ala Leu Ser Phe Met Cys Ser Val  
 305 310 315 320  
 20 Gly Ile Arg Leu Asp Asp Lys Ser Ile Phe  
 325 330

(2) INFORMATION FOR SEQ ID NO:475

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 324 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 35 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...324  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:475

Met Cys Leu Glu Pro Ile Ile Ala Pro Ile Ser Ser Glu Leu Leu Glu  
 1 5 10 15  
 45 Gln Glu Leu Thr Ala Asp Arg Phe Leu Arg Met Thr Asn Lys Ala Gly  
 20 25 30  
 Asn Glu Ile Tyr Val Phe Thr Ala Glu Glu Ala Pro His Cys Met Lys  
 35 40 45  
 50 Glu Val Gly Arg Leu Arg Glu Glu Ala Phe Arg His Tyr Gly Gly Gly  
 50 55 60  
 Thr Gly Lys Ala Ile Asp Ile Asp Glu Phe Asp Thr Met Pro Gly Ser  
 65 70 75 80  
 Tyr Lys Gln Leu Ile Val Trp Asp Pro Gln Asn Lys Ala Ile Leu Gly  
 85 90 95  
 55 Gly Tyr Arg Phe Ile Tyr Gly Arg Asp Val Ala Phe Asp Thr Asp Gly  
 100 105 110  
 Lys Pro Leu Leu Ala Thr Ala Glu Met Phe Arg Phe Ser Asp Ala Phe  
 115 120 125  
 60 Leu His Asp Tyr Leu Pro Tyr Thr Val Glu Leu Gly Arg Ser Phe Val  
 130 135 140  
 Ser Leu Gln Tyr Gln Ser Thr Arg Met Gly Thr Lys Ala Ile Phe Val  
 145 150 155 160  
 Leu Asp Asn Leu Trp Asp Gly Ile Gly Ala Leu Thr Val Val Asn Pro  
 165 170 175  
 65 Glu Ala Leu Tyr Phe Tyr Gly Lys Val Thr Met Tyr Lys Asp Tyr Asp  
 180 185 190  
 Arg Arg Ala Arg Asn Leu Ile Leu Tyr Phe Leu Arg Lys His Phe Ser  
 195 200 205  
 70 Asp Pro Glu Gly Leu Val Lys Pro Ile His Pro Leu Pro Ile Glu Ile  
 210 215 220  
 Ser Ala Glu Asp Glu Ala Leu Phe Ser Ser Ser Asp Phe Asp Thr Asn  
 225 230 235 240  
 Tyr Lys Thr Leu Asn Ile Glu Val Arg Lys Leu Gly Ile Asn Ile Pro  
 245 250 255  
 75 Pro Leu Val Ser Ala Tyr Ile Ala Leu Ser Pro Glu Met Arg Val Phe

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424/ 490

260 265 270  
 Gly Thr Ala Val Asn Glu Ser Phe Gly Glu Val Glu Glu Thr Gly Ile  
 275 280 285  
 Phe Ile Ala Val Gly Lys Ile Leu Glu Glu Lys Lys Gln Arg His Ile  
 290 295 300  
 Glu Ser Phe Ile Leu Ser Arg Asn Glu Lys Lys Gly Leu Asp Ser Ser  
 305 310 315 320  
 Asn Gly Arg Ser

10 (2) INFORMATION FOR SEQ ID NO:476  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 547 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...547  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:476

Met Lys Thr Ile Val Arg Tyr Ser Arg Leu Pro Val Ala Leu Phe Phe  
 1 5 10 15  
 Cys Leu Leu Gly Ala Val His Leu Ser Val Glu Ala Gln Met Leu Asn  
 20 25 30  
 Thr Pro Phe Glu Leu Ser Asp Gln Ile Val Leu Ser Pro Thr Glu Arg  
 35 40 45  
 Gln Tyr Arg Glu Ile Cys Val Gln Thr Lys Glu Lys Arg Gly Ala Asp  
 50 55 60  
 Leu Phe Pro Leu Ser Asp Lys Leu Arg Asp Ser Ala Tyr Val Arg Phe  
 65 70 75 80  
 Gly Ser Ala Tyr Gly Asp Ile Ala Gly Asp Tyr Leu Pro Tyr Asn Gly  
 85 90 95  
 Asn Asn Tyr Ser Ser Leu Ser Leu Glu Ser Gly Gly Arg Ile Ser Val  
 100 105 110  
 Arg Asn Tyr Gly Thr Leu Gln Gly Ser Ala Ser Tyr Ser Arg Gly Met  
 115 120 125  
 His Lys Arg Ile Gly Trp Asn Ala Leu Arg Asn Ala Glu Ala Tyr Tyr  
 130 135 140  
 Pro Tyr Leu Val Ser Asp Ser Thr Gly Gly Asp Tyr His Phe Glu Asp  
 145 150 155 160  
 Tyr Arg Leu Ala Gly Tyr Tyr Ser Phe Arg Ala Gly Arg Leu Pro Leu  
 165 170 175  
 Gly Ile Gly Phe Ser Tyr Arg Gly Glu Val Ala Tyr Arg Leu Thr Asp  
 180 185 190  
 Pro Arg Thr Thr Asn Thr Thr Gly Ala Leu Glu Leu Ser Cys Ala Thr  
 195 200 205  
 Ser Leu Thr Leu Pro Arg Glu Asn Arg Leu Ser Leu Ser Ala Ala Tyr  
 210 215 220  
 Leu Tyr His Arg Gln His Leu Thr Gln Tyr Asn Trp Arg Pro Gly Gln  
 225 230 235 240  
 Gln Asp Lys Phe Phe Val Ser Tyr Gly Phe Gly Gln Val Asp Val Ser  
 245 250 255  
 Asn Ser Pro Ile Trp Phe Gly Ile Ser Arg Met Asn Tyr Val Asn Gly  
 260 265 270  
 Trp Lys Leu Ser Ser Arg Leu Asp Thr Arg Arg Gly Asp Ala Ile Gly  
 275 280 285  
 Leu Asp Tyr Ser Gly Tyr Phe Leu Asp Thr Glu Glu Arg Ser Ser Ile  
 290 295 300  
 Asn Leu Phe Ala Leu Leu Tyr Asn Arg Leu Arg Leu Tyr Gly Ser Trp  
 305 310 315 320  
 His Leu Ser Asp Phe Asp Phe Ser Phe Ser Ala Asp Tyr Ala Leu Arg  
 325 330 335  
 Gln Gly Ile Glu Arg Ile Tyr Glu Asp Tyr Lys Pro Asp Asn Tyr  
 340 345 350  
 His Ile Tyr Asp Leu Arg Ile Leu Ala Ile Arg Arg Trp Tyr Met Leu

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355 360 365  
 Asn Glu Phe Ser Ala Gln Ala Gln Ala Ser Tyr Arg Ile Arg Thr Asp  
 370 375 380  
 5 Arg Gly Cys Ala Leu Arg Val Ser Ala Gly Ser Asp Phe Tyr Gly Tyr  
 385 390 395 400  
 Asp Glu Thr Tyr Arg Lys His Gly His His Thr Met Ser Gly Met Leu  
 405 410 415  
 Arg Pro Phe Ala Gly Ile Ala Tyr Asp His Ala Gly Ser Lys Leu Asp  
 420 425 430  
 10 Phe Gly Leu Ser Leu Ser Ala Ala Tyr Arg Met Val Leu Thr His Ser  
 435 440 445  
 Tyr Lys Ile Arg Thr Ile Gln Lys Glu Gln Leu Asp Tyr Gln Leu Ala  
 450 455 460  
 15 Tyr Leu Pro Tyr Ala Tyr Arg Asn Arg Glu Gly Val Glu Val Arg Ser  
 465 470 475 480  
 Ser Leu Tyr Val Ser Ile Pro Met Gln Asn Thr His Arg Leu Met Thr  
 485 490 495  
 Glu Leu Arg Leu Tyr Gly Asp Leu Met Lys Arg Lys Asp Gly Ile Ala  
 500 505 510  
 20 Tyr Gly Lys Thr Pro Gly Val Ile Ser His Ile Leu Ser Asp Pro Gln  
 515 520 525  
 Ala Glu Arg Thr Ser Gly His Thr Ile Gly Ala Ile Cys Asn Ile Ser  
 530 535 540  
 25 Tyr Leu Phe  
 545

(2) INFORMATION FOR SEQ ID NO:477

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 750 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 35 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 40 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...750  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:477

Met Lys Lys Leu His Met Ile Ala Ala Leu Ala Val Leu Pro Phe Cys  
 1 5 10 15  
 50 Leu Thr Ala Gln Ala Pro Val Ser Asn Ser Glu Ile Asp Ser Leu Ser  
 20 25 30  
 Asn Val Gln Leu Gln Thr Val Gln Val Val Ala Thr Arg Ala Thr Ala  
 35 40 45  
 Lys Thr Pro Val Ala Tyr Thr Asn Val Arg Lys Ala Glu Leu Ser Lys  
 50 55 60  
 55 Ser Asn Tyr Gly Arg Asp Ile Pro Tyr Leu Leu Met Leu Thr Pro Ser  
 65 70 75 80  
 Val Val Ala Thr Ser Asp Ala Gly Thr Gly Ile Gly Tyr Ser Gly Phe  
 85 90 95  
 60 Arg Val Arg Gly Thr Asp Ala Asn Arg Ile Asn Ile Thr Thr Asn Gly  
 100 105 110  
 Val Pro Leu Asn Asp Ser Glu Ser Gln Ser Val Phe Trp Val Asn Met  
 115 120 125  
 Pro Asp Phe Ala Ser Ser Ile Glu Asp Leu Gln Val Gln Arg Gly Val  
 130 135 140  
 65 Gly Thr Ser Thr Asn Gly Ala Gly Ala Phe Gly Ala Ser Val Asn Met  
 145 150 155 160  
 Arg Thr Asp Asn Leu Gly Leu Ala Pro Tyr Gly Arg Val Asp Leu Ser  
 165 170 175  
 70 Gly Gly Ser Phe Gly Thr Phe Arg Arg Ser Val Lys Leu Gly Ser Gly  
 180 185 190  
 Arg Ile Gly Arg His Trp Ala Val Asp Ala Arg Leu Ser Lys Ile Gly  
 195 200 205  
 Ser Asp Gly Tyr Val Asp Arg Gly Ser Val Asp Leu Lys Ser Tyr Phe  
 210 215 220  
 75 Ala Gln Val Gly Tyr Phe Gly Ser Asn Thr Ala Leu Arg Phe Ile Thr

SUBSTITUTE SHEET (Rule 26) (RO/AU)

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[illegible]

(2) INFORMATION FOR SEQ ID NO:478

70 (1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 494 amino acids  
(B) TYPE: amino acid  
(C) TOPOLOGY: linear

75 (11) MOLECULE TYPE: protein



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(111) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...494

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478

5 Met Lys Arg Arg Phe Leu Ser Leu Leu Leu Tyr Ile Leu Ser Ser  
 1 5 10 15  
 15 Ile Ser Asn Ser Ala Gln Arg Phe Pro Met Val Gln Gly Ile Glu Leu  
 20 20 25 30  
 Asp Thr Asp Ser Leu Phe Ser Leu Pro Lys Arg Pro Trp Arg Ala Ile  
 35 40 45  
 Gly Lys Thr Ile Gly Val Asn Leu Ala Val Trp Gly Phe Asp His Phe  
 50 55 60  
 20 Ile Met Asn Glu Asp Phe Ala Asp Ile Ser Trp Gln Thr Ile Lys Ser  
 65 70 75 80  
 Asn Phe Gln Thr Gly Phe Gly Trp Asp Asn Asp Lys Phe Val Thr Asn  
 85 90 95  
 25 Leu Phe Ala His Pro Tyr His Gly Ser Leu Tyr Phe Asn Ala Ala Arg  
 100 105 110  
 Ser Asn Gly Leu Ser Phe Arg His Ser Ala Pro Phe Ala Phe Gly  
 115 120 125  
 Ser Leu Met Trp Glu Leu Leu Met Glu Asn Glu Pro Pro Ser Ile Asn  
 130 135 140  
 30 Asp Leu Cys Ala Thr Thr Ile Gly Gly Ile Ala Leu Gly Glu Met Gly  
 145 150 155 160  
 His Arg Leu Ser Asp Leu Leu Ile Asp Asn Arg Thr Thr Gly Trp Glu  
 165 170 175  
 Arg Met Gly Arg Glu Val Ala Ile Ala Leu Ile Asn Pro Met Arg Phe  
 180 185 190  
 35 Leu Asn Arg Leu Thr Ala Gly Glu Val Thr Ser Val Gly Ser Arg Ser  
 195 200 205  
 Gly Gln Ile Phe Gln Ser Val Pro Ile Asn Ile Val Val Asp Ala Gly  
 210 215 220  
 40 Phe Arg Phe Leu Ala Asp Lys Arg His Ala Arg Thr Gly Ala Thr Ala  
 225 230 235 240  
 Leu Thr Leu Asn Leu Arg Phe Asp Tyr Gly Asp Pro Phe Arg Ser Glu  
 245 250 255  
 Thr Phe Ser Pro Tyr Asp Phe Phe Gln Phe Lys Ala Gly Leu Ser Phe  
 260 265 270  
 45 Ser Glu Ser Gln Pro Leu Leu Ser Gln Ile Asn Leu Ile Gly Ile Leu  
 275 280 285  
 Ser Gly Cys Gln Leu Leu Ala His Glu Arg Thr Val Leu Val Gly Gly  
 290 295 300  
 50 Leu Phe Gln His Phe Asp Tyr Tyr Asn Ser Glu Lys Arg Ile Ser Lys  
 305 310 315 320  
 Asn Ser Glu Glu Val Leu Val Thr Pro Tyr Arg Ile Ser Gln Val Ala  
 325 330 335  
 55 Ala Leu Gly Gly Gly Leu Ile Phe Gln His His Gly Lys Phe Arg Arg  
 340 345 350  
 Arg Pro Leu Glu Leu Tyr Ala Glu Thr Tyr Leu Asn Val Val Pro Met  
 355 360 365  
 Gly Ala Ser Leu Ser Asp His Tyr Asn Val Asp Asn Arg Asp Tyr Asn  
 370 375 380  
 60 Leu Gly Ser Gly Leu Ser Gly Lys Leu Tyr Leu Gly Ala Thr Tyr Asn  
 385 390 395 400  
 Asp Leu Trp Ser Trp Leu Leu Gly Val Glu Ser Tyr Arg Leu Tyr Thr  
 405 410 415  
 Trp Ile Gly Tyr Glu Glu Pro His Gln Lys Asn Thr Asp Val Ser Ser  
 420 425 430  
 65 Phe Met Val Gln Gly Asp Glu Ser Lys Ala Arg Leu Leu Val Thr Ser  
 435 440 445  
 Ser Glu Phe Ala Phe His Pro Gly Pro Trp His Val Ala Ile Val Ala  
 450 455 460  
 70 Arg Arg Phe Ile Arg Lys Thr Ala Tyr Gln Phe Tyr Pro Asn Val Ser  
 465 470 475 480  
 Phe Asp Thr Gly Asp Ile Gln Leu Arg Val Gly Phe His Phe  
 485 490

75 (2) INFORMATION FOR SEQ ID NO:479

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 294 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479

Met Lys Arg Leu Ile Val Phe Leu Ala Met Gly Gly Leu Leu Phe Thr  
 1 5 10 15  
 Leu Ala Asn Ala Gln Glu Ala Asn Thr Ala Ser Asp Thr Pro Lys Lys  
 20 25 30  
 Asp Trp Thr Ile Lys Gly Val Thr Gly Leu Asn Ala Ser Gln Thr Ser  
 35 40 45  
 Leu Thr Asn Trp Ala Ala Gly Gly Glu Asn Thr Val Ala Gly Asn Leu  
 50 55 60  
 Tyr Leu Asn Ile Asp Ala Asn Tyr Leu Lys Asp Lys Trp Ser Trp Asp  
 65 70 75 80  
 Asn Gly Leu Arg Thr Asp Phe Gly Leu Thr Tyr Thr Thr Ala Asn Lys  
 85 90 95  
 Trp Asn Lys Ser Val Asp Lys Ile Glu Leu Phe Thr Lys Ala Gly Tyr  
 100 105 110  
 Glu Ile Gly Lys His Trp Tyr Gly Ser Ala Leu Phe Thr Phe Leu Ser  
 115 120 125  
 Gln Tyr Ala Lys Gly Tyr Glu Lys Pro Ser Asp His Leu Thr Gly Val  
 130 135 140  
 Lys His Ile Ser Asn Phe Phe Ala Pro Ala Tyr Leu Thr Leu Gly Ile  
 145 150 155 160  
 Gly Ala Asp Tyr Lys Pro Asn Glu Lys Phe Ser Leu Tyr Leu Ser Pro  
 165 170 175  
 Thr Thr Gly Lys Leu Thr Val Val Ala Asp Asp Tyr Leu Ser Ser Leu  
 180 185 190  
 Gly Ala Phe Gly Val Lys Val Gly Glu Lys Thr Met Phe Glu Leu Gly  
 195 200 205  
 Ala Leu Val Val Gly Ser Ala Asn Ile Asn Leu Met Glu Asn Val Asn  
 210 215 220  
 Leu Ile Thr Lys Ala Ser Phe Phe Ser Ala Tyr Thr His Asp Phe Gly  
 225 230 235 240  
 Asn Ile Asp Ile Asn Trp Glu Ala Met Leu Ala Met Lys Ile Asn Lys  
 245 250 255  
 Phe Leu Thr Ala Thr Ile Ala Thr Asn Leu Ile Tyr Asp Asp Asp Val  
 260 265 270  
 Lys Ile Asn Asp Gly Pro Lys Ile Gln Phe Lys Glu Val Val Gly Val  
 275 280 285  
 Gly Val Ala Tyr Thr Phe  
 290

(2) INFORMATION FOR SEQ ID NO:480

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 204 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...204

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## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:480

5 Met Lys Lys Met Ile Leu Ala Ala Thr Met Leu Leu Ala Thr Ile Gly  
 1 5 10 15  
 Phe Ala Asn Ala Gln Ser Arg Pro Ala Leu Arg Leu Asp Ala Asn Phe  
 20 25 30  
 Val Gly Ser Asn Leu Met Gln Lys Val Ala Asn Thr Ser Val Asn Asn  
 35 40 45  
 10 Lys Met Ile Val Gly Leu Arg Val Gly Ala Ala Ala Glu Phe Ala Leu  
 50 55 60  
 Ser Asn Asp Gly Phe Tyr Leu Ala Pro Gly Leu Ala Tyr Thr Met Arg  
 65 70 75 80  
 15 Gly Ala Lys Met Glu Ser Leu Ser Glu Thr Thr Thr Arg Leu His Tyr  
 85 90 95  
 Leu Gln Ile Pro Val Asn Ala Gly Met Arg Phe Ser Phe Ala Asp Asn  
 100 105 110  
 Met Ala Ile Ser Leu Glu Ala Gly Pro Tyr Phe Ala Tyr Gly Val Ala  
 115 120 125  
 20 Gly Thr Ile Lys Thr Lys Val Ala Gly Val Thr Ala Ser Val Asp Ala  
 130 135 140  
 Phe Gly Asp Asn Gly Tyr Asn Arg Phe Asp Leu Gly Leu Gly Leu Ser  
 145 150 155 160  
 25 Ala Ala Leu Ser Tyr Asp Arg Tyr Tyr Val Gln Ile Gly Tyr Glu His  
 165 170 175  
 Gly Leu Leu Asn Met Leu Lys Asp Ala Pro Asp Lys Thr Ser Leu Arg  
 180 185 190  
 Asn His Asp Phe Phe Val Gly Leu Gly Val Arg Phe  
 195 200

## (2) INFORMATION FOR SEQ ID NO:481

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...243

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:481

50 Met Lys Arg Ile Phe Thr Val Ala Leu Val Leu Leu Ala Ser Val Thr  
 1 5 10 15  
 Met Ala Ile Gly Gln Ser Arg Pro Ala Leu Arg Val Asp Ala Asn Phe  
 20 25 30  
 55 Val Gly Ser Asn Gln Ser Met Lys Arg Asp Gly Tyr Val Trp Asp Thr  
 35 40 45  
 Lys Met Asn Val Gly Leu Arg Val Gly Ala Ala Ala Glu Phe Met Ile  
 50 55 60  
 60 Gly Ser Arg Gly Phe Tyr Leu Ala Pro Gly Leu Asn Tyr Thr Met Lys  
 65 70 75 80  
 Gly Ser Lys Thr Glu Trp Asp Ile Pro Glu Met Val Pro Gly Thr Tyr  
 85 90 95  
 Ile Thr Met Val Ser Thr Arg Leu His Tyr Leu Gln Leu Pro Ile Asn  
 100 105 110  
 65 Ala Gly Met Arg Phe Asp Leu Met Asn Asp Met Ala Val Ser Ile Glu  
 115 120 125  
 Ala Gly Pro Phe Leu Ala Tyr Gly Ile Tyr Gly Thr Tyr Arg Gln Lys  
 130 135 140  
 70 Leu Glu Gly Trp Lys Pro Asn Asn Tyr Ser Thr Glu Phe Phe Gly Pro  
 145 150 155 160  
 Thr Leu Gly Gly Pro Thr Asn Ile Arg Trp Asp Ile Gly Ala Asn Ile  
 165 170 175  
 Ile Ala Ala Phe His Tyr Lys Arg Tyr Tyr Ile Gln Ile Gly Tyr Glu  
 180 185 190  
 75 His Gly Phe Val Asp Ile Val Ser Gly Gly Gly Ser Asp Ile Pro Arg



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Met Arg Val Ser Asp Leu Cys Ser Arg Leu Ser Trp Leu Leu Pro Val  
1 5 10 15  
Ile Leu Val Gly Leu Leu Cys Ala Thr Leu Val Ala Ala Glu Arg Pro  
20 25 30  
5 Met Ala Gly Ala Val Gly Leu His His Arg Arg His Ala Ala Leu Ser  
35 40 45  
Asp Ser Thr Ala Lys Asp Thr Val Pro Leu Ala Lys Pro Ile Pro Asp  
50 55 60  
10 Ser Ala Phe Arg Asp Ser Leu Pro Ala Asp Ser Thr Gly Ser Met Arg  
65 70 75 80  
Gln Asp Ser Val Tyr Asp Asp Glu Phe Glu Leu Glu Asp Ile Val Glu  
85 90 95  
Tyr Glu Ala Ala Asp Ser Ile Val Leu Leu Gly Gln Asn Arg Ala Tyr  
100 105 110  
15 Leu Phe Gly Lys Ser Tyr Val Ser Tyr Gln Lys Ser Arg Leu Glu Ala  
115 120 125  
Asn Phe Met Tyr Leu Asn Thr Asp Ser Ser Thr Val Tyr Thr Arg Tyr  
130 135 140  
20 Val Leu Asp Thr Ala Gly Tyr Pro Met Ala Phe Pro Val Phe Lys Asp  
145 150 155 160  
Gly Glu Gln Ser Phe Glu Ala Lys Asn Phe Thr Tyr Asn Phe Arg Thr  
165 170 175  
Glu Lys Gly Ile Ile Ser Gly Val Ile Thr Gln Gln Gly Glu Gly Tyr  
180 185 190  
25 Leu Thr Ala Gly Lys Thr Lys Lys Met Pro Asp Asn Ile Met Phe Met  
195 200 205  
Gln Gly Gly Arg Tyr Thr Thr Cys Asp Asn His Asp His Pro His Phe  
210 215 220  
30 Tyr Ile Asn Leu Ser Lys Ala Lys Val His Pro Glu Lys Asp Ile Val  
225 230 235 240  
Thr Gly Pro Val Asn Leu Val Ile Ala Asp Met Pro Leu Pro Ile Gly  
245 250 255  
Leu Pro Phe Gly Tyr Phe Pro Phe Ser Asn Lys Tyr Ser Ser Gly Ile  
260 265 270  
35 Leu Met Pro Thr Tyr Gly Glu Asp Asn Arg Tyr Gly Phe Tyr Leu Arg  
275 280 285  
Asn Gly Gly Tyr Tyr Phe Ala Phe Ser Asp Tyr Ile Asp Leu Ala Leu  
290 295 300  
40 Arg Gly Glu Ile Phe Ser Lys Gly Ser Trp Gly Ile Ser Ala Gln Ser  
305 310 315 320  
Lys Tyr Lys Lys Arg Tyr Lys Tyr Asn Gly Ser Phe Glu Ala Asn Tyr  
325 330 335  
Leu Val Ser Lys Ser Gly Asp Lys Tyr Val Pro Gly Asp Tyr Ser Lys  
340 345 350  
45 Thr Thr Ser Leu Asn Ile Arg Trp Thr His Ser Gln Asp Pro Lys Ala  
355 360 365  
Asn Pro Leu Gln Thr Leu Ser Ala Asn Val Asn Phe Ala Thr Gly Ser  
370 375 380  
50 Tyr Phe Gln Asn Ser Leu Asn Thr Thr Tyr Asp Val Asn Ala Arg Thr  
385 390 395 400  
Ala Thr Thr Arg Ser Ser Ala Val Ser Tyr Ser Arg Lys Phe Pro Gly  
405 410 415  
Thr Pro Phe Ser Ile Thr Gly Ser Met Asp Ile Ser Gln Asn Met Arg  
420 425 430  
55 Asp Thr Thr Val Ser Leu Thr Leu Pro Asn Leu Ser Ile Asn Met Ser  
435 440 445  
Thr Arg Tyr Pro Phe Lys Arg Lys Thr Arg Val Gly Pro Glu Arg Trp  
450 455 460  
60 Tyr Glu Lys Leu Ser Val Gly Tyr Ser Gly Gln Leu Arg Asn Ser Ile  
465 470 475 480  
Leu Thr Lys Glu Lys Asp Leu Leu Gln Ser Asn Leu Val Arg Asp Trp  
485 490 495  
Lys Asn Gly Met Arg His Ser Val Pro Ile Ser Leu Thr Val Pro Leu  
500 505 510  
65 Leu Asp Tyr Ile Asn Leu Thr Met Gly Val Asn Tyr Asn Glu Trp Trp  
515 520 525  
Tyr Thr Lys Gly Ile Arg Lys Ser Trp Asn Glu Asp Lys Lys Thr Phe  
530 535 540  
70 Leu Pro Ser Asp Thr Tyr Lys Phe Arg Arg Leu Tyr Asp Tyr Ser  
545 550 555 560  
Leu Ser Ala Gly Leu Ser Thr Thr Leu Tyr Gly Met Phe Lys Pro Trp  
565 570 575  
Lys Pro Phe Ser Phe Gly Gly Asn Leu Ile Met Ile Arg His Arg Phe  
580 585 590  
75 Thr Pro Thr Val Ser Phe Ser Tyr Met Pro Asp Phe Thr Lys Arg Arg

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595 600 605  
 Tyr Gly Phe Trp Glu Leu Leu Glu His Thr Asp Gln Asn Gly Lys Leu  
 610 615 620  
 5 His Thr Leu Leu Tyr Ser Pro Tyr Phe Glu Gln Ile Phe Gly Ala Pro  
 625 630 635 640  
 Ser Met Gly Asn Ala Gly Ser Val Asn Phe Ser Phe Asp Asn Asn Leu  
 645 650 655  
 Glu Ala Lys Ile Lys Ser Lys Ser Asp Ser Thr Gly Ile Lys Lys Ile  
 660 665 670  
 10 Ser Leu Ile Asp Gln Phe Thr Trp Ser Thr Ser Tyr Asn Met Phe Ala  
 675 680 685  
 Asp Ser Ile Arg Trp Ser Asn Ile Ser Ala Ser Leu Ala Leu Arg Leu  
 690 695 700  
 15 Ser Lys Ser Phe Thr Leu Arg Leu Ser Gly Leu Phe Asp Pro Tyr Leu  
 705 710 715 720  
 Thr Lys Tyr Tyr Glu Gly Glu Asp Gly Lys Ile Ile Pro Tyr Lys Ser  
 725 730 735  
 Asn Asp Leu Arg Ile Phe Asn Gly Lys Gly Leu Ala Arg Leu Ile Ser  
 740 745 750  
 20 Thr Gly Thr Ser Phe Ser Tyr Thr Leu Asn Lys Glu Ser Leu Ser Gly  
 755 760 765  
 Leu Ile Ala Leu Phe Ser Gly Lys Lys Glu Arg Arg Asp Glu Lys Lys  
 770 775 780  
 25 Asn Thr Gly Ala Thr Pro His Glu Gly Asp Asp Ala Ala Asp Ile Leu  
 785 790 795 800  
 Glu Gly Gly Arg Pro Gln Asn Glu Ser Gly Gly Ser Leu Leu Glu Arg  
 805 810 815  
 Asn Arg Gln Gly Gly Ala Val Asp Gln Asp Gly Tyr Phe Ala Tyr Ser  
 820 825 830  
 30 Ile Pro Trp Ser Leu Ser Phe Asp Tyr Ser Trp Asn Ile Ala Thr Asp  
 835 840 845  
 Tyr Asn Arg Tyr Asn Val Asn Lys Met Glu His Tyr Tyr Arg Val Thr  
 850 855 860  
 35 Gln Asn Leu Ser Phe Arg Gly Asn Ile Gln Pro Thr Pro Asn Trp Ser  
 865 870 875 880  
 Phe Gly Phe Asn Ala Asn Tyr Asn Phe Asp Leu Lys Lys Ile Thr Ser  
 885 890 895  
 Leu Thr Cys Asn Val Thr Arg Asp Met His Cys Trp Ala Ile Ser Ala  
 900 905 910  
 40 Ser Phe Ile Pro Ile Gly Ala Tyr Lys Ser Tyr Asn Phe Val Ile Ser  
 915 920 925  
 Val Lys Ser Ser Leu Leu Gln Asp Leu Lys Tyr Gln Gln Ser Asn Arg  
 930 935 940  
 45 Pro Ile Thr Asn Thr Trp Tyr  
 945 950

(2) INFORMATION FOR SEQ ID NO:484

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1226 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 55 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 60 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...1226  
 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:484

Met Met Lys Arg Tyr Thr Ile Ile Leu Ala Val Phe Leu Leu Phe Cys  
 1 5 10 15  
 70 Thr Val Phe Thr Phe Gln Ile Lys Ala Arg Pro Tyr-Glu Arg Phe Ala  
 20 25 30  
 Asp Val Glu Lys Pro Trp Ile Gln Lys His Ser Met Asp Ser Lys Leu  
 35 40 45  
 Val Pro Ala Asn Lys Gly Asn Leu Ile Gln Ala Glu Ile Val Tyr Gln  
 50 55 60  
 75 Ser Val Ser Glu His Ser Asp Leu Val Ile Ser Pro Val Asn Glu Ile



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Ser Glu Trp Asp Val Thr Ser Asn Trp Thr Gly Ala Gln Val Pro Leu  
 675 680 685  
 Thr Gly Glu Asp Val Glu Phe Ala Thr Thr Glu Asn Phe Gly Ser Pro  
 690 695 700  
 5 Ala Val Ala Asp Leu His Val Pro Thr Thr Asn Pro Lys Ile Ile Gly  
 705 710 715 720  
 Asn Leu Ile Asn Asn Ser Asp Lys Asp Leu Val Val Thr Thr Ser Ser  
 725 730 735  
 10 Gln Leu Thr Ile Asn Gly Val Val Glu Asp Asn Asn Pro Asn Val Gly  
 740 745 750  
 Thr Ile Val Val Lys Ser Ser Lys Asp Asn Pro Thr Gly Thr Leu Leu  
 755 760 765  
 Phe Ala Asn Pro Gly Tyr Asn Gln Asn Val Gly Gly Thr Val Glu Phe  
 770 775 780  
 15 Tyr Asn Gln Gly Tyr Asp Cys Ala Asp Cys Gly Met Tyr Arg Arg Ser  
 785 790 795 800  
 Trp Gln Tyr Phe Gly Ile Pro Val Asn Glu Ser Gly Phe Pro Ile Asn  
 805 810 815  
 20 Asp Val Gly Gly Asn Glu Thr Val Asn Gln Trp Val Glu Pro Phe Asn  
 820 825 830  
 Gly Asp Lys Trp Arg Pro Ala Pro Tyr Ala Pro Asp Thr Glu Leu Gln  
 835 840 845  
 Lys Phe Lys Gly Tyr Gln Ile Thr Asn Asp Val Gln Ala Gln Pro Thr  
 850 855 860  
 25 Gly Val Tyr Ser Phe Lys Gly Met Ile Cys Val Cys Asp Ala Phe Leu  
 865 870 875 880  
 Asn Leu Thr Arg Thr Ser Gly Val Asn Tyr Ser Gly Ala Asn Leu Ile  
 885 890 895  
 30 Gly Asn Ser Tyr Thr Gly Ala Ile Asp Ile Lys Gln Gly Ile Val Phe  
 900 905 910  
 Pro Pro Glu Val Glu Gln Thr Val Tyr Leu Phe Asn Thr Gly Thr Arg  
 915 920 925  
 Asp Gln Trp Arg Lys Leu Asn Gly Ser Thr Val Ser Gly Tyr Arg Ala  
 930 935 940  
 35 Gly Gln Tyr Leu Ser Val Pro Lys Asn Thr Ala Gly Gln Asp Asn Leu  
 945 950 955 960  
 Pro Asp Arg Ile Pro Ser Met His Ser Phe Leu Val Lys Met Gln Asn  
 965 970 975  
 40 Gly Ala Ser Cys Thr Leu Unk Ile Leu Tyr Asp Lys Leu Leu Lys Asn  
 980 985 990  
 Thr Thr Val Asn Asn Gly Asn Gly Thr Gln Ile Thr Trp Arg Ser Gly  
 995 1000 1005  
 Asn Ser Gly Ser Ala Asn Met Pro Ser Leu Val Met Asp Val Leu Gly  
 1010 1015 1020  
 45 Asn Glu Ser Ala Asp Arg Leu Trp Ile Phe Thr Asp Gly Gly Leu Ser  
 1025 1030 1035 1040  
 Phe Gly Phe Asp Asn Gly Trp Asp Gly Arg Lys Leu Thr Glu Lys Gly  
 1045 1050 1055  
 Leu Ser Gln Leu Tyr Ala Met Ser Asp Ile Gly Asn Asp Lys Phe Gln  
 1060 1065 1070  
 50 Val Ala Gly Val Pro Glu Leu Asn Asn Leu Leu Ile Gly Phe Asp Ala  
 1075 1080 1085  
 Asp Lys Asp Gly Gln Tyr Thr Leu Glu Phe Ala Leu Ser Asp His Phe  
 1090 1095 1100  
 55 Ala Lys Gly Ala Val Tyr Leu His Asp Leu Gln Ser Gly Ala Lys His  
 1105 1110 1115 1120  
 Arg Ile Thr Asn Ser Thr Ser Tyr Ser Phe Asp Ala Lys Arg Gly Asp  
 1125 1130 1135  
 60 Ser Gly Ala Arg Phe Arg Leu Ser Tyr Gly Cys Asp Glu Asn Val Asp  
 1140 1145 1150  
 Asp Ser His Val Val Ser Thr Asn Gly Arg Glu Ile Ile Ile Leu Asn  
 1155 1160 1165  
 Gln Asp Ala Leu Asp Cys Thr Val Thr Leu Phe Thr Ile Glu Gly Lys  
 1170 1175 1180  
 65 Leu Leu Arg Arg Leu Lys Val Leu Ala Gly His Arg Glu Val Met Lys  
 1185 1190 1195 1200  
 Val Gln Thr Gly Gly Ala Tyr Ile Val His Leu Gln Asn Ala Phe Thr  
 1205 1210 1215  
 70 Asn Asp Val His Lys Val Leu Val Glu Tyr  
 1220 1225

(2) INFORMATION FOR SEQ ID NO:485

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1225 amino acids



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(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...1225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485

Met	Lys	Arg	Tyr	Thr	Ile	Ile	Leu	Ala	Val	Phe	Leu	Leu	Phe	Cys	Thr
1				5					10					15	
Val	Phe	Thr	Phe	Gln	Ile	Lys	Ala	Arg	Pro	Tyr	Glu	Arg	Phe	Ala	Asp
			20				25						30		
Val	Glu	Lys	Pro	Trp	Ile	Gln	Lys	His	Ser	Met	Asp	Ser	Lys	Leu	Val
		35				40					45				
Pro	Ala	Asn	Lys	Gly	Asn	Leu	Ile	Gln	Ala	Glu	Ile	Val	Tyr	Gln	Ser
	50				55					60					
Val	Ser	Glu	His	Ser	Asp	Leu	Val	Ile	Ser	Pro	Val	Asn	Glu	Ile	Arg
65				70					75					80	
Pro	Ala	Asn	Arg	Phe	Pro	Ser	His	Arg	Lys	Ser	Phe	Phe	Ala	Glu	Asn
		85						90					95		
Leu	Arg	Ala	Ser	Pro	Pro	Val	Val	Pro	Val	Ala	Val	Asp	Lys	Tyr	Ala
		100						105					110		
Val	Pro	Val	Ala	Asn	Pro	Met	Asp	Pro	Glu	Asn	Pro	Asn	Ala	Trp	Asp
	115					120						125			
Val	Thr	Leu	Lys	Ile	Thr	Thr	Lys	Ala	Val	Thr	Val	Pro	Val	Asp	Val
	130				135					140					
Val	Met	Val	Ile	Asp	Gln	Ser	Ser	Met	Gly	Gly	Gln	Asn	Ile	Ala	
145				150					155					160	
Arg	Leu	Lys	Ser	Ala	Ile	Ala	Ser	Gly	Gln	Arg	Phe	Val	Lys	Lys	Met
		165						170					175		
Leu	Pro	Lys	Gly	Thr	Ala	Thr	Glu	Gly	Val	Arg	Ile	Ala	Leu	Val	Ser
	180						185						190		
Tyr	Asp	His	Glu	Pro	His	Arg	Leu	Ser	Asp	Phe	Thr	Lys	Asp	Thr	Ala
	195						200					205			
Phe	Leu	Cys	Gln	Lys	Ile	Arg	Ala	Leu	Thr	Pro	Ile	Trp	Gly	Thr	His
	210				215						220				
Thr	Gln	Gly	Gly	Leu	Lys	Met	Ala	Arg	Asn	Ile	Met	Ala	Thr	Ser	Thr
225				230					235				240		
Ala	Val	Asp	Lys	His	Ile	Ile	Leu	Met	Ser	Asp	Gly	Leu	Ala	Thr	Glu
	245						250						255		
Gln	Tyr	Pro	Val	Lys	Asn	Val	Thr	Thr	Ala	Asp	Phe	Ile	Gly	Lys	Thr
	260						265						270		
Gly	Asn	Ala	Asn	Asp	Pro	Ile	Asp	Leu	Val	Ile	Gln	Gly	Ala	Ile	Asn
	275					280						285			
Phe	Pro	Thr	Asn	Tyr	Val	Ser	Asn	Asn	Pro	Ser	Thr	Pro	Leu	Thr	Pro
	290					295					300				
Asn	Tyr	Pro	Thr	His	Ser	Ser	Lys	Val	Gly	Arg	Arg	Asn	Leu	Pro	Glu
305				310					315				320		
Ser	Lys	Phe	Asp	Tyr	Ser	Asn	Leu	Ser	Ala	Arg	Ile	Thr	Phe	Asp	Gly
	325								330				335		
Val	Ala	Gly	Ala	Leu	Val	Tyr	Glu	Pro	Arg	Phe	Pro	His	Pro	Tyr	Tyr
	340						345						350		
Tyr	Tyr	Phe	Pro	Cys	Asn	Ala	Ala	Ile	Asn	Glu	Ala	Gln	Phe	Ala	Lys
	355					360						365			
Asn	Ser	Gly	Tyr	Thr	Ile	His	Thr	Ile	Gly	Tyr	Asp	Leu	Gly	Asp	Phe
	370				375						380				
Ala	Leu	Ala	Asn	Asn	Ser	Leu	Lys	Leu	Thr	Ala	Thr	Asp	Glu	Asn	His
385				390						395				400	
Phe	Phe	Thr	Ala	Thr	Pro	Ala	Asn	Leu	Ala	Ala	Ala	Phe	Asp	Asn	Ile
		405							410				415		
Ala	Gln	Thr	Ile	Asn	Ile	Gly	Ile	Gln	Arg	Gly	Glu	Val	Thr	Asp	Phe
	420						425						430		
Val	Ala	Pro	Gly	Phe	Ile	Val	Lys	Asn	Leu	Thr	Gln	Ser	Gly	Asp	Val
	435					440						445			
Thr	His	Leu	Leu	Asn	Val	Ser	Asn	Gly	Thr	Val	His	Tyr	Asp	Val	Ser
	450					455					460				
Thr	Lys	Lys	Leu	Thr	Trp	Thr	Thr	Gly	Thr	Ile	Leu	Ser	Ser	Ser	Glu

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465 470 475 480  
 Ala Thr Ile Thr Tyr Arg Ile Tyr Ala Asp Leu Asp Tyr Ile Gln Asn  
 485 490 495  
 Asn Asp Ile Pro Val Asn Thr Thr Ser Ala Ile Gly Pro Asp Leu Gly  
 500 505 510  
 Gly Phe Asp Thr Asn Thr Glu Ala Lys Leu Thr Tyr Thr Asn Ser Asn  
 515 520 525  
 Gly Glu Pro Asn Gln Gln Leu Ile Phe Pro Arg Pro Thr Val Lys Leu  
 530 535 540  
 10 Gly Tyr Gly Val Ile Lys Arg His Tyr Val Leu Val Asn Lys Asp Gly  
 545 550 555 560  
 Gln Pro Ile Gln Ala Asn Gly Thr Val Val Ser Ser Leu Ser Glu Ala  
 565 570 575  
 15 His Val Leu Gln Ser Gln Asp Phe Phe Leu Pro Ser Gly Gly Gly His  
 580 585 590  
 Ile Val Pro Lys Trp Ile Lys Leu Asp Lys Thr Thr Glu Ala Leu Gln  
 595 600 605  
 Tyr Tyr Ser Val Pro Pro Thr Asn Thr Val Ile Thr Thr Ala Asp Gly  
 610 615 620  
 20 Lys Arg Tyr Arg Phe Val Glu Val Pro Gly Ser Thr Pro Asn Pro Gly  
 625 630 635 640  
 Gln Ile Gly Ile Ser Trp Lys Lys Pro Ala Gly Asn Ala Tyr Phe Ala  
 645 650 655  
 25 Tyr Lys Leu Leu Asn Tyr Trp Met Gly Gly Thr Thr Asp Gln Gln Ser  
 660 665 670  
 Glu Trp Asp Val Thr Ser Asn Trp Thr Gly Ala Gln Val Pro Leu Thr  
 675 680 685  
 Gly Glu Asp Val Glu Phe Ala Thr Thr Glu Asn Phe Gly Ser Pro Ala  
 690 695 700  
 30 Val Ala Asp Leu His Val Pro Thr Thr Asn Pro Lys Ile Ile Gly Asn  
 705 710 715 720  
 Leu Ile Asn Asn Ser Asp Lys Asp Leu Val Val Thr Thr Ser Ser Gln  
 725 730 735  
 35 Leu Thr Ile Asn Gly Val Val Glu Asp Asn Asn Pro Asn Val Gly Thr  
 740 745 750  
 Ile Val Val Lys Ser Ser Lys Asp Asn Pro Thr Gly Thr Leu Leu Phe  
 755 760 765  
 Ala Asn Pro Gly Tyr Asn Gln Asn Val Gly Gly Thr Val Glu Phe Tyr  
 770 775 780  
 40 Asn Gln Gly Tyr Asp Cys Ala Asp Cys Gly Met Tyr Arg Arg Ser Trp  
 785 790 795 800  
 Gln Tyr Phe Gly Ile Pro Val Asn Glu Ser Gly Phe Pro Ile Asn Asp  
 805 810 815  
 45 Val Gly Gly Asn Glu Thr Val Asn Gln Trp Val Glu Pro Phe Asn Gly  
 820 825 830  
 Asp Lys Trp Arg Pro Ala Pro Tyr Ala Pro Asp Thr Glu Leu Gln Lys  
 835 840 845  
 Phe Lys Gly Tyr Gln Ile Thr Asn Asp Val Gln Ala Gln Pro Thr Gly  
 850 855 860  
 50 Val Tyr Ser Phe Lys Gly Met Ile Cys Val Cys Asp Ala Phe Leu Asn  
 865 870 875 880  
 Leu Thr Arg Thr Ser Gly Val Asn Tyr Ser Gly Ala Asn Leu Ile Gly  
 885 890 895  
 55 Asn Ser Tyr Thr Gly Ala Ile Asp Ile Lys Gln Gly Ile Val Phe Pro  
 900 905 910  
 Pro Glu Val Glu Gln Thr Val Tyr Leu Phe Asn Thr Gly Thr Arg Asp  
 915 920 925  
 Gln Trp Arg Lys Leu Asn Gly Ser Thr Val Ser Gly Tyr Arg Ala Gly  
 930 935 940  
 60 Gln Tyr Leu Ser Val Pro Lys Asn Thr Ala Gly Gln Asp Asn Leu Pro  
 945 950 955 960  
 Asp Arg Ile Pro Ser Met His Ser Phe Leu Val Lys Met Gln Asn Gly  
 965 970 975  
 65 Ala Ser Cys Thr Leu Unk Ile Leu Tyr Asp Lys Leu Leu Lys Asn Thr  
 980 985 990  
 Thr Val Asn Asn Gly Asn Gly Thr Gln Ile Thr Trp Arg Ser Gly Asn  
 995 1000 1005  
 Ser Gly Ser Ala Asn Met Pro Ser Leu Val Met Asp Val Leu Gly Asn  
 1010 1015 1020  
 70 Glu Ser Ala Asp Arg Leu Trp Ile Phe Thr Asp Gly Gly Leu Ser Phe  
 1025 1030 1035 1040  
 Gly Phe Asp Asn Gly Trp Asp Gly Arg Lys Leu Thr Glu Lys Gly Leu  
 1045 1050 1055  
 75 Ser Gln Leu Tyr Ala Met Ser Asp Ile Gly Asn Asp Lys Phe Gln Val  
 1060 1065 1070

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Ala Gly Val Pro Glu Leu Asn Asn Leu Leu Ile Gly Phe Asp Ala Asp  
 1075 1080 1085  
 Lys Asp Gly Gln Tyr Thr Leu Glu Phe Ala Leu Ser Asp His Phe Ala  
 1090 1095 1100  
 5 Lys Gly Ala Val Tyr Leu His Asp Leu Gln Ser Gly Ala Lys His Arg  
 1105 1110 1115 1120  
 Ile Thr Asn Ser Thr Ser Tyr Ser Phe Asp Ala Lys Arg Gly Asp Ser  
 1125 1130 1135  
 10 Gly Ala Arg Phe Arg Leu Ser Tyr Gly Cys Asp Glu Asn Val Asp Asp  
 1140 1145 1150  
 Ser His Val Val Ser Thr Asn Gly Arg Glu Ile Ile Ile Leu Asn Gln  
 1155 1160 1165  
 Asp Ala Leu Asp Cys Thr Val Thr Leu Phe Thr Ile Glu Gly Lys Leu  
 1170 1175 1180  
 15 Leu Arg Arg Leu Lys Val Leu Ala Gly His Arg Glu Val Met Lys Val  
 1185 1190 1195 1200  
 Gln Thr Gly Gly Ala Tyr Ile Val His Leu Gln Asn Ala Phe Thr Asn  
 1205 1210 1215  
 20 Asp Val His Lys Val Leu Val Glu Tyr  
 1220 1225

(2) INFORMATION FOR SEQ ID NO:486

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 425 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...425
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:486

Met Glu Val Lys Lys Asn Thr Val Val Leu Arg Leu Leu Ile Trp Phe  
 1 5 10 15  
 Val Ala Ile Leu Leu Phe His Ser Ser Arg Leu Trp Gly Gln Glu Gly  
 20 25 30  
 45 Glu Gly Ser Ala Arg Tyr Arg Phe Lys Gly Phe Val Asp Thr Tyr His  
 35 40 45  
 Ala Val Arg Ser Ser Ser Pro Phe Asp Phe Met Ser Ser Arg Thr Arg  
 50 55 60  
 Val Arg Gly Glu Leu Glu Arg Ser Phe Gly Asn Ser Lys Val Ala Val  
 65 70 75 80  
 Ser Val Asn Ala Thr Tyr Asn Ala Leu Leu Lys Asp Glu Thr Gly Leu  
 85 90 95  
 55 Arg Leu Arg Glu Ala Phe Phe Glu His Gln Glu Glu His Trp Gly Leu  
 100 105 110  
 Arg Leu Gly Arg Gln Ile Val Ile Trp Gly Ala Ala Asp Gly Val Arg  
 115 120 125  
 Ile Thr Asp Leu Ile Ser Pro Met Asp Met Thr Glu Phe Leu Ala Gln  
 130 135 140  
 60 Asp Tyr Asp Asp Ile Arg Met Pro Val Asn Ala Leu Arg Phe Ser Val  
 145 150 155 160  
 Phe Asn Glu Ser Met Lys Val Glu Val Val Val Leu Pro Val Phe Glu  
 165 170 175  
 65 Gly Tyr Arg Leu Pro Val Asp Pro Arg Asn Pro Trp Asn Ile Phe Ser  
 180 185 190  
 Leu Ser Pro Ile Ala Gln Gly Met Asn Ile Val Trp Lys Glu Glu Ala  
 195 200 205  
 Gly Lys Pro Ala Phe Lys Val Ala Asn Ile Glu Tyr Gly Ala Arg Trp  
 210 215 220  
 70 Ser Thr Thr Leu Ser Gly Ile Asp Phe Ala Leu Ala Ala Leu His Thr  
 225 230 235 240  
 Trp Asn Lys Met Pro Val Ile Glu Val Gln Gly Ile Val Pro Thr Glu  
 245 250 255  
 75 Ile Ile Val Ser Pro Arg Tyr Tyr Arg Met Gly Phe Val Gly Asp  
 260 265 270

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Leu Ser Val Pro Val Gly Gln Phe Val Phe Arg Gly Glu Ala Ala Phe  
 275 280 285  
 Asn Ile Asp Lys His Phe Thr Tyr Lys Ser His Ala Glu Gln Glu Gly  
 290 295 300  
 5 Phe Gln Thr Ile Asn Trp Leu Ala Gly Ala Asp Trp Tyr Ala Pro Gly  
 305 310 315 320  
 Glu Trp Met Ile Ser Gly Gln Phe Ser Met Glu Ser Ile Phe Arg Tyr  
 325 330 335  
 10 Arg Asp Phe Ile Ser Gln Arg Gln His Ser Thr Leu Ile Thr Leu Asn  
 340 345 350  
 Val Ser Lys Lys Phe Phe Gly Ser Thr Leu Gln Leu Ser Asp Phe Thr  
 355 360 365  
 Tyr Tyr Asp Leu Thr Gly Lys Gly Trp Phe Ser Arg Phe Ala Ala Asp  
 370 375 380  
 15 Tyr Ala Leu Asn Asp Gln Ile His Leu Met Ala Gly Tyr Asp Trp Phe  
 385 390 395 400  
 Ser Ser Lys Gly Ser Gly Ile Phe Asp Arg Tyr Lys Asp Asn Ser Glu  
 405 410 415  
 20 Leu Trp Phe Lys Ala Arg Tyr Ser Phe  
 420 425

(2) INFORMATION FOR SEQ ID NO:487

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 404 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 35 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...404  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:487

Met Ser Ser Cys Glu Val Ala Tyr Phe Ser Leu Lys Pro Ile Asp Leu  
 1 5 10 15  
 45 Gln Asn Ile Arg Glu Arg Asn His Ser Ser Asp Ile Ala Leu Ser Asn  
 20 25 30  
 Leu Leu Asp Asn Ser Asn Gln Leu Leu Ala Thr Ile Leu Ile Gly Asn  
 35 40 45  
 Asn Val Ile Asn Val Ala Ile Val Ile Leu Ser Asn Tyr Ala Ile Glu  
 50 55 60  
 Gln Thr Phe Val Phe Ser Ser Pro Ile Ile Gly Phe Leu Ile Gln Thr  
 65 70 75 80  
 Ile Leu Leu Thr Thr Val Leu Leu Leu Phe Gly Glu Ile Leu Pro Lys  
 85 90 95  
 Val Tyr Ala Arg Lys Asn Pro Leu Gln Tyr Ser Arg Phe Ser Ala Ala  
 100 105 110  
 55 Ala Met Ser Val Ile Tyr Lys Ile Leu Ser Pro Phe Ser Lys Leu Leu  
 115 120 125  
 Val Lys Ser Thr Gly Ile Val Thr Arg Gly Ile Ser Lys Lys Tyr  
 130 135 140  
 60 Asp Met Ser Val Asp Glu Leu Ser Lys Ala Val Ala Leu Thr Thr Thr  
 145 150 155 160  
 Glu Gly Glu Pro Glu Glu Lys Glu Met Ile Asn Glu Ile Ile Lys Phe  
 165 170 175  
 Tyr Asn Lys Thr Ala Cys Glu Ile Met Val Pro Arg Ile Asp Ile Val  
 180 185 190  
 65 Asp Val Asp Leu Ser Trp Pro Phe Arg Lys Met Leu Asp Phe Val Val  
 195 200 205  
 Ser Ser Gly Tyr Ser Arg Leu Pro Val Ser Glu Gly Ser Glu Asp Asn  
 210 215 220  
 70 Ile Lys Gly Val Ile Tyr Ile Lys Asp Leu Ile Pro His Met Asp Lys  
 225 230 235 240  
 Gly Asp Glu Phe Asp Trp His Pro Leu Ile Arg Lys Ala Tyr Phe Val  
 245 250 255  
 75 Pro Glu Asn Lys Arg Ile Asp Asp Leu Leu Glu Glu Phe Arg Ala Asn  
 260 265 270

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Lys Val His Val Ser Ile Val Val Asp Glu Phe Gly Gly Thr Cys Gly  
 275 280 285  
 Leu Ile Thr Met Glu Asp Ile Leu Glu Glu Ile Val Gly Glu Ile Thr  
 290 295 300  
 5 Asp Glu Tyr Asp Glu Glu Leu Pro Phe Lys Val Leu Gly Asp Gly  
 305 310 315 320  
 Ser Tyr Leu Phe Glu Gly Lys Thr Ser Leu Ser Asp Val Arg His Tyr  
 325 330 335  
 10 Leu Asp Leu Pro Glu Asn Ala Phe Gly Glu Leu Gly Asp Glu Val Asp  
 340 345 350  
 Thr Leu Ser Gly Leu Phe Leu Glu Ile Lys Gln Glu Leu Pro His Val  
 355 360 365  
 Gly Asp Thr Ala Val Tyr Glu Pro Phe Arg Phe Gln Val Thr Gln Met  
 370 375 380  
 15 Asp Lys Arg Arg Ile Ile Glu Ile Lys Ile Phe Pro Phe Glu Arg Thr  
 385 390 395 400  
 Trp Glu Val Glu

20 (2) INFORMATION FOR SEQ ID NO:488

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 260 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES

30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

35 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488

40 Met Lys Leu Leu Leu Tyr Leu Leu Leu Val Leu Ser Thr Leu Ser Pro  
 1 5 10 15  
 Met Tyr Ser Gln Met Leu Phe Ser Glu Asn Leu Thr Met Asn Ile Asp  
 20 25 30  
 45 Ser Thr Lys Thr Ile Gln Gly Thr Ile Leu Pro Val Leu Asp Phe Lys  
 35 40 45  
 Thr Glu Lys Glu Asn Val Phe Thr Phe Lys Asn Thr Ala Asn Leu Asn  
 50 55 60  
 Leu Leu Ile Lys His Gly Gln Val Ile Asn Leu Ile Asn Lys Leu Glu  
 65 70 75 80  
 Phe Ser Thr Tyr Gly Asn Lys Val Thr Val Ser Gly Gly Tyr Val His  
 85 90 95  
 Thr Glu Tyr Arg Tyr Leu Leu His His Val Phe Glu Val Tyr Pro Tyr  
 100 105 110  
 Val Glu Ser Gln Trp Ala Glu Ser Arg Gly Met Lys Tyr Lys Val Ser  
 115 120 125  
 55 Thr Gly Leu Gln Ser Arg Tyr Arg Leu Val Asn Ser Asp Asn Cys Leu  
 130 135 140  
 Met Phe Ala Thr Leu Gly Val Phe Phe Glu Phe Glu Lys Trp Glu Gln  
 145 150 155 160  
 60 Pro Ala Thr Ser Leu Phe Ala Gly Thr Tyr Ala Tyr Ser Arg Ser Ile  
 165 170 175  
 Lys Ser His Leu Ser Ile Ser Phe Arg His Arg Leu Gly Glu His Trp  
 180 185 190  
 Glu Phe Thr Thr Thr Ala Ile His Gln Gly Lys Pro Asp Ser Tyr Phe  
 195 200 205  
 Lys Lys Ala Arg Phe Gly Gly Ala Ile Asp Leu Lys Tyr His Ile Thr  
 210 215 220  
 Pro Thr Ile Gly Ile Arg Gly Ala Tyr Arg Ile Ile Tyr Asp Thr Ala  
 225 230 235 240  
 70 Pro Ile Val Pro Val Arg Lys Asp Tyr Asn Thr Val Asp Val Gly Ile  
 245 250 255  
 Asp Ile Ser Phe  
 260

75 (2) INFORMATION FOR SEQ ID NO:489

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 834 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489

20	Met Lys Arg Ile Val Leu Ser Ser Phe Leu Phe Val Leu Ser Ile Leu
	1 5 10 15
	Ser Leu Met Ala Gln Asn Asn Thr Leu Asp Val His Ile Ser Gly Thr
	20 25 30
25	Ile Lys Asp Ala Ser Ser Gly Glu Pro Val Pro Tyr Ala Thr Val Ser
	35 40 45
	Ile Arg Leu Thr Gly Ala Asp Thr Thr Gln Val Phe Arg Gln Val Thr
	50 55 60
	Asp Gly Asn Gly Tyr Phe Val Ile Gly Leu Pro Ala Ala Pro Ser Tyr
	65 70 75 80
30	His Leu Thr Ala Ser Phe Val Gly Met Lys Thr His Thr Met Gln Ile
	85 90 95
	Ser Arg Gly Asn Gly Gln His Asp Ile Lys Ser Ile Asp Ile Ser Leu
	100 105 110
35	Glu Ser Glu Asp Lys Gln Leu Ser Thr Val Thr Val Ser Ala Ala Arg
	115 120 125
	Pro Leu Val Lys Met Glu Ile Asp Arg Leu Ser Tyr Asn Met Lys Asp
	130 135 140
	Asp Pro Ala Ala Lys Thr Asn Asn Leu Leu Glu Met Leu Arg Asn Val
	145 150 155 160
40	Pro Leu Val Thr Val Asp Gly Gln Gly Asn Ile Gln Val Lys Gly Ser
	165 170 175
	Ser Asn Phe Lys Ile His Leu Asn Gly Arg Pro Ser Thr Met Val Ser
	180 185 190
45	Ser Asn Pro Lys Glu Val Phe Arg Ser Ile Pro Ala His Thr Ile Lys
	195 200 205
	Arg Val Glu Val Ile Thr Asp Pro Gly Val Lys Tyr Asp Ala Glu Gly
	210 215 220
	Thr Ser Ala Ile Leu Asp Ile Val Thr Glu Glu Gly Lys Lys Leu Glu
	225 230 235 240
50	Gly Tyr Ser Gly Ser Ile Thr Ala Ser Val Ser Asn Asn Pro Thr Ala
	245 250 255
	Asn Gly Ser Ile Phe Leu Thr Ala Lys Ser Gly Lys Val Gly Leu Thr
	260 265 270
	Thr Asn Tyr Asn Tyr Tyr Gly Gly Lys Asn Lys Gly Ser Arg Tyr Phe
	275 280 285
55	Thr Glu Arg Thr Thr Ser Met Leu Gln Thr Ile Glu Glu Gly Lys Gly
	290 295 300
	Gln Glu Thr Phe Gly Gly His Phe Gly Asn Ala Leu Leu Ser Phe Glu
	305 310 315 320
60	Ile Asp Ser Leu Asn Leu Phe Thr Val Gly Gly Asn Val Arg Leu Trp
	325 330 335
	Glu Met Thr Thr Asp Arg Asn Ser Val Glu Lys Ser Phe Ala Gly Ser
	340 345 350
65	Asn Leu Met Ser Tyr Ile Asp Arg Lys Leu Lys Thr Gln Met Asp Ala
	355 360 365
	Gly Ser Tyr Glu Leu Asn Ala Asp Tyr Gln His Ser Thr Arg Leu Pro
	370 375 380
	Gly Glu Leu Leu Thr Val Ser Tyr Arg Phe Thr His Asn Pro Asn Asn
	385 390 395 400
70	Ser Glu Thr Phe Ile Asp Gln Trp Lys Arg Asp Pro Leu Asn Thr Ala
	405 410 415
	Asn Thr Ile Gln Tyr Ala Gly Gln His Ser Lys Ser Asp Ala Gly Met
	420 425 430
75	Asp Glu His Thr Ala Gln Val Asp Tyr Thr Arg Pro Leu Gly Gln Ala
	435 440 445

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His Ser Leu Glu Ala Gly Leu Lys Tyr Ile Tyr Arg His Ala Thr Ser  
 450 455 460  
 Asp Pro Leu Tyr Glu Ile Arg Pro Ser Glu Asp Ala Pro Trp Gln Pro  
 465 470 475 480  
 5 Gly Ser Leu Tyr Ala Gln Asn Pro Ser Asn Gly Lys Phe Arg His Asp  
 485 490 495  
 Gln Tyr Ile Gly Ala Ala Tyr Ala Gly Tyr Asn Tyr Arg Lys Asp Gln  
 500 505 510  
 10 Tyr Ser Leu Gln Thr Gly Leu Arg Val Glu Ser Ser Arg Leu Lys Ala  
 515 520 525  
 Leu Phe Pro Glu Asn Ala Ala Ala Asp Phe Ser His Asn Ser Phe Asp  
 530 535 540  
 Trp Val Pro Gln Leu Thr Leu Gly Tyr Thr Pro Ser Pro Met Lys Gln  
 545 550 555 560  
 15 Leu Lys Leu Ala Tyr Asn Phe Arg Ile Gln Arg Pro Ala Ile Gly Gln  
 565 570 575  
 Leu Asn Pro Tyr Arg Leu Gln Thr Asn Asp Tyr Gln Val Gln Tyr Gly  
 580 585 590  
 20 Asn Pro Asp Leu Lys Ser Glu Lys Arg His His Val Gly Leu Ser Tyr  
 595 600 605  
 Asn Gln Tyr Gly Ala Lys Val Met Leu Thr Ala Ser Leu Asp Tyr Asp  
 610 615 620  
 Phe Cys Asn Asn Ala Ile Gln Asn Tyr Thr Phe Ser Asp Pro Ala Asn  
 625 630 635 640  
 25 Pro Asn Leu Phe His Gln Thr Tyr Gly Asn Ile Gly Arg Glu His Ser  
 645 650 655  
 Phe Ser Leu Asn Thr Tyr Ala Met Tyr Thr Pro Ala Val Trp Val Arg  
 660 665 670  
 Ile Met Leu Asn Gly Asn Ile Asp Arg Thr Phe Gln Lys Ser Glu Ala  
 675 680 685  
 30 Leu Gly Ile Asp Val Asn Ser Trp Ser Gly Met Val Tyr Ser Gly Leu  
 690 695 700  
 Met Phe Thr Leu Pro Lys Asp Trp Thr Val Asn Leu Phe Gly Gly Tyr  
 705 710 715 720  
 35 Tyr His Gly Gly Arg Ser Tyr Gln Thr Lys Tyr Asp Gly Asn Val Phe  
 725 730 735  
 Asn Asn Ile Gly Ile Ala Lys Gln Leu Phe Asp Lys Lys Leu Arg Val  
 740 745 750  
 40 Ser Leu Ser Ala Asn Asn Ile His Ala Lys Tyr Ser Thr Trp Lys Ser  
 755 760 765  
 Arg Thr Ile Gly Asn Gly Phe Thr Ile Tyr Ser Glu Asn Ala Gly Ile  
 770 775 780  
 Gln Arg Ser Val Ser Leu Ser Leu Thr Tyr Ser Phe Gly Lys Met Asn  
 785 790 795 800  
 45 Thr Gln Val Arg Lys Val Glu Arg Thr Ile Val Asn Asp Asp Leu Lys  
 805 810 815  
 Gln Thr Ser Ser Gln Gly Gln Gln Gly Gly Gln Gly Asn Pro Thr  
 820 825 830  
 Gly Asn

## (2) INFORMATION FOR SEQ ID NO:490

(1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 399 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...399  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:490  
 Met Arg Leu Ser Ala Ile Leu Ile Ala Leu Ile Val Met Leu Pro Ala  
 1 5 10 15  
 Val Leu Ser Gly Gln His Tyr Tyr Ser Met Ala Gly Glu Arg Leu Glu  
 20 25 30

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Thr Asp Ser Ile Arg Pro Asn Glu Leu Ser Ala Ser Ile Arg Ser Ala  
 35 40 45  
 Leu Phe Phe Arg Asn Asn Glu Tyr Asn Ala Arg Ser Val Lys Gly Tyr  
 50 55 60  
 5 Thr Leu Pro Gly Ala Arg Val Ser Ala Phe Ala Ser Tyr Ser Leu Pro  
 65 70 75 80  
 Ala Ala His Gly Val Lys Leu Ser Leu Gly Val Ser Thr Leu Asn Tyr  
 85 90 95  
 10 Trp Gly Ala Ser Arg Tyr Pro Ala Gly Ile Ala Tyr Ser Asp Leu Pro  
 100 105 110  
 Tyr Trp Thr Asp Tyr Asn Asp Tyr Val Arg Leu Arg Ile Leu Pro Tyr  
 115 120 125  
 Val Gln Ala Met Leu Lys Pro Thr Ala Thr Thr Ala Leu Met Leu Gly  
 130 135 140  
 15 Asn Ile Ala Gly Gly Thr Ala His Gly Leu Ile Glu Pro Ile Tyr Asn  
 145 150 155 160  
 Pro Glu Leu Asp Leu Thr Ala Asp Pro Glu Ala Gly Val Gln Phe Arg  
 165 170 175  
 20 Gly Asp Trp Thr Arg Phe Arg Met Asp Val Trp Val Asn Trp Met Ser  
 180 185 190  
 Met Ile Phe Lys Asn Asp Asn His Gln Glu Ser Phe Val Phe Gly Leu  
 195 200 205  
 Ser Thr Thr Ser Lys Leu Leu Ser Gly Glu Gly Lys Trp Arg Leu Glu  
 210 215 220  
 25 Leu Pro Leu Gln Ala Ile Ala Thr His Arg Gly Gly Glu Tyr Asn Trp  
 225 230 235 240  
 Ala Gln Gln Asp Thr Val His Thr Trp Val Asn Gly Ala Val Gly Leu  
 245 250 255  
 Lys Leu Ser Tyr Arg Pro Arg Thr Asp Lys Pro Met Gln Ile Trp Gly  
 260 265 270  
 30 Ser Ala Tyr Gly Val Ala Ala Leu Ser Ser Gly Gly Tyr Phe Pro Tyr  
 275 280 285  
 Glu Arg Gly Trp Gly Gly Tyr Leu Ser Leu Gly Met Asp Leu Glu His  
 290 295 300  
 35 Phe Ala Phe Arg Thr Asp Tyr Trp Tyr Gly Arg His Tyr Val Ser Pro  
 305 310 315 320  
 Phe Ala Ala Pro Phe Ala Asn Ser Leu Thr Tyr Asp Lys Gln Pro Leu  
 325 330 335  
 40 Thr Asn Gly Trp Gly Asp Tyr Ile Arg Leu Tyr Ala Asp Tyr Ser Trp  
 340 345 350  
 Arg Met Ala Arg Ser Val Ser Leu Ala Ala Val Ala Arg Val Trp Phe  
 355 360 365  
 Gln Pro Ser Asp Arg Phe Ala Met Ser His Ala Leu Glu Leu Thr Met  
 370 375 380  
 45 Arg Ile Asp Pro Lys Phe Pro Ile Ala Phe Leu Lys Gly Asn His  
 385 390 395

(2) INFORMATION FOR SEQ ID NO:491

- 50 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 382 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 55 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 60 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...382  
 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:491

Met Asn Lys Ser Leu Leu Ser Leu Ala Cys Leu Ile Leu Cys Gly Met  
 1 5 10 15  
 70 Pro Ala Ile Ala Gln Gln Thr Gly Pro Ala Glu Arg Ser Gly Glu Pro  
 20 25 30  
 Ser Leu Ala Glu Arg Val Phe Gly Leu Glu Gln Lys Gln Lys Lys Leu  
 35 40 45  
 Lys Val Tyr Leu Gly Ile Gln Ser Phe Tyr Asp Gln Pro Leu Val Asp  
 50 55 60



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    Asp Glu Ser His Ile Gly His Phe Lys Val Gln Glu Leu Arg Met Ser
    65      70      75      80
    Ala His Gly Glu Leu Asn Arg His Leu Ser Phe Asp Trp Arg Gln Arg
    85      90      95
5   Leu Asn Arg Ala Ala Asp Gly Thr Ser Phe Ala Asp Asn Leu Ser Asn
    100      105      110
    Ala Ile Asp Ile Ala Gly Val Asp Trp His Pro Asn Asp Lys Val Ser
    115      120      125
10  Phe Phe Phe Gly Arg Gln Tyr Ala Arg Phe Gly Gly Ile Glu Tyr Asp
    130      135      140
    Met Asn Pro Val Glu Ile Tyr Gln Tyr Ser Asp Leu Val Asp Tyr Met
    145      150      155      160
    Thr Cys Tyr Thr Ser Gly Val Asn Phe Ala Trp Asn Phe His Pro Glu
    165      170      175
15  Gln Gln Leu Gln Leu Gln Val Leu Asn Ala Tyr Asn Asn Arg Phe Ala
    180      185      190
    Asp Arg Tyr His Val Thr Pro Asp Val Ala Thr Ala Thr Ser Tyr Pro
    195      200      205
20  Leu Leu Tyr Ser Ala Gln Trp Asn Gly Thr Leu Leu Gly Gly Ala Leu
    210      215      220
    His Met Arg Tyr Ala Val Ser Met Ala His Gln Ala Gln Glu Arg Asn
    225      230      235      240
    Met Trp Tyr Phe Thr Ala Gly Asn Leu Phe Asn Pro Gly Lys Arg Ile
    245      250      255
25  Asn Gly Tyr Leu Asp Leu Thr Tyr Ser Ile Glu Gly Leu Asp Asp Lys
    260      265      270
    Gly Ile Met Thr Ala Arg Tyr Gly Lys Gly Lys Thr Leu Thr Asp Val
    275      280      285
30  Lys Tyr Tyr Ala Leu Val Ser Lys Trp Asn Phe Arg Ile Phe Asp Gln
    290      295      300
    Val Asn Leu Phe Leu Lys Gly Met Tyr Glu Asn Gly Tyr Ala Pro Ala
    305      310      315      320
    Gln Tyr Gly Glu Ser Ser His Thr Arg His Ser Tyr Gly Tyr Met Gly
    325      330      335
35  Gly Val Glu Tyr Tyr Pro Thr Glu Thr Asn Phe Arg Leu Phe Val Thr
    340      345      350
    Tyr Ile Gly Arg His Tyr Arg Tyr Ser Ala Thr Glu Thr Glu Ser Thr
    355      360      365
40  Asn Ala Leu Arg Ala Gly Leu Ile Tyr Gln Ile Pro Phe Leu
    370      375      380

```

## (2) INFORMATION FOR SEQ ID NO:492

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
- (A) NAME/KEY: misc feature
- (B) LOCATION 1...222
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:492

```

Met Lys His Leu Phe Lys Ser Thr Leu Val Leu Leu Cys Ala Leu Ser
1      5      10      15
Phe Ser Gly Thr Tyr Thr Phe Ala Gln Glu Asn Asn Thr Glu Lys Ser
20      25      30
65 Arg Phe Asp Phe Ser Val Arg Leu Gly Gln Gly Tyr Ile Ala Gly Ser
    35      40      45
    Thr Thr Asn Leu Met Tyr Gly Tyr Thr Ser Ala Asn Asp Arg Leu Leu
    50      55      60
70 Ser Gly Ala Ile Tyr Leu Gly Leu Thr Pro Ser Lys Lys Glu Asn Ala
    65      70      75      80
    Thr Gly Val Ala Phe Arg Phe Leu Ser Pro Ser Pro Gly Tyr Tyr Val
    85      90      95
75 Asp Ile Ser Gly Lys Glu Asn Thr Leu Asn Tyr Ala Phe Tyr Val Val
    100      105      110

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Gly Ala Tyr Asn Arg Ile Ala Ile Pro Ile Arg Pro Ile Lys Asn Phe  
 115 120 125  
 Asn Phe Ile Phe Ser Thr Glu Val Gly Met Ala Trp Met Ser Arg His  
 130 135 140  
 5 Glu Gln Ile Tyr Asn Ser Thr Ser Gln Thr Trp Asp Lys Gln Arg Lys  
 145 150 155 160  
 Ser Arg Ser Gly Leu Asp Phe Gly Leu Gly Met His Leu Gln Unk His  
 165 170 175  
 10 Ile Asn Lys Thr Val Tyr Phe Met Ala Gly Thr Asp Leu Thr Ser Cys  
 180 185 190  
 Met Phe Gly Lys Arg Ile Asn Asp Tyr Gln Gln Lys Asp Arg Thr Phe  
 195 200 205  
 15 Ile Ala Leu Ile Asp Asn Ser Ile Gly Ile Gly Leu Asn Leu  
 210 215 220  
 (2) INFORMATION FOR SEQ ID NO:493  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 391 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 25 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 30 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...391  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:493  
 35 Met Ile Ile Lys Lys Met Leu Lys Asn Lys Leu Ala Pro Leu Ala Ile  
 1 5 10 15  
 Leu Phe Leu Phe Ala Pro Lys Ala Met Lys Ala Gln Glu Gln Leu Asn  
 20 25 30  
 40 Val Val His Thr Ser Val Pro Ser Leu Asn Ile Ser Pro Asp Ala Arg  
 35 40 45  
 Ala Ala Gly Met Gly Asp Ile Gly Val Ala Thr Thr Pro Asp Ala Tyr  
 50 55 60  
 45 Ser Gln Tyr Trp Asn Pro Ser Lys Tyr Ala Phe Met Asp Thr Lys Ala  
 65 70 75 80  
 Gly Ile Ser Phe Ser Tyr Thr Pro Trp Leu Ser Lys Leu Val Asn Asp  
 85 90 95  
 Ile Ala Leu Met Gln Met Thr Gly Phe Tyr Lys Leu Gly Thr Asp Glu  
 100 105 110  
 50 Asn Gln Ala Ile Ser Ala Ser Leu Arg Tyr Phe Thr Leu Gly Lys Leu  
 115 120 125  
 Glu Thr Phe Asp Glu Leu Gly Glu Ser Met Gly Glu Ala His Pro Asn  
 130 135 140  
 55 Glu Phe Ala Val Asp Leu Gly Tyr Ser Arg Gln Leu Ser Glu Asn Phe  
 145 150 155 160  
 Ser Met Ala Val Ala Leu Arg Tyr Ile Arg Ser Asp Gln Ser Thr His  
 165 170 175  
 Asn Thr Gly Glu Asn Gln Ala Gly Asn Ala Phe Ala Ala Asp Ile Ala  
 180 185 190  
 60 Gly Tyr Leu Gln Lys Tyr Val Leu Leu Gly Asn Ala Glu Ser Leu Trp  
 195 200 205  
 Ser Leu Gly Phe Asn Val Lys Asn Ile Gly Thr Lys Ile Ser Tyr Asp  
 210 215 220  
 65 Gly Gly Val Thr Ser Phe Phe Ile Pro Thr Ser Leu Asn Leu Gly Thr  
 225 230 235 240  
 Gly Leu Leu Tyr Pro Ile Asp Asp Tyr Asn Ser Ile Asn Phe Asn Leu  
 245 250 255  
 Glu Leu Ser Lys Leu Leu Val Pro Thr Pro Ile Met Asp Gln Asn  
 260 265 270  
 70 Asp Gln Ala Gly Tyr Glu Ala Ala Leu Lys Lys Tyr Gln Glu Thr Ser  
 275 280 285  
 Ser Ile Ser Gly Ile Phe Ser Ser Phe Gly Asp Ala Pro Gly Gly Leu  
 290 295 300  
 75 Lys Glu Glu Phe Arg Glu Ile Thr Trp Gly Leu Gly Ala Glu Tyr Ser  
 305 310 315 320

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Tyr Asp Asp Lys Phe Phe Val Arg Ala Gly Tyr Ser Tyr Leu His Pro  
 325 330 335  
 Thr Lys Gly Asn Leu Gln Tyr Phe Thr Ala Gly Ala Gly Phe Lys Met  
 340 345 350  
 5 Asn Ile Phe Arg Ile Asp Ala Ser Tyr Leu Leu Ser Thr Ile Gln Ser  
 355 360 365  
 Asn Pro Leu Asp Gln Thr Leu Arg Phe Thr Leu Ala Phe Asp Met Asp  
 370 375 380  
 10 Gly Leu Arg Asn Leu Phe His  
 385 390

(2) INFORMATION FOR SEQ ID NO:494

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 446 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 20 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- 25 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...446
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:494

Met Lys Thr Thr Val Gln Gln Ile Ile Leu Cys Leu Ala Leu Met Met  
 1 5 10 15  
 35 Ser Gly Val Leu Gly Gly Asn Ala Gln Ser Phe Trp Glu Glu Ile Ala  
 20 25 30  
 Pro Pro Phe Ile Ser Asn Glu Pro Asn Val Lys Tyr Ile Ile Pro Asn  
 35 40 45  
 Met Gly Ile Asp Ser Lys Gly Thr Ile Tyr Val Thr Val Thr Lys Arg  
 50 55 60  
 40 Ile Gln Gln Gly Ala Asn Tyr Thr Ser Glu Gln Leu Gly Met Tyr Tyr  
 65 70 75 80  
 Arg Pro Leu Gly Asp Asn Glu Gln Trp Trp Lys His Asp Pro Tyr Phe  
 85 90 95  
 45 Asp Asp Lys Ile Val Ala Asp Ile Gln Thr Asp Ala Tyr Gly Arg Val  
 100 105 110  
 Tyr Val Cys Thr Thr Ser Ser Arg Asp Gln Glu Tyr Gln Leu Tyr Ile  
 115 120 125  
 Asn Glu Gln Asn Glu Trp Arg Cys Ile Phe Lys Thr Ser Val Ser Thr  
 130 135 140  
 50 Tyr Glu His Gly Met Ala Val Phe Arg Ser Ser Thr Gly Val Thr Tyr  
 145 150 155 160  
 Ile Gly Thr Arg His His Ile Phe Ala Ser Gly Val Asn Asp Phe Glu  
 165 170 175  
 55 Phe Asn Thr Ile Tyr Glu Asp Ser Thr Pro Met Ser Cys Arg Phe Ala  
 180 185 190  
 Glu Ala Thr Asn Ser Gly Thr Ile Tyr Leu Ala Leu Met His Glu Thr  
 195 200 205  
 Thr Met Ser Thr Thr Ile Leu Thr Tyr Gln Asn Gly Glu Phe Val Asp  
 210 215 220  
 60 Ile Ser Glu Ser Glu Leu Ser Asn Ser Ile Ile Ala Ser Met Cys Ser  
 225 230 235 240  
 Asn Lys Glu Gly Asp Ile Ile Ala Leu Val Thr Ser Tyr Thr Gly Phe  
 245 250 255  
 65 Met Ser Gly Thr Leu Ala Ile Arg Lys Ala Asp Glu Gly Lys Trp Gln  
 260 265 270  
 Leu Val Gly Gly Asp Ile Gln Asn Ala Ile Val Gln Asn Ile Cys Met  
 275 280 285  
 Met Asp Asp Asn Lys Ile Ala Cys Glu Val Phe Gly Thr Pro Asn Gly  
 290 295 300  
 70 Val Asp Gly Arg Thr Arg Val Cys Val Ser Asp Ala Ser Val Phe Asp  
 305 310 315 320  
 Phe Glu Trp Tyr Glu Asp Glu Ile Tyr Gly Gly Leu Ile Phe Asp Thr  
 325 330 335  
 75 Phe Phe Tyr Ser Pro Trp Asp Lys Leu Leu Tyr Ala Lys Phe Gly Gly  
 340 345 350

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Ile Met Leu Arg Ser Lys Glu Ser Phe Ile Thr Ser Phe Ile Ser Pro  
 355 360 365  
 Thr Val Val Gln Gly Val Asp Val Tyr Thr Leu Ala Gly Lys Ile Arg  
 370 375 380  
 5 Ile Glu Ser Glu Thr Pro Val Ser Glu Val Leu Leu Phe Asp Leu Ala  
 385 390 395 400  
 Gly Arg Met Val Leu Arg Gln Thr Ile Asp Asn Lys Ile Tyr Ser Asp  
 405 410 415  
 10 Ile Asp Thr Asn Gly Leu Lys Arg Ser Gly Ile Tyr Val Val Ser Val  
 420 425 430  
 Arg Leu Ser Ser Gly Gln Val Phe Ser His Lys Val Gln Val  
 435 440 445

(2) INFORMATION FOR SEQ ID NO:495

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495

Met Ile Ile Arg Cys Leu Ile Arg Arg Pro Arg Thr Val Leu Phe Gly  
 1 5 10 15  
 Leu Ile Phe Val Val Gly Leu Phe Ser Ala Met Ala Gln Glu Lys Lys  
 20 25 30  
 Asp Ser Leu Ser Thr Val Gln Pro Val Pro Asn Ser Ser Met Val Glu  
 35 40 45  
 40 Gln Thr Pro Leu Leu Ser Ile Asp His Pro Val Leu Pro Ala Ser Phe  
 50 55 60  
 Gln Asn Thr Arg Thr Leu Lys Arg Phe Arg Asp Lys His Leu Ser Asp  
 65 70 75 80  
 45 Ala Leu Leu Asn Gly Leu Lys Pro His Arg Ser Ser Leu Gln Leu Asn  
 85 90 95  
 Glu Glu Leu Asn Phe Ala Ala Glu Arg Arg Asp Phe Val Ser Pro Leu  
 100 105 110  
 Leu Gln Thr Arg His Ala Ala Gly Val Leu Ser Trp Arg Pro Thr Asp  
 115 120 125  
 50 Arg Met His Phe Tyr Thr Ser Gly Asn Ile Gly Leu Gly His Asp Leu  
 130 135 140  
 Leu Thr Gly Val Arg Lys Asp Phe Gly Trp Asn Ala Gly Ala Asp Phe  
 145 150 155 160  
 55 Leu Leu Ser Gln Asn Leu Thr Ala His Val Gln Gly Gly Trp Gln Gln  
 165 170 175  
 Asn Phe Gly Phe Ile Pro Met Thr Ala Val Asn Gly Gln Leu Arg Trp  
 180 185 190  
 Gln Ala Thr Glu Arg Leu Ser Phe Thr Thr Gly Ile Asp Tyr Arg Gln  
 195 200 205  
 60 Val Gln Trp Asn Ala Phe Asp Asn Arg Thr Phe Ser Leu Lys Gly Ser  
 210 215 220  
 Ala Arg Tyr Glu Val Met Asp Asn Val Phe Val Asn Gly Phe Gly Ser  
 225 230 235 240  
 Tyr Pro Leu Tyr Ser Ser Thr Arg Ser Gly Leu Asn Met Ala Val Pro  
 245 250 255  
 65 Met His Gly Phe Gly Pro Gln Tyr Gly Gly Ser Leu Glu Leu Lys Val  
 260 265 270  
 Ser Glu Arg Phe Gly Phe Ala Val Gly Met Glu Arg Glu Tyr Asn Ile  
 275 280 285  
 70 Trp Thr Arg Arg Trp Glu Thr His Tyr Phe Ala Tyr Pro Val Phe Tyr  
 290 295 300  
 Gly Asp Lys Lys  
 305

(2) INFORMATION FOR SEQ ID NO:496

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 315 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496

Met Lys Thr Asn Arg Arg Tyr Ala Phe Val Leu Pro Leu Leu Leu Leu  
 1 5 10 15  
 Thr Gly Leu Leu Ala Trp Gly Gln Asp Ser Ser His Gly Ser Asn Thr  
 20 25 30  
 Ala Phe Ala Thr Asp Ser Ser Ser Arg Glu Leu Pro Thr Glu Gln Ser  
 35 40 45  
 Ala Tyr Arg Ile His Ser Ala Tyr Met Val Gly Gly Gly Ser Ile  
 50 55 60  
 Thr Arg Asp Thr Tyr Leu Ser Pro Leu Arg Tyr Gly Gly Trp Thr Leu  
 65 70 75 80  
 Asn Leu Leu Gly Glu Lys Thr Phe Pro Leu Lys Ala Ser Asp Ser Arg  
 85 90 95  
 Trp Met Ile Arg Thr Gly His Glu Leu Asp Phe Ala Leu Met Asp Asn  
 100 105 110  
 Pro Ala Asn Asn Ala His Phe Tyr Ser Leu Leu Tyr Asn Gly Ser Ala  
 115 120 125  
 Ala Ala Leu Tyr Arg Leu Gly Ala Lys His Leu Arg Ala Ala Trp Met  
 130 135 140  
 Asp Asn Leu Arg Leu Ala Phe Gly Pro Gly Leu Glu Ile Gly Leu Gly  
 145 150 155 160  
 Gly Ile Tyr Ser Thr Arg Asn Gly Asn Asn Pro Ala Thr Leu Lys Leu  
 165 170 175  
 Tyr Thr Asn Ala Ile Ala Gln Ala Ser Ile Gly Tyr Tyr Val Pro Ser  
 180 185 190  
 Glu Thr Phe Pro Leu Tyr Phe Arg Leu Leu Ser Gln Ile Asn Leu Phe  
 195 200 205  
 Gly Ile Ala Tyr Gly Asn Gly Phe Gly Glu Ser Tyr Tyr Glu Asn Phe  
 210 215 220  
 Leu Leu Asn Asn Gly Ile Ala Gly Ser Leu His Phe Thr Tyr Pro Gly  
 225 230 235 240  
 Lys Phe Thr Arg Phe Thr Thr Leu Ile Thr Ala Asp Ile Pro Ile Arg  
 245 250 255  
 Asn Phe Cys Thr Leu Arg Val Gly Tyr Arg Tyr Ser His Leu Gly Ser  
 260 265 270  
 Ser Leu Asn Ala Leu Asp Thr Arg Ile His Ser His Thr Ala Phe Ile  
 275 280 285  
 Gly Phe Val Thr Glu Phe Tyr Arg Phe Arg Gly Arg Lys Ala Met Asn  
 290 295 300  
 Thr Gly Arg Arg Thr Ser Leu Tyr Tyr His Asp  
 305 310 315

(2) INFORMATION FOR SEQ ID NO:497

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 285 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

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(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497

5 Met Val Val Thr Leu Leu Val Ile Val Gly Ile Val Val Val Arg  
1 5 10 15  
Tyr Ser Leu Arg Val His Val His Lys Thr Gly Thr Val Val Ser Ala  
20 25 30  
10 Ala Ile Phe Gly Phe Ile Leu Leu Gly Lys Thr Val Pro Cys Asp Thr  
35 40 45  
Arg Asn Phe Phe Ser Ser Glu Ser Asp Glu Pro Glu Ser Arg Val Ala  
50 55 60  
Thr Glu Ile Ala His Leu Cys Glu Ile Gly Phe Gln Ile His Ala Ser  
65 70 75 80  
15 Ser Ile His Val Ala Val Arg Thr Asp Phe Gly Gln Ala Gly Ile His  
85 90 95  
Cys Pro Met Ala Thr Asp Ala Ser Ala Thr Glu Phe Asp Arg Ser Ala  
100 105 110  
20 Glu Cys Ala Glu Arg Thr Ser Ala Gln Ile Asp Thr Ala Ile Arg Ser  
115 120 125  
Gln Ser Gln Ile Ile Arg Thr His Ile Asp Thr Cys Pro Lys Ser Ser  
130 135 140  
25 Gly Thr Ile Gly Gly Ser Thr His Thr Ser Leu His Leu Lys Val Phe  
145 150 155 160  
Asp Gly Arg Gly Glu Val Gly His Ile His Pro Lys Asp Gly Leu Arg  
165 170 175  
Phe Gly Val Val Glu Gly Tyr Ser Ile Gly Ser Tyr Val Asp Ala Ile  
180 185 190  
30 Gly Ile Gly Ala Thr His Ala Lys Ala Gly Ile Ser Asp Thr Arg Thr  
195 200 205  
Gly Ile Ala Gly Gly Tyr His Gly Gly Ser Gln His Gln Gln Ile Gly  
210 215 220  
35 Asp Val Thr Thr Ile Ile Gly Leu Gly Lys Phe Gly Leu Ala Asn Val  
225 230 235 240  
Gly Val Ser Asp Arg Gly Phe Arg Arg Gly Ala Ser Ser Tyr Asp Leu  
245 250 255  
Tyr Gly Leu Glu Leu His Ile Ala Lys Thr Ile Tyr Leu Ala Val Gly  
260 265 270  
40 Asp Gly Cys Leu Cys Arg Gln Ala Glu Arg Gln Asp Gly  
275 280 285

(2) INFORMATION FOR SEQ ID NO:498

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 599 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
50 (ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: YES  
(vi) ORIGINAL SOURCE:  
55 (A) ORGANISM: Porphyromonas gingivalis  
(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1...599  
60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498

Met Glu Asn Leu Lys Asn Ile Gln Pro Arg Glu Asp Phe Asn Trp Glu  
1 5 10 15  
65 Glu Phe Glu Ala Gly Gly Val His Ala Ala Val Ser Arg Gln Glu Gln  
20 25 30  
Glu Ala Ala Tyr Asp Lys Thr Leu Asn Thr Ile Lys Glu Lys Glu Val  
35 40 45  
70 Val Met Gly Arg Val Thr Ala Ile Asn Lys Arg Glu Val Val Ile Asn  
50 55 60  
Val Gly Tyr Lys Ser Glu Gly Val Val Pro Ala Thr Glu Phe Arg Tyr  
65 70 75 80  
Asn Pro Glu Leu Lys Val Gly Asp Glu Val Glu Val Tyr Ile Glu Asn  
85 90 95  
75 Gln Glu Asp Lys Lys Gly Gln Leu Val Leu Ser His Arg Lys Gly Arg

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100 105 110  
 Ala Ala Arg Ser Trp Glu Arg Val Asn Glu Ala Leu Glu Lys Asp Glu  
 115 120 125  
 5 Ile Val Lys Gly Tyr Val Lys Cys Arg Thr Lys Gly Gly Met Ile Val  
 130 135 140  
 Asp Val Phe Gly Ile Glu Ala Phe Leu Pro Gly Ser Gln Ile Asp Val  
 145 150 155 160  
 Arg Pro Ile Arg Asp Tyr Asp Ala Phe Val Glu Lys Thr Met Glu Phe  
 165 170 175  
 10 Lys Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val Val Ser His  
 180 185 190  
 Lys Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys Glu Ile Ile  
 195 200 205  
 Gly Lys Leu Glu Lys Gly Gln Val Leu Glu Gly Ile Val Lys Asn Ile  
 210 215 220  
 15 Thr Ser Tyr Gly Val Phe Ile Asp Leu Gly Gly Val Asp Gly Leu Ile  
 225 230 235 240  
 His Ile Thr Asp Leu Ser Trp Gly Arg Val Ala His Pro Glu Glu Ile  
 245 250 255  
 20 Val Gln Leu Asp Gln Lys Ile Asn Val Val Ile Leu Asp Phe Asp Glu  
 260 265 270  
 Asp Arg Lys Arg Ile Ala Leu Gly Leu Lys Gln Leu Met Pro His Pro  
 275 280 285  
 25 Trp Asp Ala Leu Asp Ser Glu Leu Lys Val Gly Asp Lys Val Lys Gly  
 290 295 300  
 Lys Val Val Val Met Ala Asp Tyr Gly Ala Phe Val Glu Ile Ala Gln  
 305 310 315 320  
 Gly Val Glu Gly Leu Ile His Val Ser Glu Met Ser Trp Thr Gln His  
 325 330 335  
 30 Leu Arg Ser Ala Gln Asp Phe Leu His Val Gly Asp Glu Val Glu Ala  
 340 345 350  
 Val Ile Leu Thr Leu Asp Arg Glu Glu Arg Lys Met Ser Leu Gly Leu  
 355 360 365  
 35 Lys Gln Leu Lys Pro Asp Pro Trp Ala Asp Ile Glu Thr Arg Phe Pro  
 370 375 380  
 Val Gly Ser Arg His His Ala Arg Val Arg Asn Phe Thr Asn Phe Gly  
 385 390 395 400  
 Val Phe Val Glu Ile Glu Glu Gly Val Asp Gly Leu Ile His Ile Ser  
 405 410 415  
 40 Asp Leu Ser Trp Thr Lys Lys Ile Lys His Pro Ser Glu Phe Thr Glu  
 420 425 430  
 Val Gly Ala Asp Ile Glu Val Gln Val Ile Glu Ile Asp Lys Glu Asn  
 435 440 445  
 Arg Arg Leu Ser Leu Gly His Lys Gln Leu Glu Glu Asn Pro Trp Asp  
 450 455 460  
 45 Val Phe Glu Thr Val Phe Thr Val Gly Ser Ile His Glu Gly Thr Val  
 465 470 475 480  
 Ile Glu Val Met Asp Lys Gly Ala Val Val Ser Leu Pro Tyr Gly Val  
 485 490 495  
 50 Glu Gly Phe Ala Thr Pro Lys His Met Val Lys Glu Asp Gly Ser Gln  
 500 505 510  
 Ala Val Leu Glu Glu Lys Leu Pro Phe Lys Val Ile Glu Phe Asn Lys  
 515 520 525  
 55 Asp Ala Lys Arg Ile Ile Val Ser His Ser Arg Val Phe Glu Asp Glu  
 530 535 540  
 Gln Lys Met Ala Gln Arg Glu Ala Asn Ala Glu Arg Lys Ala Glu Ala  
 545 550 555 560  
 Lys Ala Ala Gln Lys Glu Ala Ala Ala Glu Ala Ala Asn Pro Ala Gln  
 565 570 575  
 60 Ala Val Glu Lys Ala Thr Leu Gly Asp Leu Gly Glu Leu Ala Ala Leu  
 580 585 590  
 Lys Glu Lys Leu Ser Glu Asn  
 595

65 (2) INFORMATION FOR SEQ ID NO:499

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 550 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

70

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

75

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499

5  
 10 Met Gly Arg Val Thr Ala Ile Asn Lys Arg Glu Val Val Ile Asn Val  
 1 5 10 15  
 Gly Tyr Lys Ser Glu Gly Val Val Pro Ala Thr Glu Phe Arg Tyr Asn  
 20 25 30  
 15 Pro Glu Leu Lys Val Gly Asp Glu Val Glu Val Tyr Ile Glu Asn Gln  
 35 40 45  
 Glu Asp Lys Lys Gly Gln Leu Val Leu Ser His Arg Lys Gly Arg Ala  
 50 55 60  
 Ala Arg Ser Trp Glu Arg Val Asn Glu Ala Leu Glu Lys Asp Glu Ile  
 65 70 75 80  
 20 Val Lys Gly Tyr Val Lys Cys Arg Thr Lys Gly Gly Met Ile Val Asp  
 85 90 95  
 Val Phe Gly Ile Glu Ala Phe Leu Pro Gly Ser Gln Ile Asp Val Arg  
 100 105 110  
 25 Pro Ile Arg Asp Tyr Asp Ala Phe Val Glu Lys Thr Met Glu Phe Lys  
 115 120 125  
 Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val Val Ser His Lys  
 130 135 140  
 Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys Glu Ile Ile Gly  
 145 150 155 160  
 30 Lys Leu Glu Lys Gly Gln Val Leu Glu Gly Ile Val Lys Asn Ile Thr  
 165 170 175  
 Ser Tyr Gly Val Phe Ile Asp Leu Gly Gly Val Asp Gly Leu Ile His  
 180 185 190  
 35 Ile Thr Asp Leu Ser Trp Gly Arg Val Ala His Pro Glu Glu Ile Val  
 195 200 205  
 Gln Leu Asp Gln Lys Ile Asn Val Val Ile Leu Asp Phe Asp Glu Asp  
 210 215 220  
 Arg Lys Arg Ile Ala Leu Gly Leu Lys Gln Leu Met Pro His Pro Trp  
 225 230 235 240  
 40 Asp Ala Leu Asp Ser Glu Leu Lys Val Gly Asp Lys Val Lys Gly Lys  
 245 250 255  
 Val Val Val Met Ala Asp Tyr Gly Ala Phe Val Glu Ile Ala Gln Gly  
 260 265 270  
 45 Val Glu Gly Leu Ile His Val Ser Glu Met Ser Trp Thr Gln His Leu  
 275 280 285  
 Arg Ser Ala Gln Asp Phe Leu His Val Gly Asp Glu Val Glu Ala Val  
 290 295 300  
 Ile Leu Thr Leu Asp Arg Glu Glu Arg Lys Met Ser Leu Gly Leu Lys  
 305 310 315 320  
 50 Gln Leu Lys Pro Asp Pro Trp Ala Asp Ile Glu Thr Arg Phe Pro Val  
 325 330 335  
 Gly Ser Arg His His Ala Arg Val Arg Asn Phe Thr Asn Phe Gly Val  
 340 345 350  
 55 Phe Val Glu Ile Glu Glu Gly Val Asp Gly Leu Ile His Ile Ser Asp  
 355 360 365  
 Leu Ser Trp Thr Lys Lys Ile Lys His Pro Ser Glu Phe Thr Glu Val  
 370 375 380  
 Gly Ala Asp Ile Glu Val Gln Val Ile Glu Ile Asp Lys Glu Asn Arg  
 385 390 395 400  
 60 Arg Leu Ser Leu Gly His Lys Gln Leu Glu Glu Asn Pro Trp Asp Val  
 405 410 415  
 Phe Glu Thr Val Phe Thr Val Gly Ser Ile His Glu Gly Thr Val Ile  
 420 425 430  
 65 Glu Val Met Asp Lys Gly Ala Val Val Ser Leu Pro Tyr Gly Val Glu  
 435 440 445  
 Gly Phe Ala Thr Pro Lys His Met Val Lys Glu Asp Gly Ser Gln Ala  
 450 455 460  
 Val Leu Glu Glu Lys Leu Pro Phe Lys Val Ile Glu Phe Asn Lys Asp  
 465 470 475 480  
 70 Ala Lys Arg Ile Ile Val Ser His Ser Arg Val Phe Glu Asp Glu Gln  
 485 490 495  
 Lys Met Ala Gln Arg Glu Ala Asn Ala Glu Arg Lys Ala Glu Ala Lys  
 500 505 510  
 75 Ala Ala Gln Lys Glu Ala Ala Ala Glu Ala Ala Asn Pro Ala Gln Ala  
 515 520 525

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Val Glu Lys Ala Thr Leu Gly Asp Leu Gly Glu Leu Ala Ala Leu Lys  
 530 535 540  
 Glu Lys Leu Ser Glu Asn  
 545 550

5

(2) INFORMATION FOR SEQ ID NO:500

10

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 458 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

20

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...458

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500

Met Ile Val Asp Val Phe Gly Ile Glu Ala Phe Leu Pro Gly Ser Gln  
 1 5 10 15  
 Ile Asp Val Arg Pro Ile Arg Asp Tyr Asp Ala Phe Val Glu Lys Thr  
 20 25 30  
 Met Glu Phe Lys Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val  
 35 40 45  
 Val Ser His Lys Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys  
 50 55 60  
 Glu Ile Ile Gly Lys Leu Glu Lys Gly Gln Val Leu Glu Gly Ile Val  
 65 70 75 80  
 Lys Asn Ile Thr Ser Tyr Gly Val Phe Ile Asp Leu Gly Gly Val Asp  
 85 90 95  
 Gly Leu Ile His Ile Thr Asp Leu Ser Trp Gly Arg Val Ala His Pro  
 100 105 110  
 Glu Glu Ile Val Gln Leu Asp Gln Lys Ile Asn Val Val Ile Leu Asp  
 115 120 125  
 Phe Asp Glu Asp Arg Lys Arg Ile Ala Leu Gly Leu Lys Gln Leu Met  
 130 135 140  
 Pro His Pro Trp Asp Ala Leu Asp Ser Glu Leu Lys Val Gly Asp Lys  
 145 150 155 160  
 Val Lys Gly Lys Val Val Met Ala Asp Tyr Gly Ala Phe Val Glu  
 165 170 175  
 Ile Ala Gln Gly Val Glu Gly Leu Ile His Val Ser Glu Met Ser Trp  
 180 185 190  
 Thr Gln His Leu Arg Ser Ala Gln Asp Phe Leu His Val Gly Asp Glu  
 195 200 205  
 Val Glu Ala Val Ile Leu Thr Leu Asp Arg Glu Glu Arg Lys Met Ser  
 210 215 220  
 Leu Gly Leu Lys Gln Leu Lys Pro Asp Pro Trp Ala Asp Ile Glu Thr  
 225 230 235 240  
 Arg Phe Pro Val Gly Ser Arg His His Ala Arg Val Arg Asn Phe Thr  
 245 250 255  
 Asn Phe Gly Val Phe Val Glu Ile Glu Glu Gly Val Asp Gly Leu Ile  
 260 265 270  
 His Ile Ser Asp Leu Ser Trp Thr Lys Lys Ile Lys His Pro Ser Glu  
 275 280 285  
 Phe Thr Glu Val Gly Ala Asp Ile Glu Val Gln Val Ile Glu Ile Asp  
 290 295 300  
 Lys Glu Asn Arg Arg Leu Ser Leu Gly His Lys Gln Leu Glu Glu Asn  
 305 310 315 320  
 Pro Trp Asp Val Phe Glu Thr Val Phe Thr Val Gly Ser Ile His Glu  
 325 330 335  
 Gly Thr Val Ile Glu Val Met Asp Lys Gly Ala Val Val Ser Leu Pro  
 340 345 350  
 Tyr Gly Val Glu Gly Phe Ala Thr Pro Lys His Met Val Lys Glu Asp  
 355 360 365  
 Gly Ser Gln Ala Val Leu Glu Glu Lys Leu Pro Phe Lys Val Ile Glu  
 370 375 380  
 Phe Asn Lys Asp Ala Lys Arg Ile Ile Val Ser His Ser Arg Val Phe  
 385 390 395 400

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Glu Asp Glu Gln Lys Met Ala Gln Arg Glu Ala Asn Ala Glu Arg Lys  
 370 375 380  
 Ala Glu Ala Lys Ala Ala Gln Lys Glu Ala Ala Ala Glu Ala Ala Asn  
 385 390 395 400  
 5 Pro Ala Gln Ala Val Glu Lys Ala Thr Leu Gly Asp Leu Gly Glu Leu  
 405 410 415  
 Ala Ala Leu Lys Glu Lys Leu Ser Glu Asn  
 420 425

## (2) INFORMATION FOR SEQ ID NO:502

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...240

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:502

30 Met Lys Lys Ala Ile Leu Ser Gly Ala Ala Leu Leu Leu Gly Leu Cys  
 1 5 10 15  
 Ala Asn Ala Gln Asn Val Gln Leu His Tyr Asp Phe Gly His Ser Ile  
 20 25 30  
 35 Tyr Asp Glu Leu Asp Gly Arg Pro Lys Leu Thr Thr Thr Val Glu Asn  
 35 40 45  
 Phe Thr Pro Asp Lys Trp Gly Ser Thr Phe Phe Phe Ile Asp Met Asp  
 50 55 60  
 Tyr Thr Gly Lys Gly Ile Gln Ser Ala Tyr Trp Glu Ile Ser Arg Glu  
 65 70 75 80  
 40 Leu Lys Phe Trp Gln Ala Pro Val Ser Ile His Leu Glu Tyr Asn Gly  
 85 90 95  
 Gly Leu Ser Thr Ser Phe Thr Phe Gly His Asp Ala Leu Ile Gly Ala  
 100 105 110  
 Thr Tyr Thr Tyr Asn Asn Pro Ser Phe Thr Arg Gly Phe Thr Ile Thr  
 115 120 125  
 45 Pro Met Tyr Lys His Leu Gly Ala His Asp Phe His Thr Tyr Gln Ile  
 130 135 140  
 Thr Gly Thr Trp Tyr Met His Phe Leu Asp Gly Leu Leu Thr Phe Asn  
 145 150 155 160  
 50 Gly Phe Leu Asp Leu Trp Gly Phe Pro Gln Glu Asn Pro Ile Gly Gly  
 165 170 175  
 Pro Val Leu Lys Glu Gly Asp Lys Phe Val Phe Leu Ser Glu Pro Gln  
 180 185 190  
 Phe Trp Ile Asn Leu Asn Arg Ile Lys Gly Ile Asp Lys Asp Phe Asn  
 195 200 205  
 55 Leu Ser Ile Gly Thr Glu Met Glu Ile Ser Arg Asn Phe Ala Arg Met  
 210 215 220  
 Asp Lys Phe Ser Cys Ile Pro Thr Leu Ala Val Lys Trp Thr Phe Asn  
 225 230 235 240

## (2) INFORMATION FOR SEQ ID NO:503

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 434 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

## (ix) FEATURE:







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Lys Asp Trp Gln Asn Gln Glu Asp Gly Tyr Gly Asp Asp Thr Glu Tyr  
 50 55 60  
 Thr Val Ala Ser Asp Arg Asp Ile Asp Ala Tyr Asn Arg Arg Asp Gly  
 65 70 75 80  
 5 Gln Ser Tyr Asp Gly Lys Lys Leu Ser Lys Asp Lys Lys Arg Asp Ser  
 85 90 95  
 Thr Arg Ser Ser Val Pro Gly Arg Tyr Ser Arg Arg Leu Ala Arg Phe  
 100 105 110  
 10 Tyr Lys Pro Asn Thr Ile Val Ile Ser Gly Ala Asp Asn Val Tyr Val  
 115 120 125  
 Thr Asp Asp Gly Glu Tyr Phe Val Tyr Gly Asp Glu Tyr Tyr Asp Asp  
 130 135 140  
 Ala Ser Ser Val Asn Ile Tyr Ile Asn Ser Pro Trp Cys Asp Pro Phe  
 145 150 155 160  
 15 Pro Tyr Thr Ser Trp Tyr Pro Ser Phe Ser Gly Trp Tyr Asn Tyr Thr  
 165 170 175  
 Trp Asn Tyr Pro Trp Phe Tyr Tyr Gly Ser His Ile Gly Trp Gly Gly  
 180 185 190  
 20 Tyr Tyr Pro Gly Tyr Asn Trp Tyr Trp Ser Tyr Tyr Tyr Asp Pro Phe  
 195 200 205  
 Tyr Asn Pro Tyr Gly Ile Gly Met Gly Trp Gly Tyr Pro Tyr Gly Trp  
 210 215 220  
 Gly Ser Tyr Tyr Gly Trp Gly Gly Tyr Pro Gly Val Ile His His Tyr  
 225 230 235 240  
 25 His His Tyr Pro Lys Lys Thr Tyr Ser Asn Gly Gln His Ser Gly Ala  
 245 250 255  
 Tyr Tyr Ser Tyr Gly Arg Pro Asn Arg Ile Lys Gly Gly Thr Ser Gly  
 260 265 270  
 30 Ala Lys Leu Gly Thr Gly Arg Tyr Asp Arg Ile Gln Asn Ser Ser Ser  
 275 280 285  
 Gln Lys Asn Lys Phe Gly Leu Gln Ser Asn Lys Pro Asn Asn Asn Leu  
 290 295 300  
 Gln Asn Val Lys Ser Gly Arg Thr Gly Arg Ala Asn Arg Asp Arg Asn  
 305 310 315 320  
 35 Ile Glu Thr Val Thr Pro Asn Asn Gly Gln Lys Gln Asn Arg Pro Val  
 325 330 335  
 Phe Gln Gln Asn Gln Ser Gly Asn Asp Arg Pro Thr Gly Arg Asn Ile  
 340 345 350  
 40 Arg Ser Glu Arg Gln Gly Glu Asn Asn Asp Arg Thr Phe Ser Thr Pro  
 355 360 365  
 Ser Arg Ser Asn Ser Asn Gly Gly Phe Ser Thr Pro Ser Arg Ser Ser  
 370 375 380  
 Ser Gly Ser Met Ser Gly Gly Gly Gly Arg Ser Gly Arg Gly Arg Asn  
 385 390 395 400

(2) INFORMATION FOR SEQ ID NO:506

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 398 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1...398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506

Met Lys Leu Ile Lys Arg Ser Leu Leu Leu Leu Gly Ala Val Leu Leu  
 1 5 10 15  
 Ile Thr Leu Pro Ala Tyr Ser Gln Asn Asp Asp Ile Phe Glu Asp Asp  
 20 25 30  
 70 Ile Tyr Thr Ser Arg Lys Glu Ile Arg Lys Gln Asn Gln Val Lys Asp  
 35 40 45  
 Trp Gln Asn Gln Glu Asp Gly Tyr Gly Asp Asp Thr Glu Tyr Thr Val  
 50 55 60  
 75 Ala Ser Asp Arg Asp Ile Asp Ala Tyr Asn Arg Arg Asp Gly Gln Ser  
 65 70 75 80

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Tyr Asp Gly Lys Lys Leu Ser Lys Asp Lys Lys Arg Asp Ser Thr Arg  
 85 90 95  
 Ser Ser Val Pro Gly Arg Tyr Ser Arg Arg Leu Ala Arg Phe Tyr Lys  
 100 105 110  
 5 Pro Asn Thr Ile Val Ile Ser Gly Ala Asp Asn Val Tyr Val Thr Asp  
 115 120 125  
 Asp Gly Glu Tyr Phe Val Tyr Gly Asp Glu Tyr Tyr Asp Asp Ala Ser  
 130 135 140  
 10 Ser Val Asn Ile Tyr Ile Asn Ser Pro Trp Cys Asp Pro Phe Pro Tyr  
 145 150 155 160  
 Thr Ser Trp Tyr Pro Ser Phe Ser Gly Trp Tyr Asn Tyr Thr Trp Asn  
 165 170 175  
 Tyr Pro Trp Phe Tyr Tyr Gly Ser His Ile Gly Trp Gly Gly Tyr Tyr  
 180 185 190  
 15 Pro Gly Tyr Asn Trp Tyr Trp Ser Tyr Tyr Tyr Asp Pro Phe Tyr Asn  
 195 200 205  
 Pro Tyr Gly Ile Gly Met Gly Trp Gly Tyr Pro Tyr Gly Trp Gly Ser  
 210 215 220  
 20 Tyr Tyr Gly Trp Gly Gly Tyr Pro Gly Val Ile His His Tyr His His  
 225 230 235 240  
 Tyr Pro Lys Lys Thr Tyr Ser Asn Gly Gln His Ser Gly Ala Tyr Tyr  
 245 250 255  
 Ser Tyr Gly Arg Pro Asn Arg Ile Lys Gly Gly Thr Ser Gly Ala Lys  
 260 265 270  
 25 Leu Gly Thr Gly Arg Tyr Asp Arg Ile Gln Asn Ser Ser Ser Gln Lys  
 275 280 285  
 Asn Lys Phe Gly Leu Gln Ser Asn Lys Pro Asn Asn Asn Leu Gln Asn  
 290 295 300  
 30 Val Lys Ser Gly Arg Thr Gly Arg Ala Asn Arg Asp Arg Asn Ile Glu  
 305 310 315 320  
 Thr Val Thr Pro Asn Asn Gly Gln Lys Gln Asn Arg Pro Val Phe Gln  
 325 330 335  
 Gln Asn Gln Ser Gly Asn Asp Arg Pro Thr Gly Arg Asn Ile Arg Ser  
 340 345 350  
 35 Glu Arg Gln Gly Glu Asn Asn Asp Arg Thr Phe Ser Thr Pro Ser Arg  
 355 360 365  
 Ser Asn Ser Asn Gly Gly Phe Ser Thr Pro Ser Arg Ser Ser Ser Gly  
 370 375 380  
 40 Ser Met Ser Gly Gly Gly Arg Ser Gly Arg Gly Arg Asn  
 385 390 395

(2) INFORMATION FOR SEQ ID NO:507

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 581 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 50 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 55 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...581  
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:507

Met Ile Arg Lys Leu Ile Leu Leu Leu Ala Leu Met Pro Val Ala Ser  
 1 5 10 15  
 Val Ala Phe Ala Val Pro Thr Asp Ser Thr Glu Ser Lys Asp Asn Arg  
 20 25 30  
 65 Ile Leu Thr Ser Met Gln Ser Ser Ser Leu Asn Arg Asp Asp Ala Pro  
 35 40 45  
 Asp Lys Trp Gln Pro Met His Ala Asn Phe Ser Ile Gln Ser Asp Met  
 50 55 60  
 70 Leu Leu Ser Thr Ala Gln Lys Ser Lys Asn Thr Trp Phe Gly Asn Ser  
 65 70 75 80  
 Tyr Ile Met Gly Ile Ile Lys Asn Asn Tyr Leu Glu Phe Gly Ala Arg  
 85 90 95  
 75 Phe Glu Asp Leu Tyr Lys Pro Leu Pro Gly His Glu Pro Glu Met Gly  
 100 105 110

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Arg Gly Val Pro His Met Tyr Val Lys Gly Ser Tyr His Trp Ala Glu  
 115 120 125  
 Leu Thr Met Gly Asp Phe Tyr Asp Gln Phe Gly Ser Gly Met Val Phe  
 130 135 140  
 5 Arg Thr Tyr Glu Glu Arg Asn Leu Gly Ile Asp Asn Ala Val Arg Gly  
 145 150 155 160  
 Gly Arg Ile Val Leu Thr Pro Phe Asp Gly Val Arg Val Lys Gly Ile  
 165 170 175  
 10 Ala Gly Gln Gln Arg Asn Tyr Phe Asp Arg Thr Gly Lys Val Phe Asn  
 180 185 190  
 Ser Gly Arg Gly Tyr Leu Leu Gly Ser Asp Leu Glu Leu Asn Val Glu  
 195 200 205  
 Arg Trp Ser Ser Ala Met Arg Asp Asn Asp Tyr His Leu Ala Ile Gly  
 210 215 220  
 15 Gly Ser Phe Val Ser Lys His Glu Ala Asp Glu Asp Ile Phe Val Gly  
 225 230 235 240  
 Val Gly Glu Asp Arg Lys Arg Leu Asn Leu Pro Leu Asn Val Pro Ile  
 245 250 255  
 20 Met Gly Leu Arg Thr Asn Phe Gln Lys Gly Gly Leu Ala Leu Tyr Ala  
 260 265 270  
 Glu Tyr Gly Tyr Lys Tyr Asn Asp Pro Ser Ala Asp Asn Asp Tyr Ile  
 275 280 285  
 Tyr His Asp Gly Gln Ala Ala Leu Leu Ser Ala Ser Tyr Ser Lys Lys  
 290 295 300  
 25 Gly Met Ser Ile Leu Leu Gln Ala Lys Arg Cys Glu Asn Phe Ala Phe  
 305 310 315 320  
 Arg Ser Lys Arg Ser Ala Gln Leu Thr Pro Leu Met Ile Asn Tyr Met  
 325 330 335  
 30 Pro Ala Phe Thr Gln Ala His Thr Tyr Thr Leu Ala Ala Ile Tyr Pro  
 340 345 350  
 Tyr Ala Thr Gln Pro Gln Gly Glu Trp Ala Phe Gln Gly Glu Leu Arg  
 355 360 365  
 Tyr Asn Phe Ala Arg Arg Thr Ala Leu Gly Gly Arg Tyr Gly Thr Gly  
 370 375 380  
 35 Leu Arg Ile Asn Val Ser His Val Arg Gly Leu Asp Lys Lys Met Leu  
 385 390 395 400  
 Lys Glu Asn Pro Asp Glu Leu Ile Gly Thr Asp Gly Tyr Thr Val Ser  
 405 410 415  
 40 Phe Phe Gly Met Gly Asp Leu Tyr Tyr Ser Asp Ile Asp Val Glu Ile  
 420 425 430  
 Thr Lys Lys Val Ser Pro Gly Phe Asn Phe Thr Leu Thr Tyr Leu Asn  
 435 440 445  
 Gln Ile Tyr Asn Asn Lys Val Leu His Gly Ala Ala Gly Glu Lys Pro  
 450 455 460  
 45 Glu Lys Ile Tyr Ala Asn Ile Phe Val Tyr Asp Gly Lys Tyr Lys Leu  
 465 470 475 480  
 Ser Asn Lys Val Ala Leu Arg Thr Glu Leu Gln Tyr Leu His Thr Lys  
 485 490 495  
 50 Gln Asp Gln Gly Asp Trp Ile Tyr Gly Met Ala Glu Leu Ser Ile Leu  
 500 505 510  
 Pro Ser Leu Met Leu Ser Leu Ser Glu Gln Tyr Asn Ile Gly Glu Thr  
 515 520 525  
 Lys Lys His Tyr Val Met Gly Ser Val Thr Tyr Thr His Gly Ala His  
 530 535 540  
 55 Arg Val Ala Phe Ser Ala Gly Lys Thr Arg Ala Gly Met Asn Cys Ser  
 545 550 555 560  
 Gly Gly Val Cys Arg Val Val Pro Glu Thr Gln Gly Phe Tyr Leu Ser  
 565 570 575  
 60 Tyr Ser Thr Asn Leu  
 580

(2) INFORMATION FOR SEQ ID NO:508

- 65 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 239 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 70 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 75 (A) ORGANISM: Porphyromonas gingivalis

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## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...239

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:508

```

Het Arg Ser Leu Phe Leu Ser Ala Leu Arg Ser Ser Ser Leu His Gly
1      5      10      15
Ser Glu Arg Arg Ser Arg Ile Ser Ser Val Val Het Ser Ile Arg
10     20     25     30
Gln Lys Ile Arg Leu Phe His Leu Ser Val Cys Ala Gln Thr His Asp
35     40     45
His Leu Ile Glu Ile His Leu Val Cys Ile Glu Phe Gly Ala Ile Asp
50     55     60
Thr Asp Glu Phe Arg Leu Ser Ser His Ala Tyr Thr Thr Ser Pro Thr
65     70     75     80
His Thr Gly Ala Ile His His Asn Cys Ile Glu Arg Ser Tyr Gly Arg
85     90     95
Tyr Leu Val Thr Phe Gly Gln Glu Arg Asn Glu Leu His His His Ser
100    105    110
Arg Pro Asp Arg Asn Ala Glu Val Tyr Arg Phe Pro Phe Asp Asn Ala
115    120    125
Phe His Ser Ile Arg Tyr Glu Ala Phe Arg Pro Ile Arg Pro Ile Val
130    135    140
Cys His Asp Asp His Phe Ile Ala Ile Gly Ser His Leu Phe Phe Lys
145    150    155    160
Asp Asn Gln Ile Phe Ser Ser Gly Ser Gln Tyr Asp Asn Tyr Thr Val
165    170    175
Ala Cys Phe Val Glu Ser Leu His Asp Arg Glu Gln Arg Ser His Thr
180    185    190
His Thr Ala Ser Gly Thr Asn His Cys Ala Asp Leu Phe Asp Het Arg
195    200    205
Thr Leu Ser Gln Arg Thr Tyr His Ile Arg Asp Ile Val Ala Asp Phe
210    215    220
Glu Phe Gly Gln Phe Leu Gly Arg Phe Ala His Gly Leu Asn His
225    230    235

```

## (2) INFORMATION FOR SEQ ID NO:509

- 40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 211 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear
- 45 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 50 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...211

## 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:509

```

Het Ser Ile Arg Gln Lys Ile Arg Leu Phe His Leu Ser Val Cys Ala
1      5      10      15
Gln Thr His Asp His Leu Ile Glu Ile His Leu Val Cys Ile Glu Phe
20     25     30
Gly Ala Ile Asp Thr Asp Glu Phe Arg Leu Ser Ser His Ala Tyr Thr
35     40     45
Thr Ser Pro Thr His Thr Gly Ala Ile His His Asn Cys Ile Glu Arg
50     55     60
Ser Tyr Gly Arg Tyr Leu Val Thr Phe Gly Gln Glu Arg Asn Glu Leu
65     70     75     80
His His His Ser Arg Pro Asp Arg Asn Ala Glu Val Tyr Arg Phe Pro
85     90     95
Phe Asp Asn Ala Phe His Ser Ile Arg Tyr Glu Ala Phe Arg Pro Ile
100    105    110
Arg Pro Ile Val Cys His Asp Asp His Phe Ile Ala Ile Gly Ser His
115    120    125
Leu Phe Phe Lys Asp Asn Gln Ile Phe Ser Ser Gly Ser Gln Tyr Asp
130    135    140

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Asn Tyr Thr Val Ala Cys Phe Val Glu Ser Leu His Asp Arg Glu Gln  
 145 150 155 160  
 Arg Ser His Thr His Thr Ala Ser Gly Thr Asn His Cys Ala Asp Leu  
 165 170 175  
 5 Phe Asp Met Arg Thr Leu Ser Gln Arg Thr Tyr His Ile Arg Asp Ile  
 180 185 190  
 Val Ala Asp Phe Glu Phe Gly Gln Phe Leu Gly Arg Phe Ala His Gly  
 195 200 205  
 10 Leu Asn His  
 210

(2) INFORMATION FOR SEQ ID NO:510

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 781 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...781

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510

Met Asp Arg Pro Lys Pro Ser Tyr Ile Val Arg Ile Ala Ala Ile Leu  
 1 5 10 15  
 Cys Leu Phe Val Gly Arg Pro Leu Phe Ala Gln Ser Tyr Val Asp Tyr  
 20 25 30  
 35 Val Asp Pro Leu Ile Gly Thr Leu Ser Ser Phe Glu Leu Ser Ala Gly  
 35 40 45  
 Asn Thr Tyr Pro Val Ile Gly Leu Pro Trp Gly Met Asn Ser Trp Thr  
 50 55 60  
 40 Pro Met Thr Gly Val Pro Gly Asp Gly Trp Gln Tyr Thr Tyr Ser Ala  
 65 70 75 80  
 His Lys Ile Arg Gly Phe Lys Gln Thr His Gln Pro Ser Pro Trp Ile  
 85 90 95  
 45 Asn Asp Tyr Gly Gln Phe Ser Leu Leu Pro Leu Thr Ala Pro Gln Lys  
 100 105 110  
 Pro Ser Ser Asn Asp Ser Ile Ala Leu Thr Lys Trp Cys Lys Gln Leu  
 115 120 125  
 Phe Ser Asp Glu Gln Thr Ser Trp Phe Ser His Lys Ala Glu Thr Ala  
 130 135 140  
 50 Thr Pro Tyr Tyr Tyr Ser Val Tyr Leu Ala Asp Tyr Asp Thr Arg Val  
 145 150 155 160  
 Glu Met Ala Pro Thr Glu Arg Ala Ala Ile Phe Arg Ile Arg Tyr Ser  
 165 170 175  
 55 Gly Asn Thr Glu Ser Gly Ser Gly Arg Trp Leu Arg Leu Asp Ala Phe  
 180 185 190  
 Thr Gly Gly Ser Glu Ile Ser Ile Val Asp Pro His Thr Val Val Gly  
 195 200 205  
 Ile Ser Arg Lys Asn Ser Gly Gly Val Pro Ala Asn Phe Ala Cys Tyr  
 210 215 220  
 60 Phe Ile Leu Gln Ser Asp Thr Pro Met Ala Asp Val Leu Leu Glu Thr  
 225 230 235 240  
 Asp Thr Gly Lys Ser Asp Glu Gly Thr Arg Ala Trp Ala Ala Cys Arg  
 245 250 255  
 65 Phe Asp Ser Gln Glu Val Thr Val Arg Val Ala Ser Ser Phe Ile Ser  
 260 265 270  
 Val Glu Gln Ala Glu Arg Asn Leu Ala Glu Val Lys Gly Gln Ser Phe  
 275 280 285  
 Asp Arg Ile Arg Leu Ala Gly Arg Glu Ala Trp Asn Lys Val Leu Gly  
 290 295 300  
 70 Arg Ile His Val Glu Gly Gly Thr Lys Asp Glu Arg Thr Thr Phe Tyr  
 305 310 315 320  
 Ser Ala Leu Tyr Arg Cys Leu Leu Phe Pro Arg Arg Phe Tyr Glu Glu  
 325 330 335  
 75 Asp Ala Ser Gly Asn Phe Val His Tyr Ser Pro Tyr Asn Gly Glu Val  
 340 345 350

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Leu Pro Gly Tyr Leu Tyr Thr Asp Thr Gly Phe Trp Asp Thr Phe Arg  
 355 360 365  
 Ala Leu Phe Pro Leu Leu Asn Leu Leu Tyr Pro Asp Glu Asn Ile Lys  
 370 375 380  
 5 Ile Gln Glu Gly Leu Leu Asn Val Tyr Arg Glu Ser Gly Phe Phe Pro  
 385 390 395 400  
 Glu Trp Ala Ser Pro Gly His Arg Asp Cys Met Ile Gly Asn Asn Ser  
 405 410 415  
 10 Ala Ser Val Leu Ala Asp Ala Tyr Leu Lys Gly Val Arg Val Glu Asp  
 420 425 430  
 Thr Arg Thr Leu Met Asn Gly Leu Leu His Ala Thr Lys Ala Val His  
 435 440 445  
 Pro Lys Ile Ser Ser Thr Gly Arg Lys Gly Trp Glu Trp Tyr Asn Ser  
 450 455 460  
 15 Leu Gly Tyr Val Pro Ala Asp Ala Gly Ile Asp Glu Ser Ala Ala Arg  
 465 470 475 480  
 Thr Leu Glu Tyr Ala Tyr Asn Asp Trp Cys Ile Leu Arg Leu Gly Arg  
 485 490 495  
 20 Thr Leu Gly Trp Asp Arg Ala Ala Leu Asp Thr Leu Ala His Arg Ser  
 500 505 510  
 Met Asn Tyr Arg His Leu Phe Asp Pro Glu Thr Lys Leu Met Arg Gly  
 515 520 525  
 Arg Asn Gln Asp Gly Ser Phe Arg Thr Pro Phe Ser Pro Phe Lys Trp  
 530 535 540  
 25 Gly Asp Val Phe Thr Glu Gly Asn Ala Trp His Tyr Thr Trp Ser Val  
 545 550 555 560  
 Phe His Asp Val Gln Gly Leu Ile Asp Leu Met Gly Gly Asp Arg Pro  
 565 570 575  
 30 Phe Val Ser Met Leu Asp Ser Val Phe Asn Thr Pro Pro Met Phe Asp  
 580 585 590  
 Glu Ser Tyr Tyr Gly Phe Val Ile His Glu Ile Arg Glu Met Gln Ile  
 595 600 605  
 Ala Asp Met Gly Asn Tyr Ala His Gly Asn Gln Pro Ile Gln His Met  
 610 615 620  
 35 Ile Tyr Leu Tyr Asn His Ala Gly His Pro Trp Lys Ala Gln Glu Arg  
 625 630 635 640  
 Leu Arg Glu Val Met Gly Arg Leu Tyr Arg Pro Thr Pro Asp Gly Tyr  
 645 650 655  
 40 Cys Gly Asp Glu Asp Asn Gly Gln Thr Ser Ala Trp Tyr Val Phe Ser  
 660 665 670  
 Ala Leu Gly Phe Tyr Pro Val Thr Pro Ala Thr Asp Gln Tyr Val Leu  
 675 680 685  
 Gly Ser Pro Ile Phe Ser Lys Val Ile Leu Ser Phe Pro Asp Gly His  
 690 695 700  
 45 Lys Thr Val Leu His Ala Pro Ala Asn Ser Ala Asp Thr Pro Tyr Ile  
 705 710 715 720  
 Arg Ser Ile Ser Val Glu Gly Lys Glu Trp Ser Cys Asn Tyr Leu Thr  
 725 730 735  
 50 His Glu Gln Leu Arg Ser Ser Ala Ser Ile Gln Trp Met Met Asp Thr  
 740 745 750  
 Lys Pro Asn Tyr Asn Arg Gly Met Lys Glu Ser Asp Arg Pro Tyr Ser  
 755 760 765  
 Phe Ser Thr Glu Gln Gln Arg Arg Ala Asn His Ser Asn  
 770 775 780

## (2) INFORMATION FOR SEQ ID NO:511

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 271 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...271  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:511

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Met Met Lys Ser Met Arg Ser Val Leu Leu Leu Phe Pro Leu Ser  
 1 5 10 15  
 Leu Ile Thr Ala Leu Gly Cys Ser Asn Asn Lys Ala Ala Glu Ser Lys  
 20 25 30  
 5 Ser Val Ser Phe Asp Ser Ala Tyr Leu Glu Arg Tyr Ile Pro Leu Arg  
 35 40 45  
 Ala Asp Ile Asp Thr Pro Ser Leu His Val Met Ile Ser Tyr Val Tyr  
 50 55 60  
 10 Pro Ser Gly Asp Asp Met Leu Thr Glu Ile Phe Asn Gly Leu Leu Phe  
 65 70 75 80  
 Gly Asp Ser Leu Met Asp Ser Ser Ser Pro Glu Asn Ala Met Glu Gly  
 85 90 95  
 Tyr Ala Gln Met Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala  
 100 105 110  
 15 Asn Leu Gln Gly Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln  
 115 120 125  
 Glu Asn Thr Ile Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile  
 130 135 140  
 20 Asn Thr Tyr Thr Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg  
 145 150 155 160  
 Phe Ala Asn Ile Leu Arg Thr Thr Gly Lys Val Leu Glu Glu Arg Asp  
 165 170 175  
 Ile Phe Lys Ile Asp Tyr Ala Glu Arg Leu Ser Ala Leu Ile Ile Gly  
 180 185 190  
 25 Gln Leu Val His Asp Phe Gly Lys Thr Thr Pro Ala Glu Leu Asp Ala  
 195 200 205  
 Ile Gly Phe Phe Asn Ala Glu Glu Ile Gln Pro Asn Gly Asn Phe Met  
 210 215 220  
 30 Ile Asp Asp Lys Gly Leu Thr Tyr Cys Phe Asn Glu Tyr Gln Ile Ala  
 225 230 235 240  
 Ala Tyr Ala Arg Gly Ala Val Tyr Val Arg Leu Gly Tyr Asp Val Leu  
 245 250 255  
 Ala Pro Leu Leu Arg Asp Asp Ser Pro Leu Lys Arg Tyr Leu Pro  
 260 265 270

(2) INFORMATION FOR SEQ ID NO:512

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature  
 (B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512

Met Lys Ser Met Arg Ser Val Leu Leu Leu Phe Pro Leu Ser Leu  
 1 5 10 15  
 Ile Thr Ala Leu Gly Cys Ser Asn Asn Lys Ala Ala Glu Ser Lys Ser  
 20 25 30  
 60 Val Ser Phe Asp Ser Ala Tyr Leu Glu Arg Tyr Ile Pro Leu Arg Ala  
 35 40 45  
 Asp Ile Asp Thr Pro Ser Leu His Val Met Ile Ser Tyr Val Tyr Pro  
 50 55 60  
 Ser Gly Asp Asp Met Leu Thr Glu Ile Phe Asn Gly Leu Leu Phe Gly  
 65 70 75 80  
 Asp Ser Leu Met Asp Ser Ser Ser Pro Glu Asn Ala Met Glu Gly Tyr  
 85 90 95  
 Ala Gln Met Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala Asn  
 100 105 110  
 70 Leu Gln Gly Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln Glu  
 115 120 125  
 Asn Thr Ile Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile Asn  
 130 135 140  
 Thr Tyr Thr Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg Phe  
 145 150 155 160

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

10 (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514

15 Met Lys Lys Thr Thr Leu Thr Gly Ser Ile Cys Ala Leu Leu Leu Phe  
 1 5 10 15  
 Leu Gly Leu Ser Ala Asn Ala Gln Ser Lys Leu Lys Ile Lys Ser Ile  
 20 20 25 30  
 Glu Ala Ala Thr Thr Phe Ser Ser Ala Thr Ala Gly Asn Gly Phe Gly  
 35 40 45  
 Gly Asn Ile Phe Gly Met Asp Met Ser Ile Arg Met Arg Val His His  
 50 55 60  
 Ser Ile Leu Pro Glu Gly Leu Asp Phe Ser Val Gly Ile His Glu Arg  
 25 65 70 75 80  
 Arg Ala His Trp Glu Glu Ala Gly Ser Pro Lys Leu Met Tyr Thr Asn  
 85 90 95  
 Val Pro Ser Ile Ile Gly Ile Val Glu Lys Val Ile Val Phe Glu Asp  
 100 105 110  
 30 Ala Glu Asp Phe Phe Asp Lys Lys Ala Leu Gly Arg Phe Leu Ile Ser  
 115 120 125  
 Leu Gly Ile Ser Tyr Thr Lys His Leu Gly Ala Tyr Trp Gly Trp Thr  
 130 135 140  
 Asn Asp Ala His Ile Leu Phe Ser Pro Ile Pro Lys Ser Lys Val His  
 35 145 150 155 160  
 Tyr Asp Thr Tyr Thr Arg Ala Gly Ser Asp Leu Val Leu Gln Ser Glu  
 165 170 175  
 Asp Val Ala Thr Val Ser Asn Gly Phe Ser Pro Gly Ile Gly Leu Lys  
 180 185 190  
 40 Ser Ser Ile Trp Trp Lys Met Pro Ile Lys Ser Lys Tyr Asp Phe Arg  
 195 200 205  
 Leu Gly Phe Ser Leu Gly Tyr Glu Tyr Leu Asn Leu Leu Tyr Pro Tyr  
 210 215 220  
 Arg Asn Phe Lys Leu Asp Gly Asn Lys Pro Leu Ser Ala Leu Ser Pro  
 45 225 230 235 240  
 Arg Met Asn His Ile Gly His Val Gly Phe Asn Phe Thr Val Gly Leu  
 245 250 255  
 Trp Thr Asn

50 (2) INFORMATION FOR SEQ ID NO:515

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1266 amino acids

55 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

60 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

65 (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515

70 Met Gly Lys Tyr Lys Arg Ala Lys Tyr Arg Tyr Trp Leu Phe Pro Phe  
 1 5 10 15  
 Cys Ser Asp Tyr Tyr Thr Phe Glu Gly Val Thr Phe Leu Cys Ala Ser  
 20 25 30  
 75 Asp Asp Met Thr Thr Lys Lys Pro Gln Ala Ile Leu Asp Leu Glu Lys

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35 40 45  
 Ala Tyr Asn Ile Glu Ile Pro Asp Leu Ser Ser Gln Glu Gly Ile Ser  
 50 55 60  
 Trp Ser Val Asn Arg Tyr Phe Lys Gln Asp Ser Ser Gly Ala Val Val  
 65 70 75 80  
 Glu Leu Cys Leu Arg Glu Cys Gln Ile Glu Ser Met Thr Trp Leu Ile  
 85 90 95  
 Asp Phe Pro Ala Leu Lys Lys Leu Asp Leu Ser Tyr Asn Gln Ile Ser  
 100 105 110  
 10 Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg Leu  
 115 120 125  
 Arg Ser Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Ser Leu Thr Ser  
 130 135 140  
 15 Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu Glu Gly  
 145 150 155 160  
 Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp Asn Gln  
 165 170 175  
 Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu  
 180 185 190  
 20 Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly Leu Arg Leu  
 195 200 205  
 Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu  
 210 215 220  
 25 Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg Leu Arg Ser  
 225 230 235 240  
 Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala  
 245 250 255  
 30 Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly Leu Glu  
 260 265 270  
 Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Ser  
 275 280 285  
 Lys Leu Glu Gly Leu Glu Arg Leu Ser Ser Leu Thr Lys Leu Arg Leu  
 290 295 300  
 35 Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser  
 305 310 315 320  
 Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu Glu Gly  
 325 330 335  
 Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp Asn Gln  
 340 345 350  
 40 Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu  
 355 360 365  
 Arg Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Asp Ser Leu  
 370 375 380  
 45 Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu  
 385 390 395 400  
 Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp  
 405 410 415  
 Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Gly Leu Ala Ser Leu Thr  
 420 425 430  
 50 Arg Leu Ser Leu Arg Arg Asn Gln Ile Ser Lys Leu Glu Gly Leu Asp  
 435 440 445  
 Arg Leu Lys Val Leu Arg Lys Leu Asp Val Ser Gly Asn Asp Ile Gln  
 450 455 460  
 55 Ser Ile Asp Asp Ile Lys Leu Leu Ala Pro Ile Leu Glu Gln Thr Leu  
 465 470 475 480  
 Glu Lys Leu Arg Ile His Asp Asn Pro Phe Val Ala Ser Ser Gly Leu  
 485 490 495  
 Ile Leu Ser Pro Tyr Asp Asn His Leu Pro Glu Ile Lys Ala Leu Leu  
 500 505 510  
 60 Glu Lys Glu Lys Glu Lys Gln Lys Lys Thr Ser Val Glu Tyr His Pro  
 515 520 525  
 Phe Cys Lys Val Met Leu Leu Glu Gly Asn His Ser Ser Gly Lys Thr Thr  
 530 535 540  
 65 Phe Leu Ser Gln Tyr Asp Thr Asn Tyr Thr Tyr Gln Lys Asn Thr His  
 545 550 555 560  
 Val Leu Ser Ile His Arg Ser Asn Asn Pro Asn Ala Ile Phe Tyr Asp  
 565 570 575  
 Phe Gly Gly Gln Asp Tyr Tyr His Gly Ile Tyr Gln Ala Phe Phe Thr  
 580 585 590  
 70 Thr Gln Ser Leu Tyr Leu Leu Phe Trp Asp Ala Lys Lys Asp Arg Asn  
 595 600 605  
 Phe Val Ser Val Asp Asp Lys Glu Tyr Gln Thr Leu Asn Phe Asn Arg  
 610 615 620  
 75 Pro Tyr Trp Leu Gly Gln Ile Ala Tyr Ala Cys Asn Arg Cys Met Ser  
 625 630 635 640

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Val Gly Gly Asn Pro Asp Gly Lys Asp Thr Pro Gln Thr Thr Asp Asp  
 645 650 655  
 Thr Ile Ile Ile Gln Thr His Ala Asp Glu Thr Gly Ala Lys Gln Gln  
 660 665 670  
 5 Thr Leu Gly Cys Ala Ala Glu Asn Gly Val Leu Glu Glu Ile Tyr Val  
 675 680 685  
 Ser Leu Glu Pro Lys Ala Asn Ser Ala Val His Ala Leu Asn Tyr Leu  
 690 695 700  
 10 Asn Glu Arg Val Arg Glu Val Val Ala Ser Arg Ser Lys Ser Ile Gln  
 705 710 715 720  
 Ile Thr Glu Lys Asp Lys Gly Leu Tyr Glu Ala Leu Pro Thr Ile Ala  
 725 730 735  
 Gly Asp Asn Lys His Ile Pro Ile Ser Leu Glu Ala Leu Ala Ala Gln  
 740 745 750  
 15 Leu Asn Lys Gly Arg Ala Glu Asn Asp Leu Tyr Thr Ile Glu Tyr Leu  
 755 760 765  
 Gln Thr Glu Leu Asn Gln Leu Ser Leu Arg Gly Glu Val Leu Tyr Tyr  
 770 775 780  
 20 Arg Glu Asn Glu Lys Leu Asn Asn Tyr Val Trp Leu Asp Pro Ala Ala  
 785 790 795 800  
 Phe Val Gln Met Ile His Gly Glu Ile Leu Gln Lys Asp Asn Ile Asn  
 805 810 815  
 Arg Gly Thr Val Pro Lys Asp Ile Phe Glu Cys Lys Leu His Asn Leu  
 820 825 830  
 25 Ser Ser Gly Ser Ile Phe Glu Glu Asp Gly Gln Asn Gly Asn Met Ile  
 835 840 845  
 Leu Gln Leu Leu Leu Glu Glu Leu Ile Val Tyr Glu Asp Lys Asp Cys  
 850 855 860  
 30 Tyr Val Ile Pro Gly Tyr Leu Pro Leu His Ser Asp Asp Glu Ala Tyr  
 865 870 875 880  
 Lys Trp Leu Thr Leu Gly Phe Glu Arg Pro Asn Phe Val Leu Lys Phe  
 885 890 895  
 Glu Arg Phe Ile Pro Phe Gly Leu Ile Asn Gln Ile Ile Ala Tyr Tyr  
 900 905 910  
 35 Gly Arg Glu Glu Gly Ala Leu Lys Arg Tyr Trp Arg Asp Gln Val Ile  
 915 920 925  
 Phe Thr Ala Gly Arg Glu Met Asp Arg Gln Thr Leu Glu Gln Glu Glu  
 930 935 940  
 40 Glu Lys Glu Gly Leu Pro Lys Thr Asn Ala Glu Asp Tyr Gln Ile Trp  
 945 950 955 960  
 Ile Lys Leu Asp Phe Thr Asp Leu Ala Ile Ser Val Phe Ile Lys Glu  
 965 970 975  
 Gln Arg Lys Thr Ser Ala Lys Asp Met Gln Arg Lys Glu Ala Thr Ile  
 980 985 990  
 45 Leu Ser Asp Met Leu Asp Met Tyr Trp Asn Asn Ile Pro Pro Arg Glu  
 995 1000 1005  
 Gln Ile Gly Asp Lys Asp Thr Glu Gln Thr Arg Ser Thr Ile Arg Glu  
 1010 1015 1020  
 50 Thr Asn Arg Lys Lys Arg Pro Ile Gln Asp Leu Tyr Leu Ser Cys Ala  
 1025 1030 1035 1040  
 Gln Ala Asp Lys Asp Leu Thr Glu Ser His Tyr Ile His Leu Gly Thr  
 1045 1050 1055  
 Leu Asp Asp Glu Ser Lys Thr Thr Ala Arg Ile Ala Ala Tyr Pro Leu  
 1060 1065 1070  
 55 Lys Asn Gly Val Ile Asp Lys Glu Arg Val Arg Glu Val Ser Thr Arg  
 1075 1080 1085  
 Pro Tyr Lys His Leu Ser Val Asn Lys Asn Leu Ala Thr Ala Lys Gln  
 1090 1095 1100  
 60 Ile Phe Ile Ser Tyr Ser Lys Glu Asp Gln Thr Glu Leu Glu Thr Cys  
 1105 1110 1115 1120  
 Leu Gln Phe Phe Lys Pro Leu Glu Lys Asn Gly Gln Ile Glu Ile Tyr  
 1125 1130 1135  
 Tyr Asp Lys Leu Thr Lys Phe Glu Thr Pro Ile His Pro Glu Ile Arg  
 1140 1145 1150  
 65 Lys Arg Ile Val Glu Ala Asp Cys Ile Ile Ala Leu Ile Ser Gln Arg  
 1155 1160 1165  
 Tyr Leu Ala Thr Asp Tyr Ile Leu Asp His Glu Leu Pro Val Phe Arg  
 1170 1175 1180  
 70 Glu Tyr Asn Lys Thr Ile Val Pro Ile Leu Ile Lys Pro Cys Thr Phe  
 1185 1190 1195 1200  
 Glu Asp Asp Glu Phe Leu Arg Glu Lys Tyr Phe Ala Gln Lys Ala Gln  
 1205 1210 1215  
 Ile Ile Asn Leu Gly Lys Glu Gly Lys Thr Ile Lys Ala Tyr Asp Ser  
 1220 1225 1230  
 75 Ile Thr Ala Ser Ala His Arg Asp Glu Asn Trp Val Ala Val Val Arg

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1235 1240 1245  
 Glu Phe Lys Glu Lys Ile Leu Arg Ile Thr Lys Gln Glu Val Asn Thr  
 1250 1255 1260  
 Asp Glu  
 1265

5 (2) INFORMATION FOR SEQ ID NO:516

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1232 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...1232

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:516

Met Thr Thr Lys Lys Pro Gln Ala Ile Leu Asp Leu Glu Lys Ala Tyr  
 1 5 10 15  
 30 Asn Ile Glu Ile Pro Asp Leu Ser Ser Gln Glu Gly Ile Ser Trp Ser  
 20 25 30  
 Val Asn Arg Tyr Phe Lys Gln Asp Ser Ser Gly Ala Val Val Glu Leu  
 35 40 45  
 Cys Leu Arg Glu Cys Gln Ile Glu Ser Met Thr Trp Leu Ile Asp Phe  
 50 55 60  
 35 Pro Ala Leu Lys Lys Leu Asp Leu Ser Tyr Asn Gln Ile Ser Lys Leu  
 65 70 75 80  
 Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg Leu Arg Ser  
 85 90 95  
 40 Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Ser Leu Thr Ser Leu Thr  
 100 105 110  
 Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu  
 115 120 125  
 Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp Asn Gln Ile Ser  
 130 135 140  
 45 Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu  
 145 150 155 160  
 Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser  
 165 170 175  
 50 Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly  
 180 185 190  
 Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg Leu Arg Ser Asn Gln  
 195 200 205  
 Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu  
 210 215 220  
 55 Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu  
 225 230 235 240  
 Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Ser Lys Leu  
 245 250 255  
 60 Glu Gly Leu Glu Arg Leu Ser Ser Leu Thr Lys Leu Arg Leu Arg Ser  
 260 265 270  
 Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr  
 275 280 285  
 Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu  
 290 295 300  
 65 Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp Asn Gln Ile Arg  
 305 310 315 320  
 Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg Leu  
 325 330 335  
 70 Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Asp Ser Leu Thr Ser  
 340 345 350  
 Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu Glu Gly  
 355 360 365  
 Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp Asn Gln  
 370 375 380  
 75 Ile Arg Lys Leu Glu Gly Leu Asp Gly Leu Ala Ser Leu Thr Arg Leu

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Arg Lys Lys Arg Pro Ile Gln Asp Leu Tyr Leu Ser Cys Ala Gln Ala  
 995 1000 1005  
 Asp Lys Asp Leu Thr Glu Ser His Tyr Ile His Leu Gly Thr Leu Asp  
 1010 1015 1020  
 5 Asp Glu Ser Lys Thr Thr Ala Arg Ile Ala Ala Tyr Pro Leu Lys Asn  
 1025 1030 1035 1040  
 Gly Val Ile Asp Lys Glu Arg Val Arg Glu Val Ser Thr Arg Pro Tyr  
 1045 1050 1055  
 10 Lys His Leu Ser Val Asn Lys Asn Leu Ala Thr Ala Lys Gln Ile Phe  
 1060 1065 1070  
 Ile Ser Tyr Ser Lys Glu Asp Gln Thr Glu Leu Glu Thr Cys Leu Gln  
 1075 1080 1085  
 Phe Phe Lys Pro Leu Glu Lys Asn Gly Gln Ile Glu Ile Tyr Tyr Asp  
 1090 1095 1100  
 15 Lys Leu Thr Lys Phe Glu Thr Pro Ile His Pro Glu Ile Arg Lys Arg  
 1105 1110 1115 1120  
 Ile Val Glu Ala Asp Cys Ile Ile Ala Leu Ile Ser Gln Arg Tyr Leu  
 1125 1130 1135  
 20 Ala Thr Asp Tyr Ile Leu Asp His Glu Leu Pro Val Phe Arg Glu Tyr  
 1140 1145 1150  
 Asn Lys Thr Ile Val Pro Ile Leu Ile Lys Pro Cys Thr Phe Glu Asp  
 1155 1160 1165  
 Asp Glu Phe Leu Arg Glu Lys Tyr Phe Ala Gln Lys Ala Gln Ile Ile  
 1170 1175 1180  
 25 Asn Leu Gly Lys Glu Gly Lys Thr Ile Lys Ala Tyr Asp Ser Ile Thr  
 1185 1190 1195 1200  
 Ala Ser Ala His Arg Asp Glu Asn Trp Val Ala Val Val Arg Glu Phe  
 1205 1210 1215  
 30 Lys Glu Lys Ile Leu Arg Ile Thr Lys Gln Glu Val Asn Thr Asp Glu  
 1220 1225 1230

(2) INFORMATION FOR SEQ ID NO:517

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1175 amino acids  
 (R) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 40 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 45 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1175  
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:517

Met Thr Trp Leu Ile Asp Phe Pro Ala Leu Lys Lys Leu Asp Leu Ser  
 1 5 10 15  
 55 Tyr Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu  
 20 25 30  
 Thr Lys Leu Arg Leu Arg Ser Asn Gln Ile Arg Lys Leu Glu Gly Leu  
 35 40 45  
 Asp Ser Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile  
 50 55 60  
 60 Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr  
 65 70 75 80  
 Leu Leu Asp Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr  
 85 90 95  
 65 Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu  
 100 105 110  
 Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn  
 115 120 125  
 Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys  
 130 135 140  
 70 Leu Arg Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg  
 145 150 155 160  
 Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys  
 165 170 175  
 75 Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser  
 180 185 190

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Gly Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Ser Ser Leu  
 195 200 205  
 Thr Lys Leu Arg Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu  
 210 215 220  
 5 Glu Arg Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile  
 225 230 235 240  
 Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr  
 245 250 255  
 10 Leu Leu Asp Asn Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr  
 260 265 270  
 Ser Leu Thr Lys Leu Arg Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu  
 275 280 285  
 Gly Leu Asp Ser Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn  
 290 295 300  
 15 Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu  
 305 310 315 320  
 Leu Tyr Leu Leu Asp Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Gly  
 325 330 335  
 20 Leu Ala Ser Leu Thr Arg Leu Ser Leu Arg Arg Asn Gln Ile Ser Lys  
 340 345 350  
 Leu Glu Gly Leu Asp Arg Leu Lys Val Leu Arg Lys Leu Asp Val Ser  
 355 360 365  
 Gly Asn Asp Ile Gln Ser Ile Asp Asp Ile Lys Leu Ala Pro Ile  
 370 375 380  
 25 Leu Glu Gln Thr Leu Glu Lys Leu Arg Ile His Asp Asn Pro Phe Val  
 385 390 395 400  
 Ala Ser Ser Gly Leu Ile Leu Ser Pro Tyr Asp Asn His Leu Pro Glu  
 405 410 415  
 30 Ile Lys Ala Leu Leu Glu Lys Glu Lys Glu Lys Gln Lys Lys Thr Ser  
 420 425 430  
 Val Glu Tyr His Pro Phe Cys Lys Val Met Leu Leu Gly Asn His Ser  
 435 440 445  
 Ser Gly Lys Thr Thr Phe Leu Ser Gln Tyr Asp Thr Asn Tyr Thr Tyr  
 450 455 460  
 35 Gln Lys Asn Thr His Val Leu Ser Ile His Arg Ser Asn Asn Pro Asn  
 465 470 475 480  
 Ala Ile Phe Tyr Asp Phe Gly Gly Gln Asp Tyr Tyr His Gly Ile Tyr  
 485 490 495  
 40 Gln Ala Phe Phe Thr Thr Gln Ser Leu Tyr Leu Leu Phe Trp Asp Ala  
 500 505 510  
 Lys Lys Asp Arg Asn Phe Val Ser Val Asp Asp Lys Glu Tyr Gln Thr  
 515 520 525  
 Leu Asn Phe Asn Arg Pro Tyr Trp Leu Gly Gln Ile Ala Tyr Ala Cys  
 530 535 540  
 45 Asn Arg Cys Met Ser Val Gly Gly Asn Pro Asp Gly Lys Asp Thr Pro  
 545 550 555 560  
 Gln Thr Thr Asp Asp Thr Ile Ile Ile Gln Thr His Ala Asp Glu Thr  
 565 570 575  
 50 Gly Ala Lys Gln Gln Thr Leu Gly Cys Ala Ala Glu Asn Gly Val Leu  
 580 585 590  
 Glu Glu Ile Tyr Val Ser Leu Glu Pro Lys Ala Asn Ser Ala Val His  
 595 600 605  
 Ala Leu Asn Tyr Leu Asn Glu Arg Val Arg Glu Val Val Ala Ser Arg  
 610 615 620  
 55 Ser Lys Ser Ile Gln Ile Thr Glu Lys Asp Lys Gly Leu Tyr Glu Ala  
 625 630 635 640  
 Leu Pro Thr Ile Ala Gly Asp Asn Lys His Ile Pro Ile Ser Leu Glu  
 645 650 655  
 60 Ala Leu Ala Ala Gln Leu Asn Lys Gly Arg Ala Glu Asn Asp Leu Tyr  
 660 665 670  
 Thr Ile Glu Tyr Leu Gln Thr Glu Leu Asn Gln Leu Ser Leu Arg Gly  
 675 680 685  
 Glu Val Leu Tyr Tyr Arg Glu Asn Glu Lys Leu Asn Asn Tyr Val Trp  
 690 695 700  
 65 Leu Asp Pro Ala Ala Phe Val Gln Met Ile His Gly Glu Ile Leu Gln  
 705 710 715 720  
 Lys Asp Asn Ile Asn Arg Gly Thr Val Pro Lys Asp Ile Phe Glu Cys  
 725 730 735  
 70 Lys Leu His Asn Leu Ser Ser Gly Ser Ile Phe Glu Glu Asp Gly Gln  
 740 745 750  
 Asn Gly Asn Met Ile Leu Gln Leu Leu Glu Glu Ile Val Tyr  
 755 760 765  
 Glu Asp Lys Asp Cys Tyr Val Ile Pro Gly Tyr Leu Pro Leu His Ser  
 770 775 780  
 75 Asp Asp Glu Ala Tyr Lys Trp Leu Thr Leu Gly Phe Glu Arg Pro Asn

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785                      790                      795                      800  
 Phe Val Leu Lys Phe Glu Arg Phe Ile Pro Phe Gly Leu Ile Asn Gln  
                          805                      810                      815  
 5    Ile Ile Ala Tyr Tyr Gly Arg Glu Glu Gly Ala Leu Lys Arg Tyr Trp  
                          820                      825                      830  
 Arg Asp Gln Val Ile Phe Thr Ala Gly Arg Glu Met Asp Arg Gln Thr  
                          835                      840                      845  
 Leu Glu Gln Glu Glu Glu Lys Glu Gly Leu Pro Lys Thr Asn Ala Glu  
                          850                      855                      860  
 10   Asp Tyr Gln Ile Trp Ile Lys Leu Asp Phe Thr Asp Leu Ala Ile Ser  
                          865                      870                      875                      880  
 Val Phe Ile Lys Glu Gln Arg Lys Thr Ser Ala Lys Asp Met Gln Arg  
                          885                      890                      895  
 15   Lys Glu Ala Thr Ile Leu Ser Asp Met Leu Asp Met Tyr Trp Asn Asn  
                          900                      905                      910  
 Ile Pro Pro Arg Glu Gln Ile Gly Asp Lys Asp Thr Glu Gln Thr Arg  
                          915                      920                      925  
 Ser Thr Ile Arg Glu Thr Asn Arg Lys Lys Arg Pro Ile Gln Asp Leu  
                          930                      935                      940  
 20   Tyr Leu Ser Cys Ala Gln Ala Asp Lys Asp Leu Thr Glu Ser His Tyr  
                          945                      950                      955                      960  
 Ile His Leu Gly Thr Leu Asp Asp Glu Ser Lys Thr Thr Ala Arg Ile  
                          965                      970                      975  
 25   Ala Ala Tyr Pro Leu Lys Asn Gly Val Ile Asp Lys Glu Arg Val Arg  
                          980                      985                      990  
 Glu Val Ser Thr Arg Pro Tyr Lys His Leu Ser Val Asn Lys Asn Leu  
                          995                      1000                      1005  
 Ala Thr Ala Lys Gln Ile Phe Ile Ser Tyr Ser Lys Glu Asp Gln Thr  
                          1010                      1015                      1020  
 30   Glu Leu Glu Thr Cys Leu Gln Phe Phe Lys Pro Leu Glu Lys Asn Gly  
                          1025                      1030                      1035                      1040  
 Gln Ile Glu Ile Tyr Tyr Asp Lys Leu Thr Lys Phe Glu Thr Pro Ile  
                          1045                      1050                      1055  
 35   His Pro Glu Ile Arg Lys Arg Ile Val Glu Ala Asp Cys Ile Ile Ala  
                          1060                      1065                      1070  
 Leu Ile Ser Gln Arg Tyr Leu Ala Thr Asp Tyr Ile Leu Asp His Glu  
                          1075                      1080                      1085  
 Leu Pro Val Phe Arg Glu Tyr Asn Lys Thr Ile Val Pro Ile Leu Ile  
                          1090                      1095                      1100  
 40   Lys Pro Cys Thr Phe Glu Asp Asp Glu Phe Leu Arg Glu Lys Tyr Phe  
                          1105                      1110                      1115                      1120  
 Ala Gln Lys Ala Gln Ile Ile Asn Leu Gly Lys Glu Gly Lys Thr Ile  
                          1125                      1130                      1135  
 45   Lys Ala Tyr Asp Ser Ile Thr Ala Ser Ala His Arg Asp Glu Asn Trp  
                          1140                      1145                      1150  
 Val Ala Val Val Arg Glu Phe Lys Glu Lys Ile Leu Arg Ile Thr Lys  
                          1155                      1160                      1165  
 Gln Glu Val Asn Thr Asp Glu  
                          1170                      1175  
 50   (2) INFORMATION FOR SEQ ID NO:518  
       (i) SEQUENCE CHARACTERISTICS:  
          (A) LENGTH: 229 amino acids  
          (B) TYPE: amino acid  
          (D) TOPOLOGY: linear  
 55       (ii) MOLECULE TYPE: protein  
 60       (iii) HYPOTHETICAL: YES  
       (vi) ORIGINAL SOURCE:  
          (A) ORGANISM: Porphyromonas gingivalis  
 65       (ix) FEATURE:  
          (A) NAME/KEY: misc\_feature  
          (B) LOCATION 1...229  
 70       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:518  
 75   Met Met Lys Lys Ala Phe Val Phe Val Leu Leu Val Cys Leu Phe Ser  
       1                      5                      10                      15  
       Ser Phe Ser Ser Ser Ala Gln Thr Thr Thr Asn Ser Ser Arg Ser Tyr  
                          20                      25                      30  
       Phe Thr Gly Arg Ile Glu Lys Val Ser Leu Asn Leu Gly Val Pro Pro



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(2) INFORMATION FOR SEQ ID NO:520

5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 540 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis

15 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...540

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:520

	Met	Lys	Thr	Lys	Val	Leu	Arg	Lys	Phe	Val	Val	Ala	Ala	Phe	Ala	Val
	1			5						10					15	
25	Ala	Thr	Leu	Cys	Pro	Leu	Ala	Gln	Ala	Gln	Thr	Met	Gly	Gly	Asp	Asp
			20						25					30		
	Val	Lys	Val	Val	Gln	Tyr	Asn	Gln	Glu	Lys	Leu	Val	Gln	Thr	Arg	Met
		35					40						45			
30	Ser	Val	Ala	Asp	Asn	Gly	Trp	Ile	Tyr	Val	Met	Thr	His	Ser	Gly	Tyr
		50					55					60				
	Asp	Thr	Gly	Asn	Ser	Asn	Val	Lys	Ile	Phe	Arg	Ser	Lys	Asp	Gln	Gly
		65				70					75				80	
	Ala	Thr	Tyr	Gln	Lys	Leu	Arg	Asp	Trp	Asp	Pro	Ser	Asp	Asp	Tyr	Gln
				85						90				95		
35	Phe	Gln	Asp	Phe	Asp	Ile	Val	Val	Thr	Gly	Lys	Asn	Glu	Ser	Asp	Ile
				100					105					110		
	Lys	Ile	Trp	Ser	Val	Glu	Leu	Met	Asn	Lys	Pro	Gly	Gly	Tyr	Lys	Ser
		115					120						125			
40	Arg	Val	Ala	Val	Phe	Ser	Arg	Asp	Ala	Asn	Ala	Gln	Asn	Ala	Lys	Leu
		130					135					140				
	Val	Tyr	Lys	Glu	Asp	Phe	Ser	Asn	Val	Gln	Leu	Tyr	Asp	Val	Asp	Ile
		145				150					155				160	
	Ala	Ser	Asn	Tyr	Arg	Ser	Pro	Ser	Ser	Leu	Asn	Asn	Gly	Gly	Asn	Pro
				165						170				175		
45	Phe	Ala	Leu	Ala	Phe	Ala	Tyr	Thr	Gly	Phe	Asn	Asn	Thr	His	Lys	Ile
			180						185					190		
	Ser	Phe	Val	Asp	Tyr	Val	Phe	Ser	Leu	Asn	Gly	Gly	Gln	Asn	Phe	Asn
			195				200						205			
50	Lys	Asn	Leu	Leu	Phe	Ser	Gln	Asp	Gly	Glu	Lys	Lys	Ile	Asp	Lys	Val
		210					215					220				
	Asp	Leu	Ser	Leu	Gly	Ser	Thr	Ser	Glu	Ser	Met	Gly	His	Asn	Ala	Trp
		225				230					235				240	
	Pro	Leu	Met	Gly	Val	Val	Phe	Glu	Met	Asn	Lys	Gln	Gly	Gly	Lys	Ser
				245						250				255		
55	Asp	Ile	Gly	Phe	Leu	Ser	Asn	Phe	Val	Asp	Asn	Asp	Pro	Glu	Phe	Gln
				260					265					270		
	Trp	Ser	Gly	Pro	Ile	Lys	Val	Ser	Glu	Ser	Asp	Met	Ser	Phe	Ser	Pro
			275				280						285			
60	Lys	Ile	Gln	Met	Leu	Leu	Asp	Glu	Asp	Asn	Asn	Thr	Ile	Asn	Gly	Glu
		290					295					300				
	Ser	Cys	His	Asn	Phe	Met	Ile	Thr	Tyr	Ser	Asp	Tyr	Asp	Ser	Glu	Tyr
				305			310				315				320	
	Ser	Asp	Trp	Asp	Ile	Arg	Tyr	Val	Tyr	Pro	Lys	Lys	Ser	Phe	Lys	Tyr
				325						330				335		
65	Glu	Lys	Gly	Lys	Thr	Pro	Thr	Met	Asp	Asp	Leu	Val	Glu	Ala	Phe	Leu
				340					345					350		
	Thr	Ala	Ser	Tyr	Gln	Ser	Glu	Thr	Asn	Ser	Gly	Leu	Gly	Tyr	Asp	Lys
				355				360					365			
70	Asn	Ala	Asn	His	Tyr	Leu	Ile	Thr	Tyr	Ala	Lys	Lys	Glu	Glu	Asn	Gly
				370			375					380				
	Thr	Asn	Thr	Leu	Lys	Tyr	Arg	Trp	Ala	Asn	Tyr	Asp	Lys	Ile	His	Asn
				385			390					395			400	
	Lys	Asp	Leu	Trp	Ser	Asp	Thr	Phe	Thr	Tyr	Thr	Ser	Ser	Ala	Asn	Ala
				405						410				415		
75	Leu	Tyr	Thr	Pro	Gln	Val	Asp	Ile	Asn	Pro	Thr	Lys	Gly	Leu	Val	Cys

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(A) NAME/KEY: misc feature  
(B) LOCATION 1...776

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:522

5 Met Cys Lys Ile Arg Phe Ser Leu Leu Gln Ala Leu Val Val Cys Leu  
1 5 10 15  
Leu Phe Thr Ser Phe Ser Leu Gln Ala Gln Glu Glu Gly Ile Trp Asn  
20 25 30  
10 Thr Leu Leu Ala Ile His Lys Thr Glu Lys Ala Val Glu Thr Pro Lys  
35 40 45  
Lys Val Phe Ala Val Ala Asn Gly Val Leu Tyr Ser Val Gly Lys Glu  
50 55 60  
15 Ala Pro His Glu Ala Lys Ile Phe Asp Arg Ile Ser Gly Leu Ser Asp  
65 70 75 80  
Thr Ser Val Ser Ser Ile Ala Tyr Ser Glu Gln Leu Lys Ser Leu Val  
85 90 95  
Ile Tyr Tyr Ala Ser Gly Asn Ile Asp Ile Leu Asp Glu Ala Gly Arg  
100 105 110  
20 Val Thr Asn Val Pro Ala Leu Lys Asp Asn Ile Asp Leu Ile Asp Lys  
115 120 125  
Thr Leu Asn Arg Leu Leu Ile Val Gly Asn Arg Ala Tyr Leu Ala Gly  
130 135 140  
25 Gly Phe Gly Leu Ser Val Leu Asp Val Ala Glu Ala Arg Ile Pro Ala  
145 150 155 160  
Thr Tyr Ala Lys Gly Thr Lys Val Thr Asp Val Ala Lys Leu Asp Asn  
165 170 175  
Asp Arg Leu Leu Met Leu Lys Glu Gly Gln Leu Phe Ile Gly Lys Glu  
180 185 190  
30 Thr Asp Asn Leu Gln Asp Pro Ala Ala Trp Thr Ala Leu Ser Leu Asn  
195 200 205  
Leu Pro Met Gly Ser Val Thr Gly Leu Gly Ile Val Gly Glu Asp Ile  
210 215 220  
35 Cys Phe Leu Leu Ala Asp Gly Arg Val Tyr Val Ala Ala Asn Gln Ser  
225 230 235 240  
Phe Glu Pro Glu Leu Leu Ser Ser Ser Ala Asp Ser Arg Leu Tyr  
245 250 255  
Val Thr Asp Arg Gly Leu Phe Ile Cys Ala Glu Asn Arg Ile Tyr Phe  
260 265 270  
40 Ile Glu Lys Gly Arg Lys Thr Thr Gln Phe Pro Ile Ala Asp Val Leu  
275 280 285  
Gly Val Gly Ala Met Asn Glu Ser Asn Thr Ala Tyr Ile Ala Leu Gly  
290 295 300  
45 Glu Glu Gly Leu Ala Ser Leu Leu Ala Glu Gly Ser Thr Ala Glu  
305 310 315 320  
Ala Met Pro Val Ala Phe Asp Gly Pro Gly Asp Asn Asp Phe Tyr Glu  
325 330 335  
Met Arg Phe Ser His Gly Arg Leu Tyr Ala Ala Ser Gly Leu Trp Gly  
340 345 350  
50 Thr Asn Leu Met Gly His Ala Gly Met Val Lys Leu Tyr Asp Gly Asn  
355 360 365  
Arg Trp Thr Asn Phe Asp Lys Lys Thr Val Gln Glu Gln Leu Gly Gly  
370 375 380  
55 Gly Phe Ser Phe Asn Asp Ala Ile Asp Ile Ala Val Ser Asn Gly Asp  
385 390 395 400  
Pro Asp His Phe Phe Val Gly Thr Trp Gly Asn Gly Leu Phe Glu Phe  
405 410 415  
Lys Asp Gly Lys Ala Ile Ala Arg Tyr Ser Gly Asn Glu Thr Ala Ile  
420 425 430  
60 Ala Glu Cys Asn Pro Gly Asp Ala Arg Val Lys Ala Ile Ala Phe Asp  
435 440 445  
Asn Lys Gly Asn Leu Trp Gly Thr Leu Gly Ala Val Gly Lys Asn Ile  
450 455 460  
65 Phe Met Tyr Asp Pro Gln Ser Ser Thr Trp His Ser Phe Ser Tyr Pro  
465 470 475 480  
Asp Val Ala Asn Leu Ala Ser Phe Gly Asn Met Ile Ile Leu Pro Asn  
485 490 495  
Gly Asp Lys Trp Val Asn Ile Leu His Arg Ser Gly Gly Ser Thr Arg  
500 505 510  
70 Lys Gly Val Leu Ile Phe Asn Asp Arg Gly Thr Pro Glu Thr Thr Ser  
515 520 525  
Asp Asp Ser His Leu Tyr Val Glu Gln Phe Val Asn Arg Leu Gly Ala  
530 535 540  
75 Ala Ile Gly His Lys Thr Ile Tyr Ala Met Ala Val Asp His Asn Gly  
545 550 555 560

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Ser Val Trp Met Gly Ser Asp Ile Gly Ile Phe Gly Val Tyr Asn Ala  
 565 570 575  
 Ala Gly Val Leu Ser Ser Thr Ser Thr Pro Ile Ala Val Arg Pro Val  
 580 585 590  
 5 Gly Gly Glu Glu Pro Asn Leu Tyr Tyr Val Leu Asp Lys Val Thr Val  
 595 600 605  
 Thr Asp Ile Val Val Asp Lys Leu Asn His Lys Trp Val Ala Thr Gln  
 610 615 620  
 10 Gly Thr Gly Leu Tyr Leu Leu Ser Glu Asp Cys Ser Lys Ile Leu Ala  
 625 630 635 640  
 Gln Phe Thr Val Glu Asn Ser Pro Leu Leu Ser Asn Asn Ile Leu Ser  
 645 650 655  
 Leu Ala Leu Asn Asp Asp Asn Gly Leu Leu Tyr Ile Gly Thr Ala Asp  
 660 665 670  
 15 Gly Leu Met Thr Phe Gln Thr Gly Thr Gly Ser Gly Ser Ala Ser Glu  
 675 680 685  
 Leu Asp Gly Val Tyr Val Tyr Pro Asn Pro Leu Arg Pro Glu Tyr Pro  
 690 695 700  
 20 Asp Gly Val Thr Ile Ala Gly Leu Gln Ala Gly Cys Ser Val Lys Ile  
 705 710 715 720  
 Thr Asp Thr Thr Gly Arg Leu Leu Tyr Gln Thr Glu Ser Val Thr Thr  
 725 730 735  
 Glu Val Lys Trp Asn Ala Arg Gly Ala Asp Gly Asn Arg Val Ala Ser  
 740 745 750  
 25 Gly Val Tyr Ala Val Ala Val Tyr Asp Pro Val Ser Lys Ser Lys  
 755 760 765  
 Leu Ile Arg Phe Ala Val Ile Arg  
 770 775  
 30 (2) INFORMATION FOR SEQ ID NO:523  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1158 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 35 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: YES  
 40 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1...1158  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:523  
 50 Met Lys Arg Ile Leu Pro Ile Val Ala Phe Leu Ser Leu Phe Leu Ala  
 1 5 10 15  
 Leu Ala Leu Pro Ala Lys Ala Gln Arg Ala Met Gly Lys Thr Ala Asp  
 20 25 30  
 55 Arg Ser Leu Met Ala Ser Gly His Trp Val Lys Ile Arg Val Asp Ala  
 35 40 45  
 Ser Gly Val Tyr Arg Leu Thr Asp Glu Gln Leu Arg Ala Asn Gly Phe  
 50 55 60  
 Ser Asp Pro Ser Lys Val Gly Val Phe Gly Tyr Gly Gly Val Leu  
 65 70 75 80  
 60 Pro Glu Asp Leu Ser Arg Ile Thr Thr Asp Asp Leu Pro Pro Val Pro  
 85 90 95  
 Val Leu Arg Gln Gly Asn Ala Leu Tyr Phe Tyr Ala Val Gly Pro Val  
 100 105 110  
 65 Thr Trp Phe Tyr Asn Pro Ala Lys Thr Thr Met Glu His Thr Val Asn  
 115 120 125  
 Thr Tyr Ser Thr His Gly Tyr Tyr Phe Leu Ser Asp Ala Ala Gly Ala  
 130 135 140  
 Pro Leu Gln Met Ser Gln Tyr Thr Gly Gly Gly Ala Ser Ala Glu Ala  
 145 150 155 160  
 70 Leu Ile Asp Tyr Tyr Asp Glu Leu Met Leu His Glu Gln Glu Leu Tyr  
 165 170 175  
 Ser Pro Lys Glu Ser Gly Arg Asp Leu Tyr Gly Glu Ser Phe Ser Ala  
 180 185 190  
 75 Val Asn Thr Arg Thr Val Lys Phe Pro Leu Arg Gly Asn Thr Arg Ser  
 195 200 205

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Ser Gly Glu Leu Gly Thr Val Phe Ser Tyr Ile Ala Lys Ala Arg Ser  
 210 215 220  
 Ala Gly Gly Arg Glu Met Ser Leu Ser Ala Asn Gly Ile Leu Ile  
 225 230 235 240  
 5 Phe Ser Asp Pro Phe Ser Met Thr Ser Asn Glu Val Ser Asn Ser Tyr  
 245 250 255  
 Leu Ala Gly Lys Lys Arg Arg Leu Tyr His Ser Thr Pro Met Asn Ser  
 260 265 270  
 10 Leu Val Asn Glu Leu Arg Leu Asp Ala Asn Tyr Ser Met Thr Gly Asp  
 275 280 285  
 Ala Val Asn Leu Asp Phe Ile Glu Val Ala Thr Gln Asn Asp Leu Arg  
 290 295 300  
 Tyr Asp Gly Ala Pro Met His Ile Arg Arg Phe Ser Asn Leu Pro Val  
 305 310 315 320  
 15 Leu Gly Gly Glu Ser Cys Arg Phe Val Ile Ser Glu Val Pro Glu Ser  
 325 330 335  
 Leu Val Val Leu Gln Ala Asn Ser Ser Leu Thr Ala Ser Leu Val Pro  
 340 345 350  
 20 Val Lys Thr Val Gly Asp Lys Thr Ile Glu Phe Val Ala Pro Pro Lys  
 355 360 365  
 Gly Gln Asp Arg Arg Thr Ile Asn Thr Phe Tyr Ala Val Asp Leu Ser  
 370 375 380  
 Gln Ala Ser Ala Pro Glu Ile Leu Gly Ala Val Pro Asn Gln Asn Leu  
 385 390 395 400  
 25 His Gly Glu Glu Ile Pro Asp Leu Ile Ile Val Ser Thr Gln Ala Leu  
 405 410 415  
 Leu Leu Glu Ala Asp Arg Leu Ala Thr Tyr Arg Arg Glu Lys Asn Gly  
 420 425 430  
 30 Leu Lys Val Leu Val Val Leu Gln Glu Gln Val Phe Asn Glu Phe Ser  
 435 440 445  
 Gly Gly Thr Pro Asp Ala Thr Ala Tyr Arg Leu Phe Ala Lys Met Phe  
 450 455 460  
 Tyr Asp Arg Trp Lys Ala Asn Ala Pro Val Gly Glu Thr Phe Pro Met  
 465 470 475 480  
 35 Gln Met Leu Leu Phe Gly Asp Gly Ala His Asp Asn Arg Lys Val Ser  
 485 490 495  
 Val Ala Trp Gln Lys Pro Tyr Leu Gln Thr Glu Phe Leu Leu Thr  
 500 505 510  
 40 Phe Gln Ala Val Asn Ser Thr Asn Val Asn Ser Tyr Val Thr Asp Asp  
 515 520 525  
 Tyr Phe Gly Leu Leu Asp Asp Gln Pro Ala Ser Val Asn Ile Gly Trp  
 530 535 540  
 Arg Asn Tyr Asn Met Ala Val Gly Arg Phe Pro Val Arg Thr Pro Ala  
 545 550 555 560  
 45 Glu Ala Arg Ile Ala Val Asp Lys Thr Ile Arg Tyr Glu Glu Asp Arg  
 565 570 575  
 Glu Ser Gly Ala Trp Arg Ile Arg Ala Cys Phe Ala Ala Asp Asn Gly  
 580 585 590  
 50 Asp Lys His Ala Thr Glu Thr Ser Arg Leu Ile Asp Thr Val Lys Arg  
 595 600 605  
 Tyr Ala Pro Ala Ile Met Pro Val Arg Ala Phe Gln Asp Val Tyr Pro  
 610 615 620  
 His Val Ile Glu Asn Gly Leu His Ser Ile Pro Gly Ala Lys Lys Lys  
 625 630 635 640  
 55 Met Leu Glu Thr Leu Gln Ser Gly Ile Ile Leu Leu Asn Tyr Ala Gly  
 645 650 655  
 His Gly Gly Pro Ala Gly Trp Ser Asp Glu His Leu Leu Thr Leu Asn  
 660 665 670  
 60 Asp Ile His Lys Phe Asn Tyr Lys His Met Pro Ile Trp Ile Thr Ala  
 675 680 685  
 Thr Cys Asp Phe Ala Asn Tyr Asp Ser Gln Thr Thr Ser Ala Gly Glu  
 690 695 700  
 Glu Val Phe Leu His Glu Lys Ser Gly Thr Pro Ile Met Phe Ser Thr  
 705 710 715 720  
 65 Thr Arg Val Val Tyr Asn Thr Gln Asn Glu Lys Ile Asn Gly Phe Met  
 725 730 735  
 Leu Arg Arg Met Phe Glu Lys Ala Lys Asp Gly Arg Tyr Arg Thr Met  
 740 745 750  
 70 Gly Glu Ile Ile Arg Ser Ala Lys Gln Gly Met Leu Ser Thr Val Phe  
 755 760 765  
 Pro Asp Ser Ile Asn Gln Leu Ser Phe Phe Leu Met Gly Asp Pro Ser  
 770 775 780  
 Val Arg Met Asn Leu Pro Thr His Lys Val Gln Leu Thr Ala Ile Asn  
 785 790 795 800  
 75 Gly Gln Asp Pro Glu Gly Gln Tyr Gly Thr Ile Met Leu Lys Ser Leu

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Arg Asp Tyr Thr Gly Trp Phe Ala Met Tyr Asp Thr Asn Lys Val Gly  
 130 135 140  
 Leu Val Asp Phe Ile Tyr Asn Arg Pro Arg Pro Asn Asp Asp Glu Phe  
 145 150 155 160  
 5 Pro Lys Tyr Glu Ala Gln Tyr Leu Gly Ile Glu Met Phe Gly Met Lys  
 165 170 175  
 Leu Lys Gln Thr Gly Gly Asn Tyr Met Thr Asp Gly Tyr Gly Ser Ala  
 180 185 190  
 10 Val Gln Ser His Ile Ala Tyr Thr Glu Asn Ser Ser Leu Ser Gln Ala  
 195 200 205  
 Gln Val Asn Gln Lys Met Lys Asp Tyr Leu Gly Ile Thr His His Asp  
 210 215 220  
 Val Val Gln Asp Pro Asn Gly Glu Tyr Ile Asn His Val Asp Cys Trp  
 225 230 235 240  
 15 Gly Lys Tyr Leu Ala Pro Asn Lys Ile Leu Ile Arg Lys Val Pro Asp  
 245 250 255  
 Asn His Pro Gln His Gln Ala Leu Glu Asp Met Ala Ala Tyr Phe Ala  
 260 265 270  
 20 Ala Gln Thr Cys Ala Trp Gly Thr Lys Tyr Glu Val Tyr Arg Ala Leu  
 275 280 285  
 Ala Thr Asn Glu Gln Pro Tyr Thr Asn Ser Leu Ile Leu Asn Asn Arg  
 290 295 300  
 Val Phe Val Pro Val Asn Gly Pro Ala Ser Val Asp Asn Asp Ala Leu  
 305 310 315 320  
 25 Asn Val Tyr Lys Thr Ala Met Pro Gly Tyr Glu Ile Ile Gly Val Lys  
 325 330 335  
 Gly Ala Ser Gly Thr Pro Trp Leu Gly Thr Asp Ala Leu His Cys Arg  
 340 345 350  
 30 Thr His Glu Val Ala Asp Lys Gly Tyr Leu Tyr Ile Lys His Tyr Pro  
 355 360 365  
 Ile Leu Gly Glu Gln Ala Gly Pro Asp Tyr Lys Ile Glu Ala Asp Val  
 370 375 380  
 Val Ser Cys Ala Asn Ala Thr Ile Ser Pro Val Gln Cys Tyr Tyr Arg  
 385 390 395 400  
 35 Ile Asn Gly Ser Gly Ser Phe Lys Ala Ala Asp Met Thr Met Glu Ser  
 405 410 415  
 Thr Gly His Tyr Thr Tyr Ser Phe Thr Gly Leu Asn Lys Asn Asp Lys  
 420 425 430  
 40 Val Glu Tyr Tyr Ile Ser Ala Ala Asp Asn Ser Gly Arg Lys Glu Thr  
 435 440 445  
 Tyr Pro Phe Ile Gly Glu Pro Asp Pro Phe Lys Phe Thr Cys Met Asn  
 450 455 460  
 Glu Thr Asn Thr Cys Thr Val Thr Gly Ala Ala Lys Ala Leu Arg Ala  
 465 470 475 480  
 45 Trp Phe Asn Ala Gly Arg Ser Glu Leu Ala Val Ser Val Ser Leu Asn  
 485 490 495  
 Ile Ala Gly Thr Tyr Arg Ile Lys Leu Tyr Asn Thr Ala Gly Glu Glu  
 500 505 510  
 50 Val Ala Ala Met Thr Lys Glu Leu Val Ala Gly Thr Ser Val Phe Ser  
 515 520 525  
 Met Asp Val Tyr Ser Gln Ala Pro Gly Thr Tyr Val Leu Val Val Glu  
 530 535 540  
 Gly Asn Gly Ile Arg Glu Thr Met Lys Ile Leu Lys  
 545 550 555  
 55 (2) INFORMATION FOR SEQ ID NO:526  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 428 amino acids  
 60 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 65 (iii) HYPOTHETICAL: YES  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 70 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...428  
 75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:526

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Met Lys Leu Ser Ser Lys Lys Ile Leu Ala Ile Ile Ala Leu Leu Thr
1      5      10      15
Met Gly His Ala Val Gln Ala Gln Phe Val Pro Ala Pro Thr Thr Gly
20      25      30
5 Ile Arg Met Ser Val Thr Thr Thr Lys Ala Val Gly Glu Lys Ile Glu
35      40      45
Leu Leu Val His Ser Ile Glu Lys Lys Gly Ile Trp Ile Asp Leu Asn
50      55      60
10 Gly Asp Ala Thr Tyr Gln Gln Gly Glu Glu Ile Thr Val Phe Asp Glu
65      70      75      80
Ala Tyr His Glu Tyr Thr Ile Gly Thr Gln Thr Leu Thr Ile Tyr Gly
85      90      95
Asn Thr Thr Arg Leu Gly Cys Arg Ser Thr Gly Ala Thr Ala Val Asp
100      105      110
15 Val Thr Lys Asn Pro Asn Leu Thr Tyr Leu Ala Cys Pro Lys Asn Asn
115      120      125
Leu Lys Ser Leu Asp Leu Thr Gln Asn Pro Lys Leu Leu Arg Val Trp
130      135      140
20 Cys Asp Ser Asn Glu Ile Glu Ser Leu Asp Leu Ser Gly Asn Pro Ala
145      150      155      160
Leu Ile Ile Leu Gly Cys Asp Arg Asn Lys Leu Thr Glu Leu Lys Thr
165      170      175
Asp Asn Asn Pro Lys Leu Ala Ser Leu Trp Cys Ser Asp Asn Asn Leu
180      185      190
25 Thr Glu Leu Glu Leu Ser Ala Asn Pro Arg Leu Asn Asp Leu Trp Cys
195      200      205
Phe Gly Asn Arg Ile Thr Lys Leu Asp Leu Ser Ala Asn Pro Leu Leu
210      215      220
30 Val Thr Leu Trp Cys Ser Asp Asn Glu Leu Ser Thr Leu Asp Leu Ser
225      230      235      240
Lys Asn Ser Asp Val Ala Tyr Leu Trp Cys Ser Ser Asn Lys Leu Thr
245      250      255
Ser Leu Asn Leu Ser Gly Val Lys Gly Leu Ser Val Leu Val Cys His
260      265      270
35 Ser Asn Gln Ile Ala Gly Glu Glu Met Thr Lys Val Val Asn Ala Leu
275      280      285
Pro Thr Leu Ser Pro Gly Ala Gly Ala Gln Ser Lys Phe Val Val Val
290      295      300
40 Asp Leu Lys Asp Thr Asp Glu Lys Asn Ile Cys Thr Val Lys Asp Val
305      310      315      320
Glu Lys Ala Lys Ser Lys Asn Trp Arg Val Phe Asp Phe Asn Gly Asp
325      330      335
Ser Asp Asn Met Leu Pro Tyr Glu Gly Ser Pro Thr Ser Asn Leu Ala
340      345      350
45 Val Asp Ala Pro Thr Val Arg Ile Tyr Pro Asn Pro Val Gly Arg Tyr
355      360      365
Ala Leu Val Glu Ile Pro Glu Ser Leu Leu Gly Gln Glu Ala Ala Leu
370      375      380
50 Tyr Asp Met Asn Gly Val Lys Val Tyr Ser Phe Ala Val Glu Ser Leu
385      390      395      400
Arg Gln Asn Ile Asp Leu Thr His Leu Pro Asp Gly Thr Tyr Phe Phe
405      410      415
Arg Leu Asp Asn Tyr Thr Thr Lys Leu Ile Lys Gln
420      425

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(2) INFORMATION FOR SEQ ID NO:527

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 310 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(1x) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1...310

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:527

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Met Arg Lys Thr Ile Ile Phe Cys Leu Leu Leu Ala Leu Phe Gly Cys
1      5      10      15
Ser Trp Ala Gln Glu Arg Val Asp Glu Lys Val Phe Ser Ala Gly Thr
20      25      30
5  Ser Ile Phe Arg Gly Ile Leu Glu Lys Val Lys Ala Pro Leu Met Tyr
35      40      45
Gly Asp Arg Glu Val Trp Gly Met Ala Arg Ala Ser Glu Asp Phe Phe
50      55      60
Phe Ile Leu Pro Val Thr Asp Asp Leu Thr Pro Val Leu Phe Tyr Asn
65      70      75      80
10 Arg Leu Thr Asn Glu Pro Cys Phe Val Ser Asp Gln Gly Ile Thr Glu
85      90      95
Tyr Phe Lys Phe Ala Gln Glu Gly Asp Tyr Ile Glu Val Glu Gly Ser
100      105      110
15 Ser Val Phe Met Ala Asn Leu Leu Tyr Tyr Arg Phe Phe Pro Thr Arg
115      120      125
Ile Thr Ser Tyr Asn Ala Pro Ile Glu Gly Val Val Ser Lys Thr Gly
130      135      140
20 Asn Pro Ala Phe Thr Ile Pro Met Leu Pro Gly Val Ser Asp Cys Ile
145      150      155      160
Glu Ile Ser Asn Asn Arg Lys Val Phe Leu Thr Asn Gln Leu Gly Val
165      170      175
Val Asn Ile Thr Asp Gly Met Glu Pro Pro Ile Ile Ala Gly Val Ser
180      185      190
25 Ala Ser Tyr Gly Ser Ser Val Arg Val Tyr Gly His Val Ser Gln Arg
195      200      205
Trp Asp Ile Ile Gly His Cys Tyr Leu Asp Ile Tyr Pro Thr Asn Cys
210      215      220
30 Tyr Pro Leu Ser Thr Lys Pro Val Ala Gly Asp Asp Glu Val Phe Val
225      230      235      240
Lys Gln Gln Gly Arg Gln Ile Glu Ile Asp Ser Asn Ser Pro Ile Val
245      250      255
Gln Val Val Val Tyr Asp Leu Glu Gly Lys Ser Val Phe Arg Lys Arg
260      265      270
35 Met Thr Glu Asn Ala Tyr Thr Leu Ser Phe Arg Ala Pro Met Leu Gly
275      280      285
Phe Met Thr Ile Met Ile Glu Thr Gln Asn Ser Ile Ile Asn Lys Lys
290      295      300
40 Leu Asn Val Thr Gln Leu
305      310

```

## (2) INFORMATION FOR SEQ ID NO:528

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 405 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION: 1...405
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:528

```

Met Lys Lys Thr Thr Ile Ile Ser Leu Ile Val Phe Gly Ala Phe Phe
1      5      10      15
Ala Ala Val Gly Gln Thr Lys Asp Asn Ser Ser Tyr Lys Pro Phe Ser
20      25      30
65 Lys Glu Asp Ile Ala Gly Gly Val Tyr Ser Leu Pro Thr Gln Asn Arg
35      40      45
Ala Gln Lys Asp Asn Ala Glu Trp Leu Leu Thr Ala Thr Val Ser Thr
50      55      60
70 Asn Gln Ser Ala Asp Thr His Phe Ile Phe Asp Glu Asn Asn Arg Tyr
65      70      75      80
Ile Ala Arg Asp Ile Lys Ala Asn Gly Val Arg Lys Ser Thr Asp Ser
85      90      95
75 Ile Tyr Tyr Asp Ala Asn Gly Arg Ile Ser His Val Asp Leu Tyr Ile
100      105      110

```

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Ser Phe Ser Gly Gly Glu Pro Ala Leu Asp Thr Arg Phe Lys Tyr Thr  
 115 120 125  
 Tyr Asp Asp Glu Gly Lys Met Thr Val Arg Glu Val Phe Met Leu Val  
 130 135 140  
 5 Met Asp Pro Asn Thr Pro Ile Ser Arg Leu Glu Tyr His Tyr Asp Ala  
 145 150 155 160  
 Gln Gly Arg Leu Thr His Trp Ile Ser Phe Ala Phe Gly Ala Glu Ser  
 165 170 175  
 10 Gln Lys Asn Thr Tyr His Tyr Asn Glu Lys Gly Leu Leu Val Ser Glu  
 180 185 190  
 Val Leu Ser Asn Ala Met Gly Thr Thr Tyr Ser Asp Thr Gly Lys Thr  
 195 200 205  
 Glu Tyr Ser Tyr Asp Asp Ala Asp Asn Met Val Lys Ala Glu Tyr Phe  
 210 215 220  
 15 Val Val Gln Gln Gly Lys Ala Trp Gln Val Leu Lys Arg Glu Glu Tyr  
 225 230 235 240  
 Thr Tyr Glu Asp Asn Ile Cys Ile Gln Tyr Leu Ala Ile Asn Gly Thr  
 245 250 255  
 20 Asp Thr Lys Val Tyr Lys Arg Asp Ile Glu Ser Asp Lys Ser Ile Ser  
 260 265 270  
 Ala Asn Val Ile Asp Ile Pro Ser Met Pro Glu Gln Thr Trp Pro Asn  
 275 280 285  
 Met Tyr Gly Phe Asn Ala Lys Arg Leu Lys Glu Thr Tyr Ser Ser Tyr  
 290 295 300  
 25 Glu Gly Asp Val Ala Thr Pro Ile Phe Asp Tyr Ile Tyr Thr Tyr Lys  
 305 310 315 320  
 Ala Leu Thr Ser Met Ala Thr Pro Ser Thr Glu Ala Gln Val Ala Val  
 325 330 335  
 30 Tyr Leu Asn Pro Ser Thr Asp Arg Leu Val Ile Leu Ala Asn Gly Ile  
 340 345 350  
 Thr His Leu Ser Met Tyr Asp Leu Gln Gly Lys Leu Ile Arg Asp Cys  
 355 360 365  
 Ala Leu Ser Gly Asp Lys Val Glu Met Gly Val Gly Ser Leu Thr Lys  
 370 375 380  
 35 Gly Thr Tyr Leu Leu Lys Val Asn Thr Asp Gln Gly Ala Phe Val Arg  
 385 390 395 400  
 Lys Val Val Ile Arg  
 405

40 (2) INFORMATION FOR SEQ ID NO:529

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2037 base pairs  
 (B) TYPE: nucleic acid  
 45 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

50 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

55 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature  
 (B) LOCATION 1...2037

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529

65 GTATGGACT ACAAACTCAC TTCTCGATTG AAGCCCAACGG GCGACCAAGCC GGAAGCCATT 60  
 CGCCAACTCG TACAGGGCAT CAACGAAGGG ATGCCGCTC AGACGCTGCT CGGCGTAACG 120  
 GGTTCGGGCA AAACCTTTTAC GGTGGCTAAC GTGGTGGCGG CGGTCAATCG TCCGACCCCTT 180  
 GTCCCTGAGTC ACAACAGAGC CTGGGCAGCA CAGCTATACG GAGAGTTCAA AGCCTTCTTC 240  
 CCCGAGATG CCGTGGAGTA TTCTGTCAGC TACTACGACT ACTATCAGCC CGAGGCCCTAC 300  
 CTCCCCGTCA CAGACACCTA TATCGAAAAG GACATGGCCA TCAACGCGGA GATCGAAAAA 360  
 CTGCGATTGA GGGCCACGGC TTCGCTCCTG TCAGGGGCGA AAGATGTGCT TGTGGTCAGC 420  
 70 TCCGTATCCT GTCTCTACGG TATGGCCAAT CCTGAAGCTT TTCCGAAAAA GGTGATCAGC 480  
 CTGCACACGG GACAAAGGGC AGACAGGGAT CATTTTATCC GCCTGCTGGT AGAGAGCTAC 540  
 TACACSAACA ATAAAGTAGA GTTCGAGAGC GGCAACTTCC GTGTCAAAGG CGACAGCGTG 600  
 GACATATTCC CCGCCGTAGA AGGTTATGAC GGCCTGGCAT ACAGGGTGGG GTTTTGGGAT 660  
 GGAGAGSTCG AAGGGCTGAG TACCTTCGAT CCGCGAACGG GACGGAATA CGGCTGCTG 720  
 75 TCGSAGCTGA AGATATATCC GSCCAATCTC TTGCTGAACA CTAAGGAGCA GGTGGATCGG 780

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5 GCAGTAGGSA AAATCGATGT GGATCTGGGC GCACAGGTG ATTTTC'GAA AGAAATCGGC 840  
 AAACCATATG AAGCCAAACG CTTGTATGAG CCGGTACCGT ATGACTTGGA AATGATCCGT 900  
 GAGTTGGGTT ATTGTTCCGG TATAGAGAAC TATTCGCGCT ACTTCGACGG CCGTGACGGG 960  
 GGGGAACGTC CTTTCTGTCT GTTGGATTAT TTCCCGGAGG ATTTCTGTGT GGTCTAGAGC 1020  
 GAAAGCCATG TAACGATACC GCAGATACGT GCCATGTACS GAGGCGATCG TTCGCGCAAG 1080  
 GAGAATCTGG TCGAATACGG ATTCCGCGTG CCGTCCGCTC TCGACAATCG GCCGCTTCGC 1140  
 TTCGACGAGT TCGAAGCTCT CACCCCGCGG ACCCTTTATA TCASTGCCAC GCCTGCCGAC 1200  
 TATGAGCTGA ACAGAAGCGA AGGCGTGATC GTCGAGCAGC TGATCCGTCC GACCGGACTG 1260  
 CTGGATCCCA TCATCGACGT CAAGCCGACG GCAAAACCAAG TGGACGATCT GATGGAGGAG 1320  
 ATAGCACGCT GCATCGAAAA GAAAGAGCGC GTACTGGTAA CGACCCGTGAC CAAACGTATG 1380  
 GCAGAGGAGC TTAGCGAATA CCTGCTACGC CACGSTATCA GCACCGGTA CATACACAGC 1440  
 GATGTGGACA CGCTGGAGCG TGTGCTATC ATGGAAGACC TCGCGAAGGG GGTCTACGAT 1500  
 GCACTCATCG GGGTGAATCT GCTCCGCGAA GGATTGSACT TCGCGGAAGT TTCGCTTGTG 1560  
 GCTATTCTGG ATGCGGATAA GGAAGGATTC CTGCGCTCGC ATCGTTCTGT CACCGAGACT 1620  
 GCAGGACGTC CCGCCCGGCA CATTCTATGG CGTGTCTAT TCTACGCGGA CAAGATCACC 1680  
 GACAGTATGC AGCTCACCAT GGAAGAGACT GCACGCGGAC GCGCAAGCA ACTGGCCTAC 1740  
 AACGAAGCGC ACGGCATCAG CCCCACACAG ATAGTGAAGA ACAGTGTGTC CATTGGGGGA 1800  
 GAAGGCGATG TGTGCGCCTT GCAATCCGAT ACAGAATCCG GTGCGTACAT AGAAGAGAGC 1860  
 AGCATGCTGG CTGCGGATCC TTGGCCGAC TATCTGAGCA AACCCAGCT GGAAGCACTC 1920  
 ATTGCTTCCA CCAAGAAGCA AATGCTGGCA GCAGCCAAAG AGCTGGACTT TCTGGAAGCG 1980  
 GCACGACTTC GGGACGAAGC CGCACGATTG GAAAAGAAAC TGGAGCAACT CACAGCC 2037

## (2) INFORMATION FOR SEQ ID NO:530

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2034 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

## (ix) FEATURE:

- (A) NAME/KEY: misc feature  
 (B) LOCATION 1...2034

## (x) SEQUENCE DESCRIPTION: SEQ ID NO:530

ATGGACTACA AACTCACTTC TCGATTCAAG CCCACGCGG ACCAGCCGGA AGCCATTCCG 60  
 CAACTCSTAC AGGGCATCAA CGAAGGGATG CCGCTCAGAG CGCTGCTCGG CGTAAACGGT 120  
 TCGGGCAAAA CTTTACGGGT GGCTAACGTG GTGGCGGCGG TCAATCGTCC GACCCTTGTC 180  
 CTGAGTCACA ACAAGACCTT GGCAGCACAG CTATACGGAG AGTTCAAAGC CTTCTTCCCC 240  
 GAGAATGCGG TGGAGTATTT CGTCAGCTAC TACGACTACT ATCAGCCCGA GGCCTACCTC 300  
 CCCGTACAG ACACCTATAT CGAAAAGGAC ATGGCCATCA ACGCGGAGAT CGAAAAACTG 360  
 CGATTGAGGG CCACGGCTTC GTCCTGTCA GGGCGGAAAG ATGTGCTTGT GGTCAAGTCC 420  
 GTATCCTGTC TCTACGGTAT GGCCAACTCT GAAGCTTTT CCGAAAAGGT GATCAGCCTG 480  
 CACACGGGAC AAAGGGCAGA CAGGGATCAT TTTATCCGCC TGCTGGTAGA GAGCTACTAC 540  
 ACGAACAATA AAGTAGAGTT CGAGAGCGGC AACTTCCGTG TCAAAGGCGA CAGCGTGGAC 600  
 ATATTCCGCG CGTAGAAGG TTATGACGGC GTGGCATA CA GGTGGAGTT TTGGGATGGA 660  
 GAGGTCGAGC GGCTGAGTAC CTTGATCCG CGAAGCGGAC GGAATACGG CCTGCTGTCG 720  
 GAGCTGAAGA TATATCCGGC CAATCTCTTC GTGACGACTA AGGAGCAGGT GGATCGGGCA 780  
 GTAGGGAAAA TCGATGTGGA TCTGGGCGCA CAGGTCGATT TTCTGAAAGA AATCGGCAAA 840  
 CCATATGAAG CCAACCGCTT GTATGAGCGG GTCACGTATG ACTTGGAAAT CATCCGTGAG 900  
 TTGGGTTATT GTTCCGGTAT AGAGAATAT TCGCGCTACT TCGACGGCGG TGACGCGGGC 960  
 GAACGTCCTT TCTGTCTGTT GGATTATTTC CCGGAGGATT TCCTGTTGGT CATAGACGAA 1020  
 AGCCATGTAA CGATACCGCA GATACGTGCC ATGTACGGAG GCGATCGTTC GCGCAAGGAG 1080  
 AATCTGGTCC AATACGGATT CCGCTGCTC GCCGCTCTCG ACAATCGGCC GCTTCGCTTC 1140  
 GACGAGTTCC AAGCTCTCAC CCCCAGGACC CTTTATATCA GTGCCAGGCC TGCCGACTAT 1200  
 GAGCTGAACA GAAGCGAAGG CTTGATCGTC GAGCAGCTGA TCCGTCCGAC CGGACTGCTG 1260  
 GATCCCATCA TCGACGTCAA GCGACGCGCA AACCAAGTGG ACATCTGAT GGAGGAGATA 1320  
 GCACGCTGCA TCGAAAGAA AGAGCGCGTA CTGGTAACGA CGTGACCAA ACGTATGGCA 1380  
 GACGAGCTTA GCGAATACCT GCTACGCCAC GGTATCGACA CCGGCTACAT ACACAGCGAT 1440  
 TGGGACACCG TGGAGCGTGT GCGTATCATG GAAGACCTGC GCAAGGGGGT CTACGATGCA 1500  
 CTCATCGGGG TGAATCTGCT CCGCGAAGGA TTGGACTTGC CGGAAGTTTC GCTTGTGGCT 1560  
 ATTCTGGATG CGGATAAGGA AGGATTCCTG CGCTCGCATC GTTCGCTCAC GCAGACTGCA 1620  
 GGACGTGCCG CCCGCGACAT TCATGGGCGT GTCATCTTCT ACGCGGACAA GATCACCGAC 1680  
 75 AGTATGCAGC TCACCATGGA CGAGACTGCA CGCGACGCG CAAAGCAACT GGCCTACAA 1740

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GAAGCGCACG GCATCACCCC CCAACAGATA GTGAAGAACA GTGCTGCCAT TTGGGGAGAA 1800  
 GGCATGTGT CGGCCTTGCA ATCCGATACA GAATCCGGTG CGTACATAGA AGAGAGCAGC 1860  
 ATGGTGGCTG CCGATCCTTT GGCCGACTAT CTGAGCAAAC CCAAGCTGGA AGCACTCATT 1920  
 GCTTCGACCA AGAAGCAAAT GCTGGCAGCA GCCAAAGAGC TGGACTTTCT GGAAGCGGCA 1980  
 5 CGACTTCGGG ACGAAGCCGC ACGATTGGAA AAGAACTGG AGCAACTCAC AGCC 2034

## (2) INFORMATION FOR SEQ ID NO:531

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 679 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...679
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:531
- Val Met Asp Tyr Lys Leu Thr Ser Arg Phe Lys Pro Thr Gly Asp Gln  
 1 5 10 15  
 30 Pro Glu Ala Ile Arg Gln Leu Val Gln Gly Ile Asn Glu Gly Met Pro  
 20 25 30  
 Ala Gln Thr Leu Leu Gly Val Thr Gly Ser Gly Lys Thr Phe Thr Val  
 35 40 45  
 Ala Asn Val Val Ala Ala Val Asn Arg Pro Thr Leu Val Leu Ser His  
 50 55 60  
 Asn Lys Thr Leu Ala Ala Gln Leu Tyr Gly Glu Phe Lys Ala Phe Phe  
 65 70 75  
 Pro Glu Asn Ala Val Glu Tyr Phe Val Ser Tyr Tyr Asp Tyr Tyr Gln  
 80 85 90  
 40 Pro Glu Ala Tyr Leu Pro Val Thr Asp Thr Tyr Ile Glu Lys Asp Met  
 100 105 110  
 Ala Ile Asn Ala Glu Ile Glu Lys Leu Arg Leu Arg Ala Thr Ala Ser  
 115 120 125  
 45 Leu Leu Ser Gly Arg Lys Asp Val Leu Val Val Ser Ser Val Ser Cys  
 130 135 140  
 Leu Tyr Gly Met Ala Asn Pro Glu Ala Phe Ser Glu Lys Val Ile Ser  
 145 150 155  
 Leu His Thr Gly Gln Arg Ala Asp Arg Asp His Phe Ile Arg Leu Leu  
 160 165 170 175  
 50 Val Glu Ser Tyr Tyr Thr Asn Asn Lys Val Glu Phe Glu Ser Gly Asn  
 180 185 190  
 Phe Arg Val Lys Gly Asp Ser Val Asp Ile Phe Pro Ala Val Glu Gly  
 195 200 205  
 55 Tyr Asp Gly Val Ala Tyr Arg Val Glu Phe Trp Asp Gly Glu Val Glu  
 210 215 220  
 Arg Leu Ser Thr Phe Asp Pro Arg Thr Gly Arg Glu Tyr Gly Leu Leu  
 225 230 235  
 Ser Glu Leu Lys Ile Tyr Pro Ala Asn Leu Phe Val Thr Thr Lys Glu  
 240 245 250 255  
 60 Gln Val Asp Arg Ala Val Gly Lys Ile Asp Val Asp Leu Gly Ala Gln  
 260 265 270  
 Val Asp Phe Leu Lys Glu Ile Gly Lys Pro Tyr Glu Ala Lys Arg Leu  
 275 280 285  
 65 Tyr Glu Arg Val Thr Tyr Asp Leu Glu Met Ile Arg Glu Leu Gly Tyr  
 290 295 300  
 Cys Ser Gly Ile Glu Asn Tyr Ser Arg Tyr Phe Asp Gly Arg Asp Ala  
 305 310 315 320  
 Gly Glu Arg Pro Phe Cys Leu Leu Asp Tyr Phe Pro Glu Asp Phe Leu  
 325 330 335  
 70 Leu Val Ile Asp Glu Ser His Val Thr Ile Pro Gln Ile Arg Ala Met  
 340 345 350  
 Tyr Gly Gly Asp Arg Ser Arg Lys Glu Asn Leu Val Glu Tyr Gly Phe  
 355 360 365  
 75 Arg Leu Pro Ala Ala Leu Asp Asn Arg Pro Leu Arg Phe Asp Glu Phe  
 370 375 380

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Glu Ala Leu Thr Pro Arg Thr Leu Tyr Ile Ser Ala Thr Pro Ala Asp  
 385 390 395 400  
 Tyr Glu Leu Asn Arg Ser Glu Gly Val Ile Val Glu Gln Leu Ile Arg  
 405 410 415  
 5 Pro Thr Gly Leu Leu Asp Pro Ile Ile Asp Val Lys Pro Thr Ala Asn  
 420 425 430  
 Gln Val Asp Asp Leu Met Glu Glu Ile Ala Arg Cys Ile Glu Lys Lys  
 435 440 445  
 10 Glu Arg Val Leu Val Thr Thr Leu Thr Lys Arg Met Ala Glu Glu Leu  
 450 455 460  
 Ser Glu Tyr Leu Leu Arg His Gly Ile Ser Thr Gly Tyr Ile His Ser  
 465 470 475 480  
 Asp Val Asp Thr Leu Glu Arg Val Arg Ile Met Glu Asp Leu Arg Lys  
 485 490 495  
 15 Gly Val Tyr Asp Ala Leu Ile Gly Val Asn Leu Leu Arg Glu Gly Leu  
 500 505 510  
 Asp Leu Pro Glu Val Ser Leu Val Ala Ile Leu Asp Ala Asp Lys Glu  
 515 520 525  
 20 Gly Phe Leu Arg Ser His Arg Ser Leu Thr Gln Thr Ala Gly Arg Ala  
 530 535 540  
 Ala Arg His Ile His Gly Arg Val Ile Phe Tyr Ala Asp Lys Ile Thr  
 545 550 555 560  
 Asp Ser Met Gln Leu Thr Met Asp Glu Thr Ala Arg Arg Ala Lys  
 565 570 575  
 25 Gln Leu Ala Tyr Asn Glu Ala His Gly Ile Thr Pro Gln Gln Ile Val  
 580 585 590  
 Lys Asn Ser Ala Ala Ile Trp Gly Glu Gly Asp Val Ser Ala Leu Gln  
 595 600 605  
 30 Ser Asp Thr Glu Ser Gly Ala Tyr Ile Glu Glu Ser Ser Met Val Ala  
 610 615 620  
 Ala Asp Pro Leu Ala Asp Tyr Leu Ser Lys Pro Lys Leu Glu Ala Leu  
 625 630 635 640  
 Ile Ala Ser Thr Lys Lys Gln Met Leu Ala Ala Ala Lys Glu Leu Asp  
 645 650 655  
 35 Phe Leu Glu Ala Ala Arg Leu Arg Asp Glu Ala Ala Arg Leu Glu Lys  
 660 665 670  
 Lys Leu Glu Gln Leu Thr Ala  
 675  
 40 (2) INFORMATION FOR SEQ ID NO:532  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 678 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45  
 (ii) MOLECULE TYPE: protein  
 50 (iii) HYPOTHETICAL: YES  
 (iv) ORIGINAL SOURCE:  
 (A) ORGANISM: Porphyromonas gingivalis  
 55 (ix) FEATURE:  
 (A) NAME/KEY: misc feature  
 (B) LOCATION 1...678  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:532  
 60 Met Asp Tyr Lys Leu Thr Ser Arg Phe Lys Pro Thr Gly Asp Gln Pro  
 1 5 10 15  
 Glu Ala Ile Arg Gln Leu Val Gln Gly Ile Asn Glu Gly Met Pro Ala  
 20 25 30  
 65 Gln Thr Leu Leu Gly Val Thr Gly Ser Gly Lys Thr Phe Thr Val Ala  
 35 40 45  
 Asn Val Val Ala Ala Val Asn Arg Pro Thr Leu Val Leu Ser His Asn  
 50 55 60  
 Lys Thr Leu Ala Ala Gln Leu Tyr Gly Glu Phe Lys Ala Phe Phe Pro  
 65 70 75 80  
 70 Glu Asn Ala Val Glu Tyr Phe Val Ser Tyr Tyr Asp Tyr Tyr Gln Pro  
 85 90 95  
 Glu Ala Tyr Leu Pro Val Thr Asp Thr Tyr Ile Glu Lys Asp Met Ala  
 100 105 110  
 75 Ile Asn Ala Glu Ile Glu Lys Leu Arg Leu Arg Ala Thr Ala Ser Leu  
 115 120 125

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Leu Ser Gly Arg Lys Asp Val Leu Val Val Ser Ser Val Ser Cys Leu  
 130 135 140  
 Tyr Gly Met Ala Asn Pro Glu Ala Phe Ser Glu Lys Val Ile Ser Leu  
 145 150 155 160  
 5 His Thr Gly Gln Arg Ala Asp Arg Asp His Phe Ile Arg Leu Leu Val  
 165 170 175  
 Glu Ser Tyr Tyr Thr Asn Asn Lys Val Glu Phe Glu Ser Gly Asn Phe  
 180 185 190  
 10 Arg Val Lys Gly Asp Ser Val Asp Ile Phe Pro Ala Val Glu Gly Tyr  
 195 200 205  
 Asp Gly Val Ala Tyr Arg Val Glu Phe Trp Asp Gly Glu Val Glu Arg  
 210 215 220  
 Leu Ser Thr Phe Asp Pro Arg Thr Gly Arg Glu Tyr Gly Leu Leu Ser  
 225 230 235 240  
 15 Glu Leu Lys Ile Tyr Pro Ala Asn Leu Phe Val Thr Thr Lys Glu Gln  
 245 250 255  
 Val Asp Arg Ala Val Gly Lys Ile Asp Val Asp Leu Gly Ala Gln Val  
 260 265 270  
 20 Asp Phe Leu Lys Glu Ile Gly Lys Pro Tyr Glu Ala Lys Arg Leu Tyr  
 275 280 285  
 Glu Arg Val Thr Tyr Asp Leu Glu Met Ile Arg Glu Leu Gly Tyr Cys  
 290 295 300  
 Ser Gly Ile Glu Asn Tyr Ser Arg Tyr Phe Asp Gly Arg Asp Ala Gly  
 305 310 315 320  
 25 Glu Arg Pro Phe Cys Leu Leu Asp Tyr Phe Pro Glu Asp Phe Leu Leu  
 325 330 335  
 Val Ile Asp Glu Ser His Val Thr Ile Pro Gln Ile Arg Ala Met Tyr  
 340 345 350  
 30 Gly Gly Asp Arg Ser Arg Lys Glu Asn Leu Val Glu Tyr Gly Phe Arg  
 355 360 365  
 Leu Pro Ala Ala Leu Asp Asn Arg Pro Leu Arg Phe Asp Glu Phe Glu  
 370 375 380  
 Ala Leu Thr Pro Arg Thr Leu Tyr Ile Ser Ala Thr Pro Ala Asp Tyr  
 385 390 395 400  
 35 Glu Leu Asn Arg Ser Glu Gly Val Ile Val Glu Gln Leu Ile Arg Pro  
 405 410 415  
 Thr Gly Leu Leu Asp Pro Ile Ile Asp Val Lys Pro Thr Ala Asn Gln  
 420 425 430  
 40 Val Asp Asp Leu Met Glu Glu Ile Ala Arg Cys Ile Glu Lys Lys Glu  
 435 440 445  
 Arg Val Leu Val Thr Thr Leu Thr Lys Arg Met Ala Glu Glu Leu Ser  
 450 455 460  
 Glu Tyr Leu Leu Arg His Gly Ile Ser Thr Gly Tyr Ile His Ser Asp  
 465 470 475 480  
 45 Val Asp Thr Leu Glu Arg Val Arg Ile Met Glu Asp Leu Arg Lys Gly  
 485 490 495  
 Val Tyr Asp Ala Leu Ile Gly Val Asn Leu Leu Arg Glu Gly Leu Asp  
 500 505 510  
 50 Leu Pro Glu Val Ser Leu Val Ala Ile Leu Asp Ala Asp Lys Glu Gly  
 515 520 525  
 Phe Leu Arg Ser His Arg Ser Leu Thr Gln Thr Ala Gly Arg Ala Ala  
 530 535 540  
 Arg His Ile His Gly Arg Val Ile Phe Tyr Ala Asp Lys Ile Thr Asp  
 545 550 555 560  
 55 Ser Met Gln Leu Thr Met Asp Glu Thr Ala Arg Arg Arg Ala Lys Gln  
 565 570 575  
 Leu Ala Tyr Asn Glu Ala His Gly Ile Thr Pro Gln Gln Ile Val Lys  
 580 585 590  
 Asn Ser Ala Ala Ile Trp Gly Glu Gly Asp Val Ser Ala Leu Gln Ser  
 595 600 605  
 60 Asp Thr Glu Ser Gly Ala Tyr Ile Glu Glu Ser Ser Met Val Ala Ala  
 610 615 620  
 Asp Pro Leu Ala Asp Tyr Leu Ser Lys Pro Lys Leu Glu Ala Leu Ile  
 625 630 635 640  
 65 Ala Ser Thr Lys Lys Gln Met Leu Ala Ala Lys Glu Leu Asp Phe  
 645 650 655  
 Leu Glu Ala Ala Arg Leu Arg Asp Glu Ala Ala Arg Leu Glu Lys Lys  
 660 665 670  
 70 Leu Glu Gln Leu Thr Ala  
 675